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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<b>(21) International Application Number:</b> PCT/US00/08621 <b>(22) International Filing Date:</b> 31 March 2000 (31.03.00)  <b>(30) Priority Data:</b> <table border="0" style="width: 100%;"> <tr> <td style="width: 30%;">60/127,607</td> <td style="width: 40%;">31 March 1999 (31.03.99)</td> <td style="width: 30%;">US</td> </tr> <tr> <td>60/127,636</td> <td>2 April 1999 (02.04.99)</td> <td>US</td> </tr> <tr> <td>60/127,728</td> <td>5 April 1999 (05.04.99)</td> <td>US</td> </tr> <tr> <td>09/540,763</td> <td>30 March 2000 (30.03.00)</td> <td>US</td> </tr> </table> <b>(63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Applications</b> <table border="0" style="width: 100%;"> <tr> <td style="width: 30%;">US</td> <td style="width: 40%;">60/127,607 (CIP)</td> <td style="width: 30%;"></td> </tr> <tr> <td>Filed on</td> <td>31 March 1999 (31.03.99)</td> <td></td> </tr> <tr> <td>US</td> <td>60/127,636 (CIP)</td> <td></td> </tr> <tr> <td>Filed on</td> <td>2 April 1999 (02.04.99)</td> <td></td> </tr> <tr> <td>US</td> <td>60/127,728 (CIP)</td> <td></td> </tr> <tr> <td>Filed on</td> <td>5 April 1999 (05.04.99)</td> <td></td> </tr> <tr> <td>US</td> <td>09/540,763 (CIP)</td> <td></td> </tr> <tr> <td>Filed on</td> <td>30 March 2000 (30.03.00)</td> <td></td> </tr> </table> <b>(71) Applicant (for all designated States except US):</b> CURAGEN CORPORATION [US/US]; 555 Long Wharf Drive, 11th Floor, New Haven, CT 06511 (US).	60/127,607	31 March 1999 (31.03.99)	US	60/127,636	2 April 1999 (02.04.99)	US	60/127,728	5 April 1999 (05.04.99)	US	09/540,763	30 March 2000 (30.03.00)	US	US	60/127,607 (CIP)		Filed on	31 March 1999 (31.03.99)		US	60/127,636 (CIP)		Filed on	2 April 1999 (02.04.99)		US	60/127,728 (CIP)		Filed on	5 April 1999 (05.04.99)		US	09/540,763 (CIP)		Filed on	30 March 2000 (30.03.00)		<b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> SHIMKETS, Richard, A. [US/US]; 191 Leete Street, West Haven, CT 06516 (US). LEACH, Martin [GB/US]; 884 School Street, Webster, MA 01570 (US).  <b>(74) Agent:</b> ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).  <b>(81) Designated States:</b> AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
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<b>(54) Title:</b> NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX"  <b>(57) Abstract</b> <p>The present invention provides open reading frames ORFX, encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.</p>																																					

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## NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY

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## BACKGROUND OF THE INVENTION

The invention relates generally to nucleic acids and polypeptides encoded thereby, and methods of using these nucleic acids and polypeptides.

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## SUMMARY OF THE INVENTION

The invention is based in part on the discovery of nucleic acids that include open reading frames encoding novel polypeptides, and on the polypeptides encoded thereby. The nucleic acids and polypeptides are collectively referred to herein as "ORFX".

15

Accordingly, in one aspect, the invention provides an isolated nucleic acid molecule (SEQ ID NO:2 $n$ -1, wherein  $n$  is an integer between 1-3161), that encodes novel polypeptide, or a fragment, homolog, analog or derivative thereof. The nucleic acid can include, *e.g.*, a nucleic acid sequence encoding a polypeptide at least 85% identical to a polypeptide comprising the amino acid sequences of SEQ ID NO:2 $n$ , wherein  $n$  is an integer between 1-3161. The nucleic acid can be, *e.g.*, a genomic DNA fragment, or a cDNA molecule.

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Also included in the invention is a vector containing one or more of the nucleic acids described herein, and a cell containing the vectors or nucleic acids described herein.

The invention is also directed to host cells transformed with a recombinant expression vector comprising any of the nucleic acid molecules described above.

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In another aspect, the invention includes a pharmaceutical composition that includes an ORFX nucleic acid and a pharmaceutically acceptable carrier or diluent.

In a further aspect, the invention includes a substantially purified ORF polypeptide, *e.g.*, any of the ORFX polypeptides encoded by an ORFX nucleic acid, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition that includes a ORFX polypeptide and a pharmaceutically acceptable carrier or diluent.

5 In a still a further aspect, the invention provides an antibody that binds specifically to an ORFX polypeptide. The antibody can be, *e.g.*, a monoclonal or polyclonal antibody, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition including ORFX antibody and a pharmaceutically acceptable carrier or diluent. The invention is also directed to isolated antibodies that bind to an epitope on a  
10 polypeptide encoded by any of the nucleic acid molecules described above.

The invention also includes kits comprising any of the pharmaceutical compositions described above.

The invention further provides a method for producing an ORFX polypeptide by providing a cell containing a ORFX nucleic acid, *e.g.*, a vector that includes a ORFX nucleic  
15 acid, and culturing the cell under conditions sufficient to express the ORFX polypeptide encoded by the nucleic acid. The expressed ORFX polypeptide is then recovered from the cell. Preferably, the cell produces little or no endogenous ORFX polypeptide. The cell can be, *e.g.*, a prokaryotic cell or eukaryotic cell.

The invention is also directed to methods of identifying an ORFX polypeptide or nucleic  
20 acids in a sample by contacting the sample with a compound that specifically binds to the polypeptide or nucleic acid, and detecting complex formation, if present.

The invention further provides methods of identifying a compound that modulates the activity of a ORFX polypeptide by contacting ORFX polypeptide with a compound and determining whether the ORFX polypeptide activity is modified.

25 The invention is also directed to compounds that modulate ORFX polypeptide activity identified by contacting a ORFX polypeptide with the compound and determining whether the compound modifies activity of the ORFX polypeptide, binds to the ORFX polypeptide, or binds to a nucleic acid molecule encoding a ORFX polypeptide.

In a another aspect, the invention provides a method of determining the presence of or  
30 predisposition of an ORFX-associated disorder in a subject. The method includes providing a sample from the subject and measuring the amount of ORFX polypeptide in the subject sample.

The amount of ORFX polypeptide in the subject sample is then compared to the amount of ORFX polypeptide in a control sample. An alteration in the amount of ORFX polypeptide in the subject protein sample relative to the amount of ORFX polypeptide in the control protein sample indicates the subject has a tissue proliferation-associated condition. A control sample is preferably taken from a matched individual, *i.e.*, an individual of similar age, sex, or other general condition but who is not suspected of having a tissue proliferation-associated condition. Alternatively, the control sample may be taken from the subject at a time when the subject is not suspected of having a tissue proliferation-associated disorder. In some embodiments, the ORFX is detected using a ORFX antibody.

In a further aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a nucleic acid sample, *e.g.*, RNA or DNA, or both, from the subject and measuring the amount of the ORFX nucleic acid in the subject nucleic acid sample. The amount of ORFX nucleic acid sample in the subject nucleic acid is then compared to the amount of an ORFX nucleic acid in a control sample. An alteration in the amount of ORFX nucleic acid in the sample relative to the amount of ORFX in the control sample indicates the subject has a tissue proliferation-associated disorder.

In a still further aspect, the invention provides method of treating or preventing or delaying a ORFX-associated disorder. The method includes administering to a subject in which such treatment or prevention or delay is desired a ORFX nucleic acid, a ORFX polypeptide, or an ORFX antibody in an amount sufficient to treat, prevent, or delay a tissue proliferation-associated disorder in the subject.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

### DETAILED DESCRIPTION OF THE INVENTION

The invention provides novel polypeptides and nucleotides encoded thereby. The polynucleotides and their encoded polypeptides can be grouped according to the functions played by their gene products. Such functions include, structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc.

Included in the invention are 3161 novel nucleic acid sequences and their encoded polypeptides. The sequences are collectively referred to as "ORFX nucleic acids" or ORFX polynucleotides" and the corresponding encoded polypeptide is referred to as a "ORFX polypeptide" or ORFX protein". For example, an ORFX nucleic acid according to the invention is a nucleic acid including an ORF1 nucleic acid, and an ORF polypeptide according to the invention is a polypeptide that includes the amino acid sequence of an ORF1 polypeptide. Unless indicated otherwise, "ORFX" is meant to refer to any of the ORF1-3161 sequences disclosed herein.

Table 1 provides a summary of the ORFX nucleic acids and their encoded polypeptides are summarized in Table 1. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention is provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 1 of Table 1, entitled "ORF #", denotes an ORF number assigned to a nucleic acid containing an open reading frame according to the invention.

Column 2 of Table 1, entitled "Internal Identification number (Nucleic Acid Sequence Identification Number, Polypeptide Sequence Identification Number), provides an internal identification number for the indicated ORF, along with sequence identification numbers (SEQ ID NOs.) corresponding to the indicated ORF. In general, for an ORF $n$  according to the invention (wherein  $n$  is any integer from 1 to 3161), a nucleic acid corresponding to the ORF is SEQ ID NO:2 $n$ -1, and an amino acid sequence encoded by the ORF is SEQ ID NO:2 $n$ . For example, a nucleic acid sequence corresponding to an ORF1 nucleic acid is SEQ ID NO:1, and a polypeptide sequence corresponding to an ORF1 polypeptide is SEQ ID NO:2. Similarly, a

nucleic acid sequence corresponding to an ORF4 nucleic acid is SEQ ID NO:7, and a polypeptide sequence corresponding to an ORF4 polypeptide is SEQ ID NO:8; a nucleic acid sequence corresponding to an ORF198 nucleic acid sequence is SEQ ID NO:395, and a polypeptide sequence corresponding to an ORF198 polypeptide is SEQ ID NO:396. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention are provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 2 of Table 1, entitled "Protein Similarity", lists previously described proteins that are related to polypeptides encoded by the ORFs. Genbank identifiers for the previously described proteins are provided. These can be retrieved from <http://www.ncbi.nlm.nih.gov/>.

To determine similarity to previously described proteins, polypeptides encoded by ORFX DNA sequences were tested using the Framesearch Algorithm against a nonredundant version of the GenPept Database from NCBI/Genbank. DNA sequences that had a score of '90' or above (Framesearch algorithm score, Edelman et. al. GCG Genetics) to a known protein were selected. Open reading frames were extended beyond the region of the protein matched using standard DNA translation and codon tables. Novel proteins that lacked a protein match were translated against the standard genetic codons and proteins with an ORF at least 80 amino acids and containing a Methionine start are included in the Table.

Column 3 of Table 3, entitled "Protein Domains", lists previously described protein domains, designated by pfam entries, that are present in polypeptides encoded by the ORFs. Also included in column 3 are proteins in which these domains are present. The pfam entries can be retrieved from <http://pfam.wustl.edu/>. DNA sequences were translated in all six frames and tested using the Hmmer Algorithm against the Pfam Database (References to the algorithm and Pfam database can be found at <http://pfam.wustl.edu/>). Translated DNA sequences that matched a protein domain entry in the Pfam database AND had a score of '7.5' were selected.

Column 4 of Table 3, entitled "Protein Classification", lists the type of classification assigned for the protein, based on its homology. Examples of proteins in the classification include the following proteins:

### **Amylases**

Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

### 5      **Amyloid**

The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, 15 results in a pathological condition, called amyloidosis, which affects the liver, kidney and spleen and which is characterized by the highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. 15 Amyloid deposition is also associated with type II diabetes mellitus.

### **Angiopoeitin**

Members of the angiopoeitin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an 20 essential step in tumor growth in order for the tumor to get the blood supply it needs to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various antihypertensive drugs and chemotherapeutic and anti-tumor agents.

### 25      **Apoptosis-related proteins**

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell

death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of anti-aging drugs.

#### 5           **Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases**

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form  
10 of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and anti-tumor agents.

#### **Colony-stimulating factor-related proteins**

Granulocyte/macrophage colony-stimulating factors are cytokines that act in  
15 hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

#### **Complement-related proteins**

Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a  
20 membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent  
25 cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I diabetes mellitus, meningitis neurological disorders such as nemaline myopathy, neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

### **Cytochrome**

The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia  
5 areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

### **Kinesins**

Kinesins are tubulin molecular motors that function to transport organelles within cells and to move chromosomes along microtubules during cell division. Modifications of these genes  
10 may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

### **Cytokines, Interferon, Interleukin**

Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the  
15 proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

### **G-protein coupled receptors**

G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by  
20 interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological conditions. These include blood pressure regulation, renal dysfunctions, male infertility, dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and  
25 dwarfism.



**Thioesterases**

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipoffiscinosis, Neuronal 1, Infantile, Santavuori disease and more.

The key to the molecule type is as follows:

10	Abbrev:	Title:
	amylase	amylase protein
	amylaseinhib	amylase inhibitor
	amyloid	amyloid protein
15	apoptosis	apoptosis associated protein
	apoptosisinhib	apoptosis inhibitors
	apoptosisrecep	apoptosis receptors
	ATPase_associated	ATPase associated protein
	biotindep	biotin dependent enzyme/protein
20	cadherin	cadherin protein
	calcium_channel	calcium channel protein
	carboxylase	carboxylase protein
	cathepsin	cathepsin/carboxypeptidases
	cathepsininhib	cathepsin/carboxypeptidase inhibitor
25	chloride_channel	chloride channel protein
	collagen	collagen
	complement	complement protein
	complementrecept	complement receptor protein
	complementinhib	complement inhibitor
30	csf	colony stimulating factor
	csfrecept	colony stimulating factor receptor
	cyclin	cyclin protein
	cyto450	cytochrome p450 protein
	cytochrome	cytochrome related protein
35	deaminase	deaminase
	dehydrogenase	dehydrogenase
	desaturase	desaturase
	dna_rna_bind	DNA/RNA binding protein/factor
	dna_rna_inhib	DNA/RNA binding protein/factor inhibitor
40	dynein	dynein

	elastase	elastase
	elastaseinhib	elastase inhibitor
	eph	EPH family of tyrosine kinases
	esterase	esterase
5	esteraseinhib	esterase inhibitor
	fgf	fibroblast growth factor
	fgfreceptor	fibroblast growth factor receptor
	gaba	GABA receptor
	glucoamylase	glucoamylase
10	glucoronidase	glucoronidase
	glycoprotein	glycoprotein
	Guanylyl	guanylylate cyclase
	helicase	helicase
	histone	histone
15	HOM	homologous
	homeobox	homeobox protein
	hydrolase	hydrolase
	hydroxysteroid	hydroxysteroid associated protein
	hypoxanthine	hypoxanthine associated protein
20	immunoglob	immunoglobulin
	immunoglobrecept	immunoglobulin receptor
	interferon	interferon
	interleukin	interleukin
	interleukinrecept	interleukin receptor
25	isomerase	isomerase
	isomeraseinhibitor	isomerase inhibitor
	isomerasereceptor	isomerase receptor
	kinase	kinase
	kinaseinhibitor	kinase inhibitor
30	kinasereceptor	kinase receptor
	kinesin	kinesin
	laminin	laminin associated protein
	lipase	lipase
	metallothionein	metallothionein
35	MHC	major histocompatibility complex
	misc_channel	miscellaneous channel
	ngf	nerve growth factor
	nuci_recpt	nuclear receptor
	nuclease	nuclease
40	oncogene	oncogene associated protein
	oxidase	oxidase
	oxygenase	oxygenase
	peptidase	peptidase
	peroxidase	peroxidase
45	phosphatase	phosphatase
	phosphataseinhib	phosphatase inhibitor

	phosphorylase PIR	phosphorylase PIR DATABASE (release 56, 29-OCT-1998)
5	polymerase potassium channel prostaglandin protease proteaseinhib reductase	polymerase potassium channel protein prostaglandin protease protease inhibitor reductase
10	ribosomalprot RTR	ribosomal associated protein EMBLDATABASE translated entries not to be incorporated into SWISS-PROT (20-JUL-1998)
15	SIM SPTR	similar EMBL DATABASE translated entries to be incorporated into SWISS-PROT (20-JUL-1998)
20	struct sulfotransferase SWP	structural associated protein sulfotransferase SWISS-PROT DATABASE (release 18-OCT-1998)
	SWPN synthase tgf	SWISS-PROT Update (release 11-NOV-98) synthase transforming growth factor
25	tgfreceptor thioesterase thiolase tm7	transforming growth factor receptor thioesterase thiolase seven transmembrane domain G-protein coupled receptor
30	tnf traffic tnfreceptor TRN	necrosis factor receptor tumor necrosis factor tumor trafficking associated protein EMBL DATABASE translated entries update (20-JUL-1998)
35	transcriptfactor transferase transport tubulin ubiquitin	transcription factor transferase transport protein tubulin ubiquitin
40	unclassified  water channel	Protein not categorized into one of the aforementioned protein families water channel protein

Column 5 of Table 1, entitled, "Cells or Tissues in Which Gene is Expressed", denotes tissues, represented by five digit numbers, in which RNA homologous to the ORF nucleic acid sequences is present. Tissues or cells corresponding to the numbers are provided in Table 2.

ORFX nucleic acids, and their encoded polypeptides, according to the invention are  
 5 useful in a variety of applications and contexts. For example, various ORFX nucleic acids and polypeptides according to the invention are useful, *inter alia*, as novel members of the protein families indicated in Table 1, and/or according to the presence of domains and sequence relatedness to previously described proteins as summarized in Table 1.

ORFX nucleic acids and polypeptides according to the invention can also be used to  
 10 identify cell types listed in Table 1 for an indicated ORFX according to the invention. Additional utilities for ORFX nucleic acids and polypeptides according to the invention are disclosed herein.

### ORFX Nucleic Acids

15 The novel nucleic acids of the invention include those that encode an ORFX or ORFX-like protein, or biologically active portions thereof. The nucleic acids include nucleic acids encoding polypeptides that include the amino acid sequence of one or more of SEQ ID NO:2*n*, wherein *n* = 1 to 3161. The encoded polypeptides can thus include, *e.g.*, the amino acid sequences of SEQ ID NO: 2, 4, 6, 8, 10, . . . , 6310, 6312, 6314, 6316, 6318, 6320, and/or 6322.

20 In some embodiments, a nucleic acid encoding a polypeptide having the amino acid sequence of one or more of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) includes the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof. Additionally, the invention includes mutant or variant nucleic acids of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof, any of whose bases may be changed from the  
 25 disclosed sequence while still encoding a protein that maintains its ORFX-like activities and physiological functions. The invention further includes the complement of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), including fragments, derivatives,

analogues and homolog thereof. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications.

Also included are nucleic acid fragments sufficient for use as hybridization probes to identify ORFX-encoding nucleic acids (*e.g.*, ORFX mRNA) and fragments for use as  
5 polymerase chain reaction (PCR) primers for the amplification or mutation of ORFX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is  
10 double-stranded DNA.

"Probes" refer to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as about, *e.g.*, 6,000 nt, depending on use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are usually obtained from a natural or recombinant source, are highly specific and  
15 much slower to hybridize than oligomers. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

An "isolated" nucleic acid molecule is one that is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Examples of isolated nucleic  
20 acid molecules include, but are not limited to, recombinant DNA molecules contained in a vector, recombinant DNA molecules maintained in a heterologous host cell, partially or substantially purified nucleic acid molecules, and synthetic DNA or RNA molecules. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism  
25 from which the nucleic acid is derived. For example, in various embodiments, the isolated ORFX nucleic acid molecule can contain less than about 50 kb, 25 kb, 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular  
30 material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement of any of this nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n*=1 to 3161) as a hybridization probe, ORFX nucleic acid sequences can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, eds., MOLECULAR CLONING: A LABORATORY MANUAL 2<sup>nd</sup> Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, eds., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to ORFX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement thereof. Oligonucleotides may be chemically synthesized and may be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion of this nucleotide sequence. A nucleic acid molecule that is complementary to the nucleotide sequence shown in

is one that is sufficiently complementary to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161),, thereby forming a stable duplex.

- 5           As used herein, the term “complementary” refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term “binding” means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, Von der Waals, hydrophobic interactions, etc. A physical interaction can be either direct or indirect.
- 10       Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

- Moreover, the nucleic acid molecule of the invention can comprise only a portion of the
- 15       nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), *e.g.*, a fragment that can be used as a probe or primer, or a fragment encoding a biologically active portion of ORFX. Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively,
- 20       and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but
- 25       differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type.

- Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or
- 30       analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the

invention, in various embodiments, by at least about 70%, 80%, 85%, 90%, 95%, 98%, or even 99% identity (with a preferred identity of 80-99%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below. An exemplary program is the Gap program (Wisconsin Sequence Analysis Package, Version 8 for UNIX, Genetics Computer Group, University Research Park, Madison, WI) using the default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2: 482-489, which is incorporated herein by reference in its entirety).

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of ORFX polypeptide. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the present invention, homologous nucleotide sequences include nucleotide sequences encoding for a ORFX polypeptide of species other than humans, including, but not limited to, mammals, and thus can include, *e.g.*, mouse, rat, rabbit, dog, cat cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the nucleotide sequence encoding human ORFX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in any of SEQ ID NO:2 $n$  (wherein  $n = 1$  to 3161) as well as a polypeptide having ORFX activity. Biological activities of the ORFX proteins are described below. A homologous amino acid sequence does not encode the amino acid sequence of a human ORFX polypeptide.

The nucleotide sequence determined from the cloning of the human ORFX gene allows for the generation of probes and primers designed for use in identifying the cell types disclosed and/or cloning ORFX homologues in other cell types, *e.g.*, from other tissues, as well as ORFX homologues from other mammals. The probe/primer typically comprises a substantially purified



oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 or more consecutive sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or an anti-sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161);  
5 or of a naturally occurring mutant of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

Probes based on the human ORFX nucleotide sequence can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.*, the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be  
10 used as a part of a diagnostic test kit for identifying cells or tissue which misexpress a ORFX protein, such as by measuring a level of a ORFX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting ORFX mRNA levels or determining whether a genomic ORFX gene has been mutated or deleted.

"A polypeptide having a biologically active portion of ORFX" refers to polypeptides  
15 exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically active portion of ORFX" can be prepared by isolating a portion of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), that encodes a polypeptide having a ORFX biological activity (biological activities of the ORFX  
20 proteins are summarized in Table 1), expressing the encoded portion of ORFX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of ORFX. For example, a nucleic acid fragment encoding a biologically active portion of ORFX can optionally include a domain as shown in Table 1, column 4.

## 25 ORFX variants

The invention further encompasses nucleic acid molecules that differ from the disclosed ORFX nucleotide sequences due to degeneracy of the genetic code. These nucleic acids thus encode the same ORFX protein as that encoded by the nucleotide sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of  
30 the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

In addition to the human ORFX nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of ORFX may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the ORFX gene may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a ORFX protein, preferably a mammalian ORFX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the ORFX gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in ORFX that are the result of natural allelic variation and that do not alter the functional activity of ORFX are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding ORFX proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the ORFX cDNAs of the invention can be isolated based on their homology to the human ORFX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

In another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500 or 750 nucleotides in length. In another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding ORFX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. The  $T_m$  is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at  $T_m$ , 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (e.g., 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions is hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C. This hybridization is followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of any of SEQ ID NO:2*n*-1 (wherein  $n = 1$  to 3161) corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein  $n = 1$  to 3161), or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are

hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well known in the art. See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and  
5 Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A  
10 non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at  
15 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations). See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981, *Proc Natl Acad Sci USA* 78: 6789-6792.

#### Conservative mutations

20 In addition to naturally-occurring allelic variants of the ORFX sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), thereby leading to changes in the amino acid sequence of the encoded ORFX protein, without altering the functional ability of the ORFX protein. For example, nucleotide substitutions  
25 leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of ORFX without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are conserved among the ORFX proteins of the present  
30 invention, are predicted to be particularly unamenable to alteration.

Amino acid residues that are conserved among members of an ORFX family members are predicted to be less amenable to alteration. For example, an ORFX protein according to the present invention can contain at least one domain (*e.g.*, as shown in Table 1) that is a typically conserved region in an ORFX family member. As such, these conserved domains are not likely to be amenable to mutation. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved among members of the ORFX family) may not be as essential for activity and thus are more likely to be amenable to alteration.

Another aspect of the invention pertains to nucleic acid molecules encoding ORFX proteins that contain changes in amino acid residues that are not essential for activity. Such ORFX proteins differ in amino acid sequence from any of any of SEQ ID NO:2 $n$  (wherein  $n = 1$  to 3161), yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 75% homologous to the amino acid sequence of any of SEQ ID NO:2 $n$  (wherein  $n = 1$  to 3161). Preferably, the protein encoded by the nucleic acid is at least about 80% homologous to any of SEQ ID NO:2 $n$  (wherein  $n = 1$  to 3161), more preferably at least about 90%, 95%, 98%, and most preferably at least about 99% homologous to SEQ ID NO:2.

An isolated nucleic acid molecule encoding a ORFX protein homologous to the protein of any of SEQ ID NO:2 $n$  (wherein  $n = 1$  to 3161) can be created by introducing one or more nucleotide substitutions, additions or deletions into the corresponding nucleotide sequence, *i.e.* SEQ ID NO:2 $n$ -1 for the corresponding  $n$ , such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NO:2 $n$ -1 (wherein  $n = 1$  to 3161) by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline,

phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in ORFX is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a ORFX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ORFX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

In one embodiment, a mutant ORFX protein can be assayed for (1) the ability to form protein:protein interactions with other ORFX proteins, other cell-surface proteins, or biologically active portions thereof, (2) complex formation between a mutant ORFX protein and a ORFX receptor; (3) the ability of a mutant ORFX protein to bind to an intracellular target protein or biologically active portion thereof; (*e.g.*, avidin proteins); (4) the ability to bind BRA protein; or (5) the ability to specifically bind an anti-ORFX protein antibody.

#### Antisense

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire ORFX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a ORFX protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) or antisense nucleic acids complementary to a ORFX nucleic acid sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid

residues (*e.g.*, the protein coding region of a human ORFX that corresponds to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161)). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding ORFX disclosed herein (*e.g.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of ORFX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of ORFX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of ORFX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (*v*), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (*v*), 5-methyl-2-thiouracil,

3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a ORFX protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

#### Ribozymes and PNA moieties

Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are



carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme.

- 5 Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave ORFX mRNA transcripts to thereby inhibit translation of ORFX mRNA. A ribozyme having specificity for a ORFX-encoding
- 10 nucleic acid can be designed based upon the nucleotide sequence of a ORFX DNA disclosed herein (*i.e.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a ORFX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742.
- 15 Alternatively, ORFX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

- Alternatively, ORFX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the ORFX (*e.g.*, the ORFX promoter and/or
- 20 enhancers) to form triple helical structures that prevent transcription of the ORFX gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

- In various embodiments, the nucleic acids of ORFX can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of
- 25 the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has
- 30 been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide

synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of ORFX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of ORFX can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of ORFX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of ORFX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or

the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

### ORFX polypeptides

The novel protein of the invention includes the ORFX-like protein whose sequence is provided in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in FIG. 1 while still encoding a protein that maintains its ORFX-like activities and physiological functions, or a functional fragment thereof. For example, the invention includes the polypeptides encoded by the variant ORFX nucleic acids described above. In the mutant or variant protein, up to 20% or more of the residues may be so changed.

In general, an ORFX-like variant that preserves ORFX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above. Furthermore, without limiting the scope of the invention, positions of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) may be substituted such that a mutant or variant protein may include one or more substitutions

The invention also includes isolated ORFX proteins, and biologically active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-ORFX antibodies. In one embodiment, native ORFX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, ORFX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a ORFX

protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the ORFX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of ORFX protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of ORFX protein having less than about 30% (by dry weight) of non-ORFX protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-ORFX protein, still more preferably less than about 10% of non-ORFX protein, and most preferably less than about 5% non-ORFX protein. When the ORFX protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein having less than about 30% (by dry weight) of chemical precursors or non-ORFX chemicals, more preferably less than about 20% chemical precursors or non-ORFX chemicals, still more preferably less than about 10% chemical precursors or non-ORFX chemicals, and most preferably less than about 5% chemical precursors or non-ORFX chemicals.

Biologically active portions of a ORFX protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the ORFX protein, *e.g.*, the amino acid sequence shown in SEQ ID NO:2 that include fewer amino acids than the full length ORFX proteins, and exhibit at least one activity of a ORFX protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the ORFX protein. A biologically active portion of a ORFX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

A biologically active portion of a ORFX protein of the present invention may contain at least one of the above-identified domains conserved between the FGF family of proteins. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native ORFX protein.

In an embodiment, the ORFX protein has an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). In other embodiments, the ORFX protein is substantially homologous to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail below. Accordingly, in another embodiment, the ORFX protein is a protein that comprises an amino acid sequence at least about 45% homologous, and more preferably about 55, 65, 70, 75, 80, 85, 90, 95, 98 or even 99% homologous to the amino acid sequence of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the ORFX proteins of the corresponding polypeptide having the sequence of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

#### **Determining homology between two or more sequences**

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in either of the sequences being compared for optimal alignment between the sequences). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. See, *Needleman and Wunsch 1970 J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a

degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NO:2n-1 (wherein n = 1 to 3161).

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region. The term "percentage of positive residues" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical and conservative amino acid substitutions, as defined above, occur in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of positive residues.

#### **Chimeric and fusion proteins**

The invention also provides ORFX chimeric or fusion proteins. As used herein, a ORFX "chimeric protein" or "fusion protein" includes a ORFX polypeptide operatively linked to a non-ORFX polypeptide. A "ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to ORFX, whereas a "non-ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the ORFX protein, *e.g.*, a protein that is different from the ORFX protein and that is derived from the same or a different organism. Within a ORFX fusion protein the ORFX polypeptide can correspond to all or a portion of a ORFX protein. In one embodiment, a ORFX fusion protein comprises at least one biologically active portion of a ORFX protein. In another embodiment, a ORFX fusion protein comprises at least two biologically active portions of a

ORFX protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the ORFX polypeptide and the non-ORFX polypeptide are fused in-frame to each other. The non-ORFX polypeptide can be fused to the N-terminus or C-terminus of the ORFX polypeptide.

5 For example, in one embodiment a ORFX fusion protein comprises a ORFX polypeptide operably linked to the extracellular domain of a second protein. Such fusion proteins can be further utilized in screening assays for compounds that modulate ORFX activity (such assays are described in detail below).

10 In another embodiment, the fusion protein is a GST-ORFX fusion protein in which the ORFX sequences are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant ORFX.

15 In yet another embodiment, the fusion protein is a ORFX protein containing a heterologous signal sequence at its N-terminus. For example, the native ORFX signal sequence can be removed and replaced with a signal sequence from another protein. In certain host cells (e.g., mammalian host cells), expression and/or secretion of ORFX can be increased through use of a heterologous signal sequence.

20 In another embodiment, the fusion protein is a ORFX-immunoglobulin fusion protein in which the ORFX sequences comprising one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The ORFX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ORFX ligand and a ORFX protein on the surface of a cell, to thereby suppress ORFX-mediated signal transduction *in vivo*. In one nonlimiting example, a contemplated ORFX ligand of the invention is an ORFX receptor. The ORFX-immunoglobulin fusion proteins can be used to modulate the bioavailability of a ORFX  
25 cognate ligand. Inhibition of the ORFX ligand/ORFX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the ORFX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-ORFX antibodies in a subject, to purify ORFX ligands, and in screening assays to identify molecules that inhibit the interaction of  
30 ORFX with a ORFX ligand.

A ORFX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A ORFX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the ORFX protein.

#### **ORFX agonists and antagonists**

The present invention also pertains to variants of the ORFX proteins that function as either ORFX agonists (mimetics) or as ORFX antagonists. Variants of the ORFX protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the ORFX protein. An agonist of the ORFX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the ORFX protein. An antagonist of the ORFX protein can inhibit one or more of the activities of the naturally occurring form of the ORFX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the ORFX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the ORFX proteins.

Variants of the ORFX protein that function as either ORFX agonists (mimetics) or as ORFX antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the ORFX protein for ORFX protein agonist or antagonist activity. In one



embodiment, a variegated library of ORFX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of ORFX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential ORFX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of ORFX sequences therein. There are a variety of methods which can be used to produce libraries of potential ORFX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential ORFX sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu Rev Biochem* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucl Acid Res* 11:477.

#### **Polypeptide libraries**

In addition, libraries of fragments of the ORFX protein coding sequence can be used to generate a variegated population of ORFX fragments for screening and subsequent selection of variants of a ORFX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a ORFX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the ORFX protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of ORFX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors,

transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify ORFX variants (Arkin and Yourvan (1992) PNAS 89:7811-7815; Delgrave *et al.* (1993) Protein Engineering 6:327-331).

#### Anti-ORFX Antibodies

The invention further encompasses antibodies and antibody fragments, such as  $F_{ab}$  or  $(F_{ab})_2$ , that bind immunospecifically to any of the proteins of the invention.

An isolated ORFX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind ORFX using standard techniques for polyclonal and monoclonal antibody preparation. Full-length ORFX protein can be used. Alternatively, the invention provides antigenic peptide fragments of ORFX for use as immunogens. The antigenic peptide of ORFX comprises at least 4 amino acid residues of the amino acid sequence shown in any of SEQ ID NO:2n (wherein n = 1 to 3161). The antigenic peptide encompasses an epitope of ORFX such that an antibody raised against the peptide forms a specific immune complex with ORFX. The antigenic peptide may comprise at least 6 aa residues, at least 8 aa residues, at least 10 aa residues, at least 15 aa residues, at least 20 aa residues, or at least 30 aa residues. In one embodiment of the invention, the antigenic peptide comprises a polypeptide comprising at least 6 contiguous amino acids of any of SEQ ID NO:2n (wherein n = 1 to 3161).

In an embodiment of the invention, epitopes encompassed by the antigenic peptide are regions of ORFX that are located on the surface of the protein, *e.g.*, hydrophilic regions. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each incorporated herein by reference in their entirety.

As disclosed herein, an ORFX protein sequence of any of SEQ ID NO:2n (wherein n = 1 to 3161), or derivatives, fragments, analogs or homologs thereof, may be utilized as immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and

immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as ORFX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain,  $F_{ab}$  and  $F_{(ab)2}$  fragments, and an  $F_{ab}$  expression library. In a specific embodiment, antibodies to human ORFX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to a ORFX protein sequence of any of SEQ ID NO:2n (wherein  $n = 1$  to 3161) or derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed ORFX protein or a chemically synthesized ORFX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against ORFX can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of ORFX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular ORFX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular ORFX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND

CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND  
5 CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations are incorporated herein by reference in their entirety

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a ORFX protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F<sub>ab</sub> expression libraries (see *e.g.*, Huse, *et al.*,  
10 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F<sub>ab</sub> fragments with the desired specificity for a ORFX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Each of the above citations are incorporated herein by reference. Antibody fragments that contain the idiotypes to a ORFX protein may be produced by  
15 techniques known in the art including, but not limited to: (i) an F<sub>(ab)<sub>2</sub></sub> fragment produced by pepsin digestion of an antibody molecule; (ii) an F<sub>ab</sub> fragment generated by reducing the disulfide bridges of an F<sub>(ab)<sub>2</sub></sub> fragment; (iii) an F<sub>ab</sub> fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F<sub>v</sub> fragments.

Additionally, recombinant anti-ORFX antibodies, such as chimeric and humanized  
20 monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent  
25 Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988), *J.*  
30 *Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525;

Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060. Each of the above citations are incorporated herein by reference.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of a ORFX protein is facilitated by generation of hybridomas that bind to the fragment of a ORFX protein possessing such a domain. Antibodies that are specific for one or more domains within a ORFX protein, *e.g.*, the domain spanning the first fifty amino-terminal residues specific to ORFX when compared to FGF-9, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-ORFX antibodies may be used in methods known within the art relating to the localization and/or quantitation of a ORFX protein (*e.g.*, for use in measuring levels of the ORFX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for ORFX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds [hereinafter "Therapeutics"].

An anti-ORFX antibody (*e.g.*, monoclonal antibody) can be used to isolate ORFX by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-ORFX antibody can facilitate the purification of natural ORFX from cells and of recombinantly produced ORFX expressed in host cells. Moreover, an anti-ORFX antibody can be used to detect ORFX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the ORFX protein. Anti-ORFX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase,  $\beta$ -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or

phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^3\text{H}$ .

### **ORFX Recombinant Vectors and Host Cells**

5        Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding ORFX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can  
10    be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are  
15    replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the  
20    invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

      The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the  
25    recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation  
30    system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements

(*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the  
5 nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as  
10 described herein (*e.g.*, ORFX proteins, mutant forms of ORFX, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of ORFX in prokaryotic or eukaryotic cells. For example, ORFX can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY:  
15 METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or  
20 non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (1) to increase expression of recombinant protein; (2) to increase the solubility of the recombinant protein; and (3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is  
25 introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and  
30 pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

5 One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons  
10 for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the ORFX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*,  
15 (1987) *EMBO J* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (Invitrogen Corp, San Diego, Calif.).

Alternatively, ORFX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*,  
20 SF9 cells) include the pAc series (Smith *et al.* (1983) *Mol Cell Biol* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J*  
25 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells. See, *e.g.*, Chapters 16 and 17 of Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory,  
30 Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.



In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv Immunol* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the  $\alpha$ -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to ORFX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, "Antisense RNA as a molecular tool for genetic analysis," Reviews--Trends in Genetics, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant

host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, ORFX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding ORFX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) ORFX protein. Accordingly, the invention further provides methods for producing ORFX protein using the host cells of the invention. In one embodiment,

the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding ORFX has been introduced) in a suitable medium such that ORFX protein is produced. In another embodiment, the method further comprises isolating ORFX from the medium or the host cell.

## 5           **Transgenic animals**

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which ORFX-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous ORFX sequences  
10 have been introduced into their genome or homologous recombinant animals in which endogenous ORFX sequences have been altered. Such animals are useful for studying the function and/or activity of ORFX and for identifying and/or evaluating modulators of ORFX activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal  
15 includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous  
20 recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous ORFX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing ORFX-encoding  
25 nucleic acid into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The human ORFX DNA sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue of the human ORFX gene, such as a mouse ORFX gene, can be isolated based on hybridization to  
30 the human ORFX cDNA (described further above) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of

expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the ORFX transgene to direct expression of ORFX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan 1986, In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the ORFX transgene in its genome and/or expression of ORFX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding ORFX can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of a ORFX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the ORFX gene. The ORFX gene can be a human gene (*e.g.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)), but more preferably, is a non-human homologue of a human ORFX gene. For example, a mouse homologue of human ORFX gene of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be used to construct a homologous recombination vector suitable for altering an endogenous ORFX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous ORFX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous ORFX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous ORFX protein). In the homologous recombination vector, the altered portion of the ORFX gene is flanked at its 5' and 3' ends by additional nucleic acid of the ORFX gene to allow for homologous recombination to occur between the exogenous ORFX gene carried by the vector and an endogenous ORFX gene in an embryonic stem cell. The additional flanking ORFX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector. See *e.g.*, Thomas *et al.* (1987) *Cell* 51:503 for a description of

homologous recombination vectors. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced ORFX gene has homologously recombined with the endogenous ORFX gene are selected (see e.g., Li *et al.* (1992) *Cell* 69:915).

The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras. See e.g., Bradley 1987, In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Curr Opin Biotechnol* 2:823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, see, e.g., Lakso *et al.* (1992) *PNAS* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.* (1991) *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813. In brief, a cell, e.g., a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G<sub>0</sub> phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of

this female foster animal will be a clone of the animal from which the cell, *e.g.*, the somatic cell, is isolated.

### Pharmaceutical Compositions

5 The ORFX nucleic acid molecules, ORFX proteins, and anti-ORFX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, 10 antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human 15 serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

20 A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent 25 such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with 30 acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a ORFX protein or anti-ORFX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use

as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature; a binder  
5 such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

10 For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated  
15 are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

20 The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible  
25 polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as  
30 pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Pat. No. 4,522,811.



It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired  
5 therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by any of a number of  
10 routes, *e.g.*, as described in U.S. Patent Nos. 5,703,055. Delivery can thus also include, *e.g.*, intravenous injection, local administration (see U.S. Pat. No. 5,328,470) or stereotactic injection (see *e.g.*, Chen *et al.* (1994) *PNAS* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the  
15 complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

## 20 Additional Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: (a) screening assays; (b) detection assays (*e.g.*, chromosomal mapping, cell and tissue typing, forensic biology), (c) predictive medicine (*e.g.*, diagnostic assays, prognostic assays, monitoring clinical trials, and  
25 pharmacogenomics); and (d) methods of treatment (*e.g.*, therapeutic and prophylactic).

The isolated nucleic acid molecules of the invention can be used to express ORFX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect ORFX mRNA (*e.g.*, in a biological sample) or a genetic lesion in a ORFX gene, and to modulate ORFX activity, as described further below. In addition, the ORFX proteins can be  
30 used to screen drugs or compounds that modulate the ORFX activity or expression as well as to treat disorders characterized by insufficient or excessive production of ORFX protein, for

example proliferative or differentiative disorders, or production of ORFX protein forms that have decreased or aberrant activity compared to ORFX wild type protein. In addition, the anti-ORFX antibodies of the invention can be used to detect and isolate ORFX proteins and modulate ORFX activity.

5           This invention further pertains to novel agents identified by the above described screening assays and uses thereof for treatments as described herein.

### Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides,  
10   peptidomimetics, small molecules or other drugs) that bind to ORFX proteins or have a stimulatory or inhibitory effect on, for example, ORFX expression or ORFX activity.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a ORFX protein or polypeptide or biologically active portion thereof. The test compounds of the present invention can be obtained  
15   using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are  
20   applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam (1997) *Anticancer Drug Des* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc Natl Acad Sci U.S.A.* 90:6909; Erb *et al.* (1994) *Proc Natl Acad Sci U.S.A.* 91:11422; Zuckermann *et al.* (1994) *J Med Chem* 37:2678; Cho *et al.* (1993)  
25   *Science* 261:1303; Carrell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2059; Carell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2061; and Gallop *et al.* (1994) *J Med Chem* 37:1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), on chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner U.S. Pat. No. 5,223,409), spores (Ladner USP '409),  
30   plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and

Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406; Cwirla *et al.* (1990) *Proc Natl Acad Sci U.S.A.* 87:6378-6382; Felici (1991) *J Mol Biol* 222:301-310; Ladner above.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to a ORFX protein determined. The cell, for example, can be of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the ORFX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the ORFX protein or biologically active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with  $^{125}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$ , or  $^3\text{H}$ , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or a biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX or a biologically active portion thereof can be accomplished, for example, by determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule. As used herein, a "target molecule" is a molecule with which a ORFX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses a ORFX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule

associated with the internal surface of a cell membrane or a cytoplasmic molecule. A ORFX target molecule can be a non-ORFX molecule or a ORFX protein or polypeptide of the present invention. In one embodiment, a ORFX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.*, a signal generated by binding of a compound to a membrane-bound ORFX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with ORFX.

Determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular  $\text{Ca}^{2+}$ , diacylglycerol,  $\text{IP}_3$ , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising a ORFX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting a ORFX protein or biologically active portion thereof with a test compound and determining the ability of the test compound to bind to the ORFX protein or biologically active portion thereof. Binding of the test compound to the ORFX protein can be determined either directly or indirectly as described above. In one embodiment, the assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-free assay comprising contacting ORFX protein or biologically active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or

biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX can be accomplished, for example, by determining the ability of the ORFX protein to bind to a ORFX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of ORFX can be accomplished by determining the ability of the ORFX protein further modulate a ORFX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the ORFX protein to preferentially bind to or modulate the activity of a ORFX target molecule.

The cell-free assays of the present invention are amenable to use of both the soluble form or the membrane-bound form of ORFX. In the case of cell-free assays comprising the membrane-bound form of ORFX, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of ORFX is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton<sup>®</sup> X-100, Triton<sup>®</sup> X-114, Thesit<sup>®</sup>, Isotridecypoly(ethylene glycol ether)<sub>n</sub>, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl)dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either ORFX or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to ORFX, or interaction of ORFX with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For

example, GST-ORFX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or ORFX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of ORFX binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either ORFX or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated ORFX or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with ORFX or target molecules, but which do not interfere with binding of the ORFX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or ORFX trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the ORFX or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the ORFX or target molecule.

In another embodiment, modulators of ORFX expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of ORFX mRNA or protein in the cell is determined. The level of expression of ORFX mRNA or protein in the presence of the candidate compound is compared to the level of expression of ORFX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of ORFX expression based on this comparison. For example, when expression of ORFX mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of ORFX mRNA or protein expression. Alternatively, when expression of ORFX mRNA or protein is less (statistically significantly less) in the presence of the candidate

compound than in its absence, the candidate compound is identified as an inhibitor of ORFX mRNA or protein expression. The level of ORFX mRNA or protein expression in the cells can be determined by methods described herein for detecting ORFX mRNA or protein.

In yet another aspect of the invention, the ORFX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (see, *e.g.*, U.S. Pat. No. 5,283,317; Zervos *et al.* (1993) *Cell* 72:223-232; Madura *et al.* (1993) *J Biol Chem* 268:12046-12054; Bartel *et al.* (1993) *Biotechniques* 14:920-924; Iwabuchi *et al.* (1993) *Oncogene* 8:1693-1696; and Brent WO94/10300), to identify other proteins that bind to or interact with ORFX ("ORFX-binding proteins" or "ORFX-bp") and modulate ORFX activity. Such ORFX-binding proteins are also likely to be involved in the propagation of signals by the ORFX proteins as, for example, upstream or downstream elements of the ORFX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for ORFX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a ORFX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with ORFX.

This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

#### Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a

minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample.

The ORFX sequences of the present invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the present invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Pat. No. 5,272,057).

Furthermore, the sequences of the present invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the ORFX sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the present invention can be used to obtain such identification sequences from individuals and from tissue. The ORFX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences of SEQ ID NO:2 $n$ -1 (wherein  $n = 1$  to 3161), as described above, can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences are used, a more appropriate number of primers for positive individual identification would be 500-2,000.



### **Predictive Medicine**

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

### **Use of Partial ORFX Sequences in Forensic Biology**

DNA-based identification techniques can also be used in forensic biology. Forensic biology is a scientific field employing genetic typing of biological evidence found at a crime scene as a means for positively identifying, for example, a perpetrator of a crime. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues, *e.g.*, hair or skin, or body fluids, *e.g.*, blood, saliva, or semen

found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

The sequences of the present invention can be used to provide polynucleotide reagents, *e.g.*, PCR primers, targeted to specific loci in the human genome, that can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (*i.e.* another DNA sequence that is unique to a particular individual). As mentioned above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NOs: \_\_ are particularly appropriate for this use as greater numbers of polymorphisms occur in the noncoding regions, making it easier to differentiate individuals using this technique. Examples of polynucleotide reagents include the ORFX sequences or portions thereof, *e.g.*, fragments derived from the noncoding regions of one or more of SEQ ID NO:2*n*-1 (where *n* = 1 to 3161), having a length of at least 20 bases, preferably at least 30 bases.

The ORFX sequences described herein can further be used to provide polynucleotide reagents, *e.g.*, labeled or label-able probes that can be used, for example, in an *in situ* hybridization technique, to identify a specific tissue, *e.g.*, brain tissue, etc. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such ORFX probes can be used to identify tissue by species and/or by organ type.

In a similar fashion, these reagents, *e.g.*, ORFX primers or probes can be used to screen tissue culture for contamination (*i.e.* screen for the presence of a mixture of different types of cells in a culture).

### Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic

acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

5           Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

10           Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

          These and other agents are described in further detail in the following sections.

#### **Diagnostic Assays**

15           Other conditions in which proliferation of cells plays a role include tumors, restenosis, psoriasis, Dupuytren's contracture, diabetic complications, Kaposi's sarcoma and rheumatoid arthritis.

          An ORFX polypeptide may be used to identify an interacting polypeptide a sample or tissue. The method comprises contacting the sample or tissue with ORFX, allowing formation of a complex between the ORFX polypeptide and the interacting polypeptide, and detecting the complex, if present.

20           The proteins of the invention may be used to stimulate production of antibodies specifically binding the proteins. Such antibodies may be used in immunodiagnostic procedures to detect the occurrence of the protein in a sample. The proteins of the invention may be used to stimulate cell growth and cell proliferation in conditions in which such growth would be favorable. An example would be to counteract toxic side effects of chemotherapeutic agents on, for example, hematopoiesis and platelet formation, linings of the gastrointestinal tract, and hair follicles. They may also be used to stimulate new cell growth in neurological disorders including, for example, Alzheimer's disease. Alternatively, antagonistic treatments may be administered in which an antibody specifically binding the ORFX-like proteins of the invention

30

would abrogate the specific growth-inducing effects of the proteins. Such antibodies may be useful, for example, in the treatment of proliferative disorders including various tumors and benign hyperplasias.

Polynucleotides or oligonucleotides corresponding to any one portion of the ORFX nucleic acids of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) may be used to detect DNA containing a corresponding ORF gene, or detect the expression of a corresponding ORFX gene, or ORFX-like gene. For example, an ORFX nucleic acid expressed in a particular cell or tissue, as noted in Table 2, can be used to identify the presence of that particular cell type.

An exemplary method for detecting the presence or absence of ORFX in a biological sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting ORFX protein or nucleic acid (e.g., mRNA, genomic DNA) that encodes ORFX protein such that the presence of ORFX is detected in the biological sample. An agent for detecting ORFX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to ORFX mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length ORFX nucleic acid, such as the nucleic acid of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to ORFX mRNA or genomic DNA, as described above. Other suitable probes for use in the diagnostic assays of the invention are described herein.

An agent for detecting ORFX protein is an antibody capable of binding to ORFX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (e.g., Fab or F(ab')<sub>2</sub>) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect ORFX mRNA, protein, or genomic DNA in a biological sample *in vitro* as

well as *in vivo*. For example, *in vitro* techniques for detection of ORFX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of ORFX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of ORFX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of ORFX protein include introducing into a subject a labeled anti-ORFX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting ORFX protein, mRNA, or genomic DNA, such that the presence of ORFX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of ORFX protein, mRNA or genomic DNA in the control sample with the presence of ORFX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of ORFX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting ORFX protein or mRNA in a biological sample; means for determining the amount of ORFX in the sample; and means for comparing the amount of ORFX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect ORFX protein or nucleic acid.

### **Prognostic Assays**

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity in, *e.g.*, proliferative or differentiative disorders such as hyperplasias, tumors, restenosis, psoriasis, Dupuytren's

contracture, diabetic complications, or rheumatoid arthritis, etc.; and glia-associated disorders such as cerebral lesions, diabetic neuropathies, cerebral edema, senile dementia, Alzheimer's disease, etc. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the present invention provides a method for  
5 identifying a disease or disorder associated with aberrant ORFX expression or activity in which a test sample is obtained from a subject and ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. As used herein, a "test sample" refers to a biological sample obtained  
10 from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder  
15 associated with aberrant ORFX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder, such as a proliferative disorder, differentiative disorder, glia-associated disorders, etc. Thus, the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant ORFX expression or activity in which a test sample  
20 is obtained and ORFX protein or nucleic acid is detected (*e.g.*, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant ORFX expression or activity.)

The methods of the invention can also be used to detect genetic lesions in a ORFX gene, thereby determining if a subject with the lesioned gene is at risk for, or suffers from, a  
25 proliferative disorder, differentiative disorder, glia-associated disorder, etc. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding a ORFX-protein, or the mis-expression of the ORFX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of (1) a deletion  
30 of one or more nucleotides from a ORFX gene; (2) an addition of one or more nucleotides to a ORFX gene; (3) a substitution of one or more nucleotides of a ORFX gene, (4) a chromosomal

rearrangement of a ORFX gene; (5) an alteration in the level of a messenger RNA transcript of a ORFX gene, (6) aberrant modification of a ORFX gene, such as of the methylation pattern of the genomic DNA, (7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a ORFX gene, (8) a non-wild type level of a ORFX-protein, (9) allelic loss of a ORFX gene, and (10) inappropriate post-translational modification of a ORFX-protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in a ORFX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, *e.g.*, U.S. Pat. Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, *e.g.*, Landegran *et al.* (1988) *Science* 241:1077-1080; and Nakazawa *et al.* (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the ORFX-gene (see Abravaya *et al.* (1995) *Nucl Acids Res* 23:675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to a ORFX gene under conditions such that hybridization and amplification of the ORFX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990, *Proc Natl Acad Sci USA* 87:1874-1878), transcriptional amplification system (Kwoh, *et al.*, 1989, *Proc Natl Acad Sci USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *BioTechnology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in a ORFX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Pat. No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in ORFX can be identified by hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotides probes (Cronin *et al.* (1996) *Human Mutation* 7: 244-255; Kozal *et al.* (1996) *Nature Medicine* 2: 753-759). For example, genetic mutations in ORFX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin *et al.* above. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the ORFX gene and detect mutations by comparing the sequence of the sample ORFX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert (1977) *PNAS* 74:560 or Sanger (1977) *PNAS* 74:5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (Naeve *et al.*, (1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, *e.g.*, PCT International Publ. No. WO 94/16101; Cohen *et al.* (1996) *Adv Chromatogr* 36:127-162; and Griffin *et al.* (1993) *Appl Biochem Biotechnol* 38:147-159).

Other methods for detecting mutations in the ORFX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA



heteroduplexes (Myers *et al.* (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type ORFX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that  
5 cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest  
10 mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton *et al* (1988) *Proc Natl Acad Sci USA* 85:4397; Saleeba *et al* (1992) *Methods Enzymol* 217:286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

15 In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in ORFX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T  
20 mismatches (Hsu *et al.* (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on a ORFX sequence, *e.g.*, a wild-type ORFX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Pat. No. 5,459,039.

25 In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in ORFX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.* (1989) *Proc Natl Acad Sci USA*: 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments  
30 of sample and control ORFX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting

alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA, rather than DNA, in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. See, *e.g.*, Keen *et al.* (1991) *Trends Genet* 7:5.

In yet another embodiment the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). See, *e.g.*, Myers *et al.* (1985) *Nature* 313:495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. See, *e.g.*, Rosenbaum and Reissner (1987) *Biophys Chem* 265:12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. See, *e.g.*, Saiki *et al.* (1986) *Nature* 324:163; Saiki *et al.* (1989) *Proc Natl Acad. Sci USA* 86:6230. Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs *et al.* (1989) *Nucleic Acids Res* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. See, *e.g.*, Gasparini *et al.* (1992) *Mol Cell Probes* 6:1. It is anticipated that in certain embodiments amplification may also be performed using Taq ligase

for amplification. See, *e.g.*, Barany (1991) *Proc Natl Acad Sci USA* 88:189. In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

5       The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving a ORFX gene.

10       Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which ORFX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

#### **Pharmacogenomics**

15       Agents, or modulators that have a stimulatory or inhibitory effect on ORFX activity (*e.g.*, ORFX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (*e.g.*, neurological, cancer-related or gestational disorders) associated with aberrant ORFX activity. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be  
20       considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate  
25       dosages and therapeutic regimens. Accordingly, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

30       Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996, *Clin Exp Pharmacol Physiol*, 23:983-985 and Linder, 1997, *Clin Chem*, 43:254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic

conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a ORFX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

### Monitoring Clinical Efficacy

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied in basic drug screening and in clinical trials. For example, the effectiveness of an agent  
5 determined by a screening assay as described herein to increase ORFX gene expression, protein levels, or upregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting decreased ORFX gene expression, protein levels, or downregulated ORFX activity.

Alternatively, the effectiveness of an agent determined by a screening assay to decrease ORFX gene expression, protein levels, or downregulate ORFX activity, can be monitored in clinical  
10 trials of subjects exhibiting increased ORFX gene expression, protein levels, or upregulated ORFX activity. In such clinical trials, the expression or activity of ORFX and, preferably, other genes that have been implicated in, for example, a proliferative or neurological disorder, can be used as a "read out" or marker of the responsiveness of a particular cell.

For example, genes, including ORFX, that are modulated in cells by treatment with an  
15 agent (*e.g.*, compound, drug or small molecule) that modulates ORFX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of ORFX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by  
20 Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of ORFX or other genes. In this way, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the  
25 agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, nucleic acid, peptidomimetic, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (*i*) obtaining a pre-administration sample from a  
30 subject prior to administration of the agent; (*ii*) detecting the level of expression of a ORFX protein, mRNA, or genomic DNA in the preadministration sample; (*iii*) obtaining one or more

post-administration samples from the subject; (iv) detecting the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the pre-administration sample with the ORFX protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of ORFX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of ORFX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

#### Methods of Treatment

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant ORFX expression or activity.

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, (i) a ORFX polypeptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to a ORFX peptide; (iii) nucleic acids encoding a ORFX peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to a ORFX peptide) that are utilized to "knockout" endogenous function of a ORFX peptide by homologous recombination (see, *e.g.*, Capecchi, 1989, *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between a ORFX peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized

include, but are not limited to, a ORFX peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of a ORFX peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, etc.).

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant ORFX expression or activity, by administering to the subject an agent that modulates ORFX expression or at least one ORFX activity. Subjects at risk for a disease that is caused or contributed to by aberrant ORFX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the ORFX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of ORFX aberrancy, for example, a ORFX agonist or ORFX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

Another aspect of the invention pertains to methods of modulating ORFX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of ORFX protein activity associated with the cell. An agent that modulates ORFX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of a ORFX protein, a peptide, a ORFX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more ORFX protein activity. Examples of such stimulatory agents include active ORFX protein and a nucleic acid molecule encoding ORFX that has been introduced into the cell. In another embodiment, the agent inhibits one or more ORFX protein activity. Examples of such inhibitory agents include antisense ORFX nucleic acid molecules and anti-ORFX antibodies. These modulatory methods can be performed *in vitro*

(*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of a ORFX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay described herein), or combination of agents that modulates (*e.g.*, upregulates or downregulates) ORFX expression or activity. In another embodiment, the method involves administering a ORFX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant ORFX expression or activity.

#### **Determination of the Biological Effect of a Therapeutic**

In various embodiments of the present invention, suitable *in vitro* or *in vivo* assays are utilized to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

#### **Malignancies**

Some ORFX polypeptides are expressed in cancerous cells (*see, e.g.*, Tables 1 and 2). Accordingly, the corresponding ORF protein is involved in the regulation of cell proliferation. Accordingly, Therapeutics of the present invention may be useful in the therapeutic or prophylactic treatment of diseases or disorders that are associated with cell hyperproliferation and/or loss of control of cell proliferation (*e.g.*, cancers, malignancies and tumors). For a review of such hyperproliferation disorders, *see e.g.*, Fishman, *et al.*, 1985. MEDICINE, 2nd ed., J.B. Lippincott Co., Philadelphia, PA.

Therapeutics of the present invention may be assayed by any method known within the art for efficacy in treating or preventing malignancies and related disorders. Such assays include,



but are not limited to, *in vitro* assays utilizing transformed cells or cells derived from the patient's tumor, as well as *in vivo* assays using animal models of cancer or malignancies. Potentially effective Therapeutics are those that, for example, inhibit the proliferation of tumor-derived or transformed cells in culture or cause a regression of tumors in animal models, in comparison to the controls.

In the practice of the present invention, once a malignancy or cancer has been shown to be amenable to treatment by modulating (*i.e.*, inhibiting, antagonizing or agonizing) activity, that cancer or malignancy may subsequently be treated or prevented by the administration of a Therapeutic that serves to modulate protein function.

#### **Premalignant conditions**

The Therapeutics of the present invention that are effective in the therapeutic or prophylactic treatment of cancer or malignancies may also be administered for the treatment of pre-malignant conditions and/or to prevent the progression of a pre-malignancy to a neoplastic or malignant state. Such prophylactic or therapeutic use is indicated in conditions known or suspected of preceding progression to neoplasia or cancer, in particular, where non-neoplastic cell growth consisting of hyperplasia, metaplasia or, most particularly, dysplasia has occurred. For a review of such abnormal cell growth see *e.g.*, Robbins & Angell, 1976. BASIC PATHOLOGY, 2nd ed., W.B. Saunders Co., Philadelphia, PA.

Hyperplasia is a form of controlled cell proliferation involving an increase in cell number in a tissue or organ, without significant alteration in its structure or function. For example, it has been demonstrated that endometrial hyperplasia often precedes endometrial cancer. Metaplasia is a form of controlled cell growth in which one type of mature or fully differentiated cell substitutes for another type of mature cell. Metaplasia may occur in epithelial or connective tissue cells. Dysplasia is generally considered a precursor of cancer, and is found mainly in the epithelia. Dysplasia is the most disorderly form of non-neoplastic cell growth, and involves a loss in individual cell uniformity and in the architectural orientation of cells. Dysplasia characteristically occurs where there exists chronic irritation or inflammation, and is often found in the cervix, respiratory passages, oral cavity, and gall bladder.

Alternatively, or in addition to the presence of abnormal cell growth characterized as hyperplasia, metaplasia, or dysplasia, the presence of one or more characteristics of a transformed or malignant phenotype displayed either *in vivo* or *in vitro* within a cell sample derived from a patient, is indicative of the desirability of prophylactic/therapeutic administration of a Therapeutic that possesses the ability to modulate activity of An aforementioned protein.

Characteristics of a transformed phenotype include, but are not limited to: (i) morphological changes; (ii) looser substratum attachment; (iii) loss of cell-to-cell contact inhibition; (iv) loss of anchorage dependence; (v) protease release; (vi) increased sugar transport; (vii) decreased serum requirement; (viii) expression of fetal antigens, (ix) disappearance of the 250 kDal cell-surface protein, and the like. See *e.g.*, Richards, *et al.*, 1986. MOLECULAR PATHOLOGY, W.B. Saunders Co., Philadelphia, PA.

In a specific embodiment of the present invention, a patient that exhibits one or more of the following predisposing factors for malignancy is treated by administration of an effective amount of a Therapeutic: (i) a chromosomal translocation associated with a malignancy (*e.g.*, the Philadelphia chromosome (*bcr/abl*) for chronic myelogenous leukemia and t(14;18) for follicular lymphoma, etc.); (ii) familial polyposis or Gardner's syndrome (possible forerunners of colon cancer); (iii) monoclonal gammopathy of undetermined significance (a possible precursor of multiple myeloma) and (iv) a first degree kinship with persons having a cancer or pre-cancerous disease showing a Mendelian (genetic) inheritance pattern (*e.g.*, familial polyposis of the colon, Gardner's syndrome, hereditary exostosis, polyendocrine adenomatosis, Peutz-Jeghers syndrome, neurofibromatosis of Von Recklinghausen, medullary thyroid carcinoma with amyloid production and pheochromocytoma, retinoblastoma, carotid body tumor, cutaneous melanocarcinoma, intraocular melanocarcinoma, xeroderma pigmentosum, ataxia telangiectasia, Chediak-Higashi syndrome, albinism, Fanconi's aplastic anemia and Bloom's syndrome).

In another embodiment, a Therapeutic of the present invention is administered to a human patient to prevent the progression to breast, colon, lung, pancreatic, or uterine cancer, or melanoma or sarcoma.

### **Hyperproliferative and dysproliferative disorders**

In one embodiment of the present invention, a Therapeutic is administered in the therapeutic or prophylactic treatment of hyperproliferative or benign dysproliferative disorders. The efficacy in treating or preventing hyperproliferative diseases or disorders of a Therapeutic of the present invention may be assayed by any method known within the art. Such assays include *in vitro* cell proliferation assays, *in vitro* or *in vivo* assays using animal models of hyperproliferative diseases or disorders, or the like. Potentially effective Therapeutics may, for example, promote cell proliferation in culture or cause growth or cell proliferation in animal models in comparison to controls.

Specific embodiments of the present invention are directed to the treatment or prevention of cirrhosis of the liver (a condition in which scarring has overtaken normal liver regeneration processes); treatment of keloid (hypertrophic scar) formation causing disfiguring of the skin in which the scarring process interferes with normal renewal; psoriasis (a common skin condition characterized by excessive proliferation of the skin and delay in proper cell fate determination); benign tumors; fibrocystic conditions and tissue hypertrophy (*e.g.*, benign prostatic hypertrophy).

### **Neurodegenerative disorders**

Some ORFX proteins are found in cell types have been implicated in the deregulation of cellular maturation and apoptosis, which are both characteristic of neurodegenerative disease. Accordingly, Therapeutics of the invention, particularly but not limited to those that modulate (or supply) activity of an aforementioned protein, may be effective in treating or preventing neurodegenerative disease. Therapeutics of the present invention that modulate the activity of an aforementioned protein involved in neurodegenerative disorders can be assayed by any method known in the art for efficacy in treating or preventing such neurodegenerative diseases and disorders. Such assays include *in vitro* assays for regulated cell maturation or inhibition of apoptosis or *in vivo* assays using animal models of neurodegenerative diseases or disorders, or any of the assays described below. Potentially effective Therapeutics, for example but not by way of limitation, promote regulated cell maturation and prevent cell apoptosis in culture, or reduce neurodegeneration in animal models in comparison to controls.

Once a neurodegenerative disease or disorder has been shown to be amenable to treatment by modulation activity, that neurodegenerative disease or disorder can be treated or prevented by administration of a Therapeutic that modulates activity. Such diseases include all degenerative disorders involved with aging, especially osteoarthritis and neurodegenerative disorders.

#### Disorders related to organ transplantation

Some ORFX can be associated with disorders related to organ transplantation, in particular but not limited to organ rejection. Therapeutics of the invention, particularly those that modulate (or supply) activity, may be effective in treating or preventing diseases or disorders related to organ transplantation. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity of an aforementioned protein) can be assayed by any method known in the art for efficacy in treating or preventing such diseases and disorders related to organ transplantation. Such assays include *in vitro* assays for using cell culture models as described below, or *in vivo* assays using animal models of diseases and disorders related to organ transplantation, see *e.g.*, below. Potentially effective Therapeutics, for example but not by way of limitation, reduce immune rejection responses in animal models in comparison to controls.

Accordingly, once diseases and disorders related to organ transplantation are shown to be amenable to treatment by modulation of activity, such diseases or disorders can be treated or prevented by administration of a Therapeutic that modulates activity.

#### Cardiovascular Disease

GENX has been implicated in cardiovascular disorders, including in atherosclerotic plaque formation. Diseases such as cardiovascular disease, including cerebral thrombosis or hemorrhage, ischemic heart or renal disease, peripheral vascular disease, or thrombosis of other major vessel, and other diseases, including diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage disease, systemic lupus erythematosus, homocysteinemia, and familial protein or lipid processing diseases, and the like, are either directly or indirectly associated with atherosclerosis. Accordingly, Therapeutics of the invention, particularly those that modulate (or supply) activity or formation may be effective in treating or preventing

atherosclerosis-associated diseases or disorders. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity) can be assayed by any method known in the art, including those described below, for efficacy in treating or preventing such diseases and disorders.

5           A vast array of animal and cell culture models exist for processes involved in atherosclerosis. A limited and non-exclusive list of animal models includes knockout mice for premature atherosclerosis (Kurabayashi and Yazaki, 1996, *Int. Angiol.* 15: 187-194), transgenic mouse models of atherosclerosis (Kappel *et al.*, 1994, *FASEB J.* 8: 583-592), antisense oligonucleotide treatment of animal models (Callow, 1995, *Curr. Opin. Cardiol.* 10: 569-576),  
10       transgenic rabbit models for atherosclerosis (Taylor, 1997, *Ann. N.Y. Acad. Sci.* 811: 146-152), hypercholesterolemic animal models (Rosenfeld, 1996, *Diabetes Res. Clin. Pract.* 30 Suppl.: 1-11), hyperlipidemic mice (Paigen *et al.*, 1994, *Curr. Opin. Lipidol.* 5: 258-264), and inhibition of lipoxygenase in animals (Sigal *et al.*, 1994, *Ann. N.Y. Acad. Sci.* 714: 211-224). In addition, *in vitro* cell models include but are not limited to monocytes exposed to low density lipoprotein  
15       (Frostegard *et al.*, 1996, *Atherosclerosis* 121: 93-103), cloned vascular smooth muscle cells (Suttles *et al.*, 1995, *Exp. Cell Res.* 218: 331-338), endothelial cell-derived chemoattractant exposed T cells (Katz *et al.*, 1994, *J. Leukoc. Biol.* 55: 567-573), cultured human aortic endothelial cells (Farber *et al.*, 1992, *Am. J. Physiol.* 262: H1088-1085), and foam cell cultures (Libby *et al.*, 1996, *Curr Opin Lipidol* 7: 330-335). Potentially effective Therapeutics, for  
20       example but not by way of limitation, reduce foam cell formation in cell culture models, or reduce atherosclerotic plaque formation in hypercholesterolemic mouse models of atherosclerosis in comparison to controls.

          Accordingly, once an atherosclerosis-associated disease or disorder has been shown to be amenable to treatment by modulation of activity or formation, that disease or disorder can be  
25       treated or prevented by administration of a Therapeutic that modulates activity.

#### **Cytokine and Cell Proliferation/Differentiation Activity**

A GENX protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered

to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D,  
5 DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+ ), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for T-cell or thymocyte proliferation include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan *et al.*, Greene Publishing  
10 Associates and Wiley-Interscience (Chapter 3 and Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bertagnoli *et al.*, *J Immunol* 145:1706-1712, 1990; Bertagnoli *et al.*, *Cell Immunol* 133:327-341, 1991; Bertagnoli, *et al.*, *J Immunol* 149:3778-3783, 1992; Bowman *et al.*, *J Immunol* 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or  
15 thymocytes include, without limitation, those described by Kruisbeek and Shevach, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1, pp. 3.12.1-14, John Wiley and Sons, Toronto 1994; and by Schreiber, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan eds. Vol 1 pp. 6.8.1-8, John Wiley and Sons, Toronto 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells  
20 include, without limitation, those described by Bottomly *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto 1991; deVries *et al.*, *J Exp Med* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 336:690-692, 1988; Greenberger *et al.*, *Proc Natl Acad Sci U.S.A.* 80:2931-2938, 1983; Nordan, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.6.1-5, John Wiley and Sons,  
25 Toronto 1991; Smith *et al.*, *Proc Natl Acad Sci U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, *et al.* In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto 1991; Ciarletta, *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto 1991.

30 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and

cytokine production) include, without limitation, those described in: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds., Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 6, Chapter 7); Weinberger *et al.*, *Proc Natl Acad Sci USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur J Immunol* 11:405-411, 1981; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988.

### Immune Stimulating or Suppressing Activity

A GENX protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* species., malaria species. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response.

The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or energy  
5 in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon re-exposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without  
10 limitation B lymphocyte antigen functions (such as, for example, B7), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells,  
15 followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding  
20 of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to energize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte  
25 antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples  
30 of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the



immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc Natl Acad Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and auto-antibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of auto-antibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the

patient. Another method of enhancing anti-vital immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor

specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bowman *et al.*, *J Virology* 61:1992-1998; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *Cell Immunol* 133:327-341, 1991; Brown *et al.*, *J Immunol* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J Immunol* 144:3028-3033, 1990; and Mond and Brunswick In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, (eds.) Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *J Immunol* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery *et al.*, *J Immunol* 134:536-544, 1995; Inaba *et al.*, *J Exp Med* 173:549-559, 1991; Macatonia *et al.*, *J Immunol* 154:5071-5079, 1995; Porgador *et al.*, *J Exp Med* 182:255-260, 1995; Nair *et al.*, *J Virol* 67:4062-4069, 1993; Huang *et al.*, *Science* 264:961-965, 1994; Macatonia *et al.*, *J Exp Med* 169:1255-1264, 1989; Bhardwaj *et al.*, *J Clin Investig* 94:797-807, 1994; and Inaba *et al.*, *J Exp Med* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz *et al.*, *Cytometry* 13:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res* 53:1945-1951, 1993; Itoh *et al.*, *Cell* 66:233-243, 1991; Zacharchuk, *J Immunol* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-897, 1993; Gorczyca *et al.*, *Internat J Oncol* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica *et al.*, *Blood* 84:111-117, 1994; Fine *et al.*, *Cell Immunol* 155: 111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc Nat Acad Sci USA* 88:7548-7551, 1991.

#### **Hematopoiesis Regulating Activity**

A GENX protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (*i.e.*, in conjunction with bone marrow

transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

5        Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson *et al.* *Cellular Biology* 15:141-151, 1995; Keller *et al.*, *Mol. Cell.*  
10 *Biol.* 13:473-486, 1993; McClanahan *et al.*, *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama *et al.*,  
15 *Proc Natl Acad Sci USA* 89:5907-5911, 1992; McNiece and Briddeli, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben *et al.*, *Exp Hematol* 22:353-359, 1994; Ploemacher, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Spoonceret *et al.*, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp.  
20 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Sutherland, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

#### **Tissue Growth Activity**

A GENX protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for  
25 wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation  
30 employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation

induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein

may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, EPIDERMAL WOUND HEALING, pp. 71-112 (Maibach and Rovee, eds.), Year Book Medical

Publishers, Inc., Chicago, as modified by Eaglstein and Menz, *J. Invest. Dermatol* 71:382-84 (1978).

#### **Activin/Inhibin Activity**

5 A GENX protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-b group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

20 Assays for activin/inhibin activity include, without limitation, those described in: Vale *et al.*, *Endocrinology* 91:562-572, 1972; Ling *et al.*, *Nature* 321:779-782, 1986; Vale *et al.*, *Nature* 321:776-779, 1986; Mason *et al.*, *Nature* 318:659-663, 1985; Forage *et al.*, *Proc Natl Acad Sci USA* 83:3091-3095, 1986.

#### **Chemotactic/Chemokinetic Activity**

25 A protein of the present invention may have chemotactic or chemokinetic activity (*e.g.*, act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example,

30



attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by following methods:

10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Coligan *et al.*,  
15 eds. (Chapter 6.12, MEASUREMENT OF ALPHA AND BETA CHEMOKINES 6.12.1-6.12.28); Taub *et al. J Clin Invest* 95:1370-1376, 1995; Lind *et al. APMIS* 103:140-146, 1995; Muller *et al., Eur J Immunol* 25: 1744-1748; Gruber *et al. J Immunol* 152:5860-5867, 1994; Johnston *et al., J Immunol* 153: 1762-1768, 1994.

#### **Hemostatic and Thrombolytic Activity**

20 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for  
25 treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those  
30 described in: Linet *et al., J. Clin. Pharmacol.* 26:131-140, 1986; Burdick *et al., Thrombosis Res.*

45:413-419, 1987; Humphrey *et al.*, *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

### Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor  
5 ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell—cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation,  
10 antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

15 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan, *et al.*, Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions  
20 7.28.1-7.28.22), Takai *et al.*, *Proc Natl Acad Sci USA* 84:6864-6868, 1987; Bierer *et al.*, *J. Exp. Med.* 168:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* 169:149-160 1989; Stoltenborg *et al.*, *J Immunol Methods* 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995.

### Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The  
25 anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell—cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins  
30 exhibiting such activities can be used to treat inflammatory conditions including chronic or acute

conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

#### **Tumor Inhibition Activity**

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

#### **Other Activities**

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting

deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Neural disorders in general include Parkinson's disease, Alzheimer's disease, Huntington's disease, multiple sclerosis, amyotrophic lateral sclerosis (ALS), peripheral neuropathy, tumors of the nervous system, exposure to neurotoxins, acute brain injury, peripheral nerve trauma or injury, and other neuropathies, epilepsy, and/or tremors.

## **10 EQUIVALENTS**

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that particular novel compositions and methods involving nucleic acids, polypeptides, antibodies, detection and treatment have been described. Although these particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made as a matter of routine for a person of ordinary skill in the art to the invention without departing from the spirit and scope of the invention as defined by the claims. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

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Table 1

ORF#	Internal Identification Number	Protein similarity	Protein domain	Protein Classification	Cells or Tissues in which Gene is Expressed
1	13076366 (1, 2)	Novel Protein sim. GBank gij4691395[emb]CAB41562.1] - (AL049727) putative large secreted protein [Streptomyces coelicolor]		UNCLASSIFIED	264636
2	80248091 (3, 4)	Novel Protein sim. GBank gij2829508[sp]P71559[SUCC_MYCTU - SUCCINYL-COA SYNTHETASE BETA CHAIN (SCS-BETA)]	Contains protein domain (PF00549) - CoA-ligases	UNCLASSIFIED	264907, 264600, 264602, 264762, 264769, 264689, 264638, 264567
3	80415924 (5, 6)			UNCLASSIFIED	264910, 264604, 264634, 264905, 264636, 264691, 264907, 264692, 264629
4	82018837 (7, 8)			UNCLASSIFIED	264908, 264909, 264780, 264628, 264635
5	79970035 (9, 10)			UNCLASSIFIED	22279002, 264563
6	79842462 (11, 12)		Contains protein domain (PF00127) - Copper binding proteins, plastocyanin/azurin family	UNCLASSIFIED	264908
7	85515576 (13, 14)	Novel Protein sim. GBank gij4415926[sp]AAD20157] - (AC006282) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	20281099, 35695052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 265009, 264910, 264595, 264596, 264758, 264603, 264604, 264760, 264762, 264683, 264766, 264767, 264689, 35695917, 264690, 264692, 264693, 33657109, 264628, 264629, 35696423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264566, 264486
8	56924278 (15, 16)	Novel Protein sim. GBank gij585562[sp]Q06458[NIRB_KLEPN - NITRITE REDUCTASE (NAD(P)H) LARGE SUBUNIT]		reductase	264907
9	79394457 (17, 18)			UNCLASSIFIED	265007, 265019, 263972
10	79556459 (19, 20)			UNCLASSIFIED	264906
11	20414027 (21, 22)			UNCLASSIFIED	264605
12	94141210 (23, 24)	Novel Protein sim. GBank gij3878145[emb]CAA99871] - (Z75543) similar to potassium channel protein [Caenorhabditis elegans]		misc_channel	264259, 265007, 83373044
13	20750551 (25, 26)			UNCLASSIFIED	264556, 264557, 264564
14	95105114 (27, 28)	Novel Protein sim. GBank gij2832781[emb]CAA12645] - (AJ225805) inward potassium channel alpha subunit [Egeria densa]	Contains protein domain (PF00023) - Ank repeat	potassium_channel	35696286, 35696052, 264510, 35695917, 264691, 264628, 35696423, 264555, 264558, 264559, 83373044
15	20458307 (29, 30)	Novel Protein sim. GBank gij1710791[sp]Q10234[RT05_SCHPO - PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S5]	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	264604
16	20760356 (31, 32)				264555

17	20292744 (33, 34)	Novel Protein sim. GBank gi 1174884 sp P44391 URE1_HAEIN - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	Contains protein domain (PF00449) - Urease	264800	
18	80246804 (35, 36)	Novel Protein sim. GBank gi 2281102 (AC002333) - SF16 Isolog [Arabidopsis thaliana]		29331827, 264555, 264557, 264638, 264558	
19	80076624 (37, 38)		UNCLASSIFIED	22278996, 264907, 264910, 264600, 264693	
20	20724558 (39, 40)	Novel Protein sim. GBank gi 2506112 sp P43672 UUP_ECOLI - ABC TRANSPORTER ATP-BINDING PROTEIN UUP	transport	264602	
21	80417554 (41, 42)	Novel Protein sim. GBank gi 1730203 sp P50442 GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)	UNCLASSIFIED	22278995, 264906, 265008, 265010, 265011, 264602, 264605, 264766, 264688, 21908784, 264691, 18108376, 264636, 18108387, 264486	
22	11705858 (43, 44)			264685	
23	80419176 (45, 46)	Novel Protein sim. GBank gi 1677329 emb CAB07077  - (Z92771) tadE25 [Mycobacterium tuberculosis]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	264488, 264907, 264909, 264600, 264602, 264603, 264605, 264682, 264766, 32833986, 264636, 264486	
24	20291697 (47, 48)			264600	
25	80253774 (49, 50)			264593	
26	80255394 (51, 52)		UNCLASSIFIED	22278996, 56182435, 285018, 264568	
27	80235795 (53, 54)	Novel Protein sim. GBank gi 480369 emb CAB42783.1  - (AL049841) putative 30S ribosomal protein S14 [Streptomyces coelicolor]	Contains protein domain (PF00253) - Ribosomal protein S14p/S29e	18108370, 35696423, 264635, 264555	
28	79483581 (55, 56)		UNCLASSIFIED	264638	
29	82448765 (57, 58)	Novel Protein sim. GBank gi 3122280 sp O08333 K8PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)	Contains protein domain (PF00365) - Phosphofructokinase	264601, 264762, 264766, 264769, 264638	
30	78195333 (59, 60)		UNCLASSIFIED	264908, 265019, 264687, 21906764,	
31	19848158 (61, 62)		UNCLASSIFIED	21906766	
32	82448495 (63, 64)	Novel Protein sim. GBank gi 3580504 (AF027770) - unknown [Mycobacterium smegmatis]	UNCLASSIFIED	264534	
33	79582628 (65, 66)	Novel Protein sim. GBank gi 2129003 prj G64507 - hypothetical protein MJ1665 - Methanococcus jannaschii	UNCLASSIFIED	264689	
34	87487657 (67, 68)		UNCLASSIFIED	264687	
35	95005170 (69, 70)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	60432289, 264600, 264602, 264760, 18108357, 264768, 265020, 264691	
36	19642042 (71, 72)	Novel Protein sim. GBank gi 3287739 sp P73538 BIOB_SYNY3 - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)	UNCLASSIFIED	264689, 264558, 264639	
37	20369215 (73, 74)	Novel Protein sim. GBank gi 2313134 gb AAD07126.1  - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26695]	synthase	264566	
			dehydrogenase	264603	

38	20466334 (75, 76)	Novel Protein sim. GBank gi 3805970 emb CAA06231  - (A004933) periplasmic nitrate reductase, large subunit [Rhodospseudomonas sp.]		reductase	264605
39	94300715 (77, 78)	Novel Protein sim. GBank gi 1929449 (L63543) - endodermis [Xenopus laevis]	Contains protein domain (PF00207) - Alpha-2-macroglobulin family	complement	264905, 264906, 264907, 66712502, 264908, 264909, 264511, 265009, 264910, 55812038, 264758, 265011, 264762, 264882, 264763, 264784, 264766, 265022, 264893, 264628, 264631, 264634, 264635, 264555, 264638, 18108381, 264558, 18108385, 264482
40	20635625 (79, 80)			UNCLASSIFIED	264592
41	80023287 (81, 82)	Novel Protein sim. GBank gi 854065 emb CAA583371 - (X83413) U88 [Human herpesvirus 6]			264591, 35695917
42	20724566 (83, 84)			UNCLASSIFIED	264602
43	20467069 (85, 86)	Novel Protein sim. GBank gi 3820584 (AF086791) - carbamoylphosphate synthetase large subunit [Zymomonas mobilis]		synthase	264605
44	13085297 (87, 88)	Novel Protein sim. GBank gi 2494764 sp Q50729 GUAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)	Contains protein domain (PF00958) - GMP synthase C terminal domain	synthase	264769, 264636
45	39384711 (89, 90)	Novel Protein sim. GBank gi 1881738 (U89688) - myosin-I binding protein Acan125 [Acanthamoeba castellanii]		UNCLASSIFIED	264769, 264510, 264508
46	95003398 (91, 92)			ngl	264566
47	11698624 (93, 94)			UNCLASSIFIED	264689
48	79407218 (95, 96)				18108385, 264635, 264828
49	21659844 (97, 98)			UNCLASSIFIED	264603
50	80503996 (99, 100)				264508, 264603, 264769, 264689, 264636, 264558, 264486
51	80255569 (101, 102)	Novel Protein sim. GBank gi 3411177 (AF076240) - MocC [Rhizobium leguminosarum bv. viciae]		UNCLASSIFIED	264593, 18108387
52	79208528 (103, 104)	Novel Protein sim. GBank gi 3914992 sp Q26264 SM41 - HEMPU - 41 KD SPICULE MATRIX PROTEIN PRECURSOR (HSM41) (HPSMC)		struct	264634
53	36996970 (105, 106)	Novel Protein sim. GBank gi 3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]		UNCLASSIFIED	264762
54	79570897 (107, 108)			UNCLASSIFIED	264630, 264909, 264766
55	80202703 (109, 110)	Novel Protein sim. GBank gi 1633572 (U52064) - Herpesvirus salmomi ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]			29331824, 264102, 265018, 18108376
56	8758408 (111, 112)	Novel Protein sim. GBank gi 4321580 gb AA015785  - (AF050114) alginate lyase [Pseudomonas sp. W7]			284604
57	11223386 (113, 114)		Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264557

58	91227506 (115, 116)	Novel Protein sim. GBank gll172920jgb AAD45816.1 AF06194 - (AF061943) protease- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00009) - Eukaryotic protein kinase domain	kinase	56182575, 264259, 60432049, 35896052, 66712502, 264909, 265008, 265010, 265011, 264681, 29148784, 35895917, 60170615, 264691, 264692, 264693, 18108374, 35896423, 56182323, 60432113 264600, 264689, 264638
59	80077371 (117, 118)	Novel Protein sim. GBank gll172920jgb P45830 RFE_MYCLE - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N- ACETYLGLUCOSAMINYL TRANSFERASE	Contains protein domain (PF00953) - Glycosyl transferase	transferase	
60	12958341 (119, 120)				
61	80426606 (121, 122)	Novel Protein sim. GBank gll1710216 (U79260) - unknown [Homo sapiens]		glycoprotein	264689 264786
62	13504866 (123, 124)				264630
63	18474553 (125, 126)			UNCLASSIFIED	265019
64	20724578 (127, 128)	Novel Protein sim. GBank gll420945 pir A47041 - transposase homolog (insertion element ISAE1) - Alcaligenes eutrophus		UNCLASSIFIED	264602
65	79326308 (129, 130)	Novel Protein sim. GBank gll3122312 sp O06134 KPYK_MYCTU - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	kinase	264563
66	46854384 (131, 132)	Novel Protein sim. GBank gll3928723 emb CAA2219  - (AL034355) putative ABC transporter [Streptomyces coelicolor]		transport	22278996, 264558
67	78952543 (133, 134)	Novel Protein sim. GBank gll231985 sp P30234 DHA_MYCTU - ALANINE DEHYDROGENASE (40 KD ANTIGEN)		dehydrogenase	265021
68	79817382 (135, 136)				
69	79841764 (137, 138)				264909
70	79871329 (139, 140)			UNCLASSIFIED	264908
71	65897456 (141, 142)				264906, 264908
72	87734877 (143, 144)	Novel Protein sim. GBank gll4415926 gb AAD20157  - (AC006282) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264602, 265021
73	80025241 (145, 146)			UNCLASSIFIED	264488, 264905, 264906, 264907, 264908, 264511, 265008, 264910, 264758, 87168474, 264682, 264766, 264686, 264689, 35895917, 265021, 60170615, 264691, 33557023, 264692, 264693, 264629, 264631, 264639, 22279000
74	20377410 (147, 148)			UNCLASSIFIED	60424179, 264508, 264908, 265007, 264603, 264687, 264689, 264692, 18108387
75	11819032 (149, 150)	Novel Protein sim. GBank gll283509 emb CAA16914  - (AL021787) vacuolar protein sorting [Schizosaccharomyces pombe]		UNCLASSIFIED	264605 264689
76	95105303 (151, 152)	Novel Protein sim. GBank gll4468811 emb CAB38212  - (AL035601) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	83373044, 264908, 264557
77	10144718 (153, 154)	Novel Protein sim. GBank gll854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264563
78	8758256 (155, 156)			UNCLASSIFIED	264604



79	94140190 (157, 158)	Novel Protein sim. GBank gij5689453dbj BAA83010.1  - (AB028981) KIAA1058 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain	35696286, 22278998, 29331822, 29331824, 29331825, 29331827, 284905, 284906, 284907, 66712502, 284908, 284909, 285008, 285009, 284910, 60170831, 55812038, 33109954, 265017, 265018, 284288, 284768, 56181562, 21906765, 21906769, 29148784, 265020, 284690, 284691, 284692, 284693, 60431528, 35696423, 284631, 284632, 284634, 284636, 284639, 83373044, 284564, 284586, 284587
80	82314840 (159, 160)		UNCLASSIFIED	284769, 284601, 265006, 284910, 284604, 284605, 284634, 284835, 284905, 284782, 284637, 264592, 284628, 284907, 284691, 284908, 284587, 284909, 284766
81	20467247 (161, 162)	Novel Protein sim. GBank gij1723442 sp Q10258 YD2A_SCHPO - HYPOTHETICAL 69.0 KD PROTEIN C56F8.10 IN CHROMOSOME I	reductase	284605
82	16331388 (163, 164)	Novel Protein sim. GBank gij2895866 (AF045770) - methylmalonate semi-aldehyde dehydrogenase [Oryza saliva]	dehydrogenase	284587
83	94741180 (165, 166)	Novel Protein sim. GBank gij3402673 (AC004697) - unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	284488, 284508, 284509, 284905, 284908, 284909, 284511, 284591, 284593, 284594, 284595, 284596, 284758, 284603, 284760, 284681, 18108351, 284762, 284682, 284784, 284684, 284766, 284686, 284632, 284637, 284537, 284638, 284639, 18108385, 284566
84	80355375 (167, 169)	Novel Protein sim. GBank gij1173354 sp P45380 SAT1_RAT - SULFATE ANION TRANSPORTER 1 (CANALICULAR SULFATE TRANSPORTER) (SULFATE/CARBONATE ANTI-PORTER)	transport	284508, 284906, 284907, 284908, 284909, 284910, 284760, 284763, 284764, 284765, 284768, 284769, 35695855, 284636, 284637
85	80499600 (169, 170)	Novel Protein sim. GBank gij2120998 pir S70682 - glycosyltransferase homolog - Bordetella pertussis (AL021897) hypothetical protein Rv1112 [Mycobacterium tuberculosis]	transferase	284605, 284762, 284687, 284769, 18108374, 284636, 284485
86	39559043 (171, 172)	Novel Protein sim. GBank gij3256023 emb CAA17228.1  - (AL021897) hypothetical protein Rv1112 [Mycobacterium tuberculosis]		284910
87	13856808 (173, 174)		UNCLASSIFIED	284093

88	95344718 (175, 176)	Novel Protein sim. GBank gj1559703[dbj BA07552] - (D38549) ha1025 is new [Homo sapiens]			52644507, 52646365, 18108398, 65274572, 56182575, 56994075, 35896286, 22278997, 22278998, 22278999, 264092, 264093, 264094, 264095, 264259, 29331822, 29331824, 56182181, 66714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35896052, 33656970, 264105, 264508, 264905, 264906, 264907, 264908, 29331830, 68712502, 52644045, 56182435, 265007, 265009, 264910, 60170831, 264592, 60431735, 60433358, 33657402, 264757, 60433438, 55812038, 264758, 21906754, 52646317, 33109954, 52644298, 87168474, 265011, 87168559, 264601, 265017, 265018, 264604, 265019, 264448, 264369, 264288, 264766, 52644229, 21906786, 21906787, 21906768, 21906769, 55811957, 35895917, 265020, 265021, 265022, 60170815, 52644150, 33657023, 65274620, 33657109, 27486261, 27486264, 33657349, 35895763, 264628, 263972, 18108374, 55810764, 35696423, 55811576, 66274781, 35895855, 60431850, 264636, 52644332, 58182323, 60170394, 83373044, 18108385, 18108387, 18108388, 56526486, 87168518, 60432113, 22279000, 22279002, 264482, 264564, 264486, 264600
89	80077389 (177, 178)	Novel Protein sim. GBank gj11710383[sp P46352 RIPX_BACSU - PROBABLE INTEGRASE/RECOMBINASE RIPX			
90	82115999 (178, 180)	Novel Protein sim. GBank gj12499891[sp P78403 VEGQ_ECOLI - PUTATIVE PROTEASE IN BAER-OGRK INTERGENIC REGION	UNCLASSIFIED	protease	264760 265006
91	78906950 (181, 182)	Novel Protein sim. GBank gj13367754[emb CAA20079] - (AL031155) hypothetical protein SC3A7.16c [Streptomyces coelicolor]	UNCLASSIFIED		264691
92	79554871 (183, 184)	Novel Protein sim. GBank gj2885095 (AF011337) - putative E1-E2 ATPase [Mus musculus]			
93	80496778 (185, 186)	Novel Protein sim. GBank gj1171919[sp P46920 OPUA_BACSU - GLYCINE BETAINES TRANSPORT ATP-BINDING PROTEIN OPUA	ATPase-associated		264907, 264908, 264910, 265008, 264605, 264769
94	79646649 (187, 188)		Contains protein domain (PF00571) - CBS domain		264906
95	11090238 (189, 190)				264594

98	94322125 (191, 192)	Novel Protein sim. GBank gj4589560[d]BAA76802.1] - (AB023175) KIA0958 protein [Homo sapiens]	UNCLASSIFIED	22278995, 22278998, 264259, 29331822, 29331826, 35896052, 28146499, 264509, 284906, 264907, 264908, 264909, 265007, 265008, 264910, 265009, 264593, 265010, 265017, 264604, 265019, 18108351, 264288, 264766, 264768, 264769, 21906765, 21906767, 21906769, 265020, 264892, 33657182, 35695763, 264628, 264629, 18108379, 264631, 264636, 18108381, 264559, 18108382, 83373044, 22278002, 264508
97	79605200 (193, 194)	Novel Protein sim. GBank gj4583559[emb]CAB40388.1] - (AJ005255) OxyR [Erwinia chrysanthemi]	UNCLASSIFIED	
98	79427000 (195, 196)	Novel Protein sim. GBank gj1001693[d]BAA10430] - (D84002) hypothetical protein [Synecocystis sp.]	UNCLASSIFIED	264909
99	20466524 (197, 198)	Novel Protein sim. GBank gj1169479[sp]P43925[EF]G_HAEIN - ELONGATION FACTOR G (EF-G)	UNCLASSIFIED	264805
100	79640113 (199, 200)	Novel Protein sim. GBank gj480897[pir]S37485 - gene msg1 protein - mouse	UNCLASSIFIED	264693
101	80203298 (201, 202)	Novel Protein sim. GBank gj2894166[emb]CAA11773.1] - (AJ223996) PCZA361.18 [Amycolatopsis orientalis]	UNCLASSIFIED	265020, 264102, 263972
102	20467259 (203, 204)	Novel Protein sim. GBank	synthase	264605
103	20466368 (205, 206)	Novel Protein sim. GBank gj1731040[sp]P54509[YQH] - BACSU - HYPOTHETICAL HELICASE IN SINI-GCVT INTERGENIC REGION	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	264605
104	80247572 (207, 208)	Novel Protein sim. GBank gj1854063[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	264591, 264595, 264602
105	79605206 (209, 210)	Novel Protein sim. GBank gj11685117 [U70770] - furrowed [Drosophila melanogaster]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	264508
106	28382058 (211, 212)	Novel Protein sim. GBank gj1705505[sp]P54729[BS4] - MOUSE - BS4 PROTEIN	Contains protein domain (PF00627) - UBA domain	264511, 265009
107	80057791 (213, 214)	Novel Protein sim. GBank gj4887229[gb]AAD3244.1[AF150755] - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	ATPase-associated	29331824, 264591, 21906754, 265019
108	80237936 (215, 216)	Novel Protein sim. GBank gj263577[emb]CAB15264] - (Z99120) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis]	transport	18108374, 35695917, 22278996, 264113, 264600, 264602, 264603, 265017, 264910, 264906, 264636, 264766
109	95194148 (217, 218)	Novel Protein sim. GBank gj233079[emb]CAB11265] - (Z98601) carboxypeptidase 6 precursor [Schizosaccharomyces pombe]	UNCLASSIFIED	264758, 264603, 264630, 264636, 264637
110	79582823 (219, 220)			264687
111	39565458 (221, 222)			264564
112	79856038 (223, 224)		UNCLASSIFIED	264908
113	17959439 (225, 226)		UNCLASSIFIED	265007
114	80502101 (227, 228)		UNCLASSIFIED	264769

115	80251003 (229, 230)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	52645156, 52645080, 33656970, 264592, 21906754, 27486264, 18108378, 35698423, 264635, 52644332, 18108382
116	81286888 (231, 232)				264905, 264906, 264907, 264908, 264909, 264910, 264758, 265010, 264763, 264682, 264764, 264766, 264685, 264686, 264768, 264769, 33657023, 264893, 33857109, 264628, 18108374, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 56526488, 264555, 264566
117	79636695 (233, 234)		Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	264639, 264693
118	80222170 (235, 236)				263974
119	91013071 (237, 238)	Novel Protein sim. GBank gij732526 (U2327) - alpha2(IV) collagen [Caenorhabditis elegans]		UNCLASSIFIED	22278996, 29331824, 60432289, 265007, 60433438, 264603, 264605, 18108351, 264769, 264688, 265020, 264534, 27486261, 264558, 83373044, 18108385, 264564
120	8756481 (239, 240)	Novel Protein sim. GBank gij2131219iprj[S50157] - cyclin-dependent kinase chain SRB10 - yeast (Saccharomyces cerevisiae)		kinase	264603
121	80028153 (241, 242)				264595
122	20457620 (243, 244)	Novel Protein sim. GBank gij2052147[emb CAB08137] - (294752) ksgA [Mycobacterium tuberculosis]	Contains protein domain (PF00399) - Ribosomal RNA adenine dimethylases	transferase	294605
123	8758278 (245, 246)				264604
124	79104017 (247, 248)	Novel Protein sim. GBank gij2833385sp Q43134 UGST_SORBI - GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR		synthase	18108394, 18108397, 265006, 265007, 265008, 265010, 265011, 18108355, 18108379, 18108380, 18108384
125	87797988 (249, 250)	Novel Protein sim. GBank gij475542 (U09255) - glutamate receptor delta-1 subunit [Rattus norvegicus]	Contains protein domain (PF00080) - Ligand-gated ion channel	misc_channel	264508, 264906, 265009, 264596, 22279002
126	56701283 (251, 252)	Novel Protein sim. GBank gij5102785[emb CAB45200.1] - (AL079308) putative transcriptional regulator [Streptomyces coelicolor]			264511
127	20467267 (253, 254)				
128	80248473 (255, 256)	Novel Protein sim. GBank gij130120sp P23620 PHOB_PSEAE - PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN PHOB	Contains protein domain (PF00072) - Response regulator receiver domain	UNCLASSIFIED - phosphatase	264605, 264907, 264909, 264910, 264600, 264601, 264603, 264605, 18108351, 264693, 264557
129	95280543 (257, 258)	Novel Protein sim. GBank gij2506493sp P38036 YGCB_ECOLI - HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	35696423, 35695855, 264600, 264602, 264603, 264604, 264605, 264508, 264806, 264564, 264628, 264682, 264565, 264683
130	80085583 (259, 260)	Novel Protein sim. GBank gij854055[emb CAA58337] - (X83413) U88 [Human herpesvirus 6]			264634
131	94995022 (261, 262)	Novel Protein sim. GBank gij1076038iprj[S54860] - ABC transporter PstC-2 chain - Mycobacterium tuberculosis	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	18108376, 264769, 29331826, 264689, 22278996, 265021, 264600, 264511, 264601, 264602, 264605, 264905, 264838

132	10837692 (263, 264)	Novel Protein sim. GBank gij1877340[embjCAB07068] - (Z92771) accA3 [Mycobacterium tuberculosis]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	carboxylase	264636 264905, 264689
133	94630883 (265, 266)	Novel Protein sim. GBank gij4585838[embjCAB40932.1] - (AL049630) putative NADH dehydrogenase [Streptomyces coelicolor]		dehydrogenase	264905, 264605, 265021
134	79834860 (267, 268)	Novel Protein sim. GBank gij1460074[embjCAB01049] - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]			264634
135	19885057 (269, 270)	Novel Protein sim. GBank gij2125896[embjCAA73511] - (Y13070) folypolyglutamate synthase [Streptomyces coelicolor]		synthase	264508
136	79846083 (271, 272)	Novel Protein sim. GBank gij2125896[embjCAA73511] - (Y13070) folypolyglutamate synthase [Streptomyces coelicolor]			
137	79819770 (273, 274)				264683, 264685, 264686, 264691, 264692, 264693
138	79635971 (275, 276)	Novel Protein sim. GBank gij5420387[embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	18108374, 18108385, 33657109, 33657182, 265010, 22278998, 265008, 265007, 265008, 265009, 264693
139	86880076 (277, 278)	Novel Protein sim. GBank gij5689912[embjCAB52075.1] - (AL109732) putative mutase [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01817) - Chorismate mutase	dehydrogenase	22278996, 265007, 264910, 60433356, 265010, 264602, 264605, 264768, 264688, 264769, 264693, 32833986, 18108374, 18108387
140	79825759 (279, 280)			UNCLASSIFIED	264908
141	20700094 (281, 282)				264600
142	80028104 (283, 284)	Novel Protein sim. GBank gij3581916[embjCAA20855] - (AL031545) muS family DNA mismatch repair protein [Schizosaccharomyces pombe]		nuclease	264602, 265017
143	11072274 (285, 286)				
144	95009102 (287, 288)	Novel Protein sim. GBank gij3334127[spP97303]BAC2_MOUSE - TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2)		UNCLASSIFIED	264600
145	80027058 (289, 290)	Novel Protein sim. GBank gij3757569[embjCAA21315] - (AL031863) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=66.31; 1-evidence_end [Drosophila melanogaster]			263978, 264600, 264910, 264632, 264508, 264563, 264564, 264591, 264558, 264908, 264629, 264639
146	13085662 (281, 292)	Novel Protein sim. GBank gij140807[epP24536]Y121_BURCE - INSERTION ELEMENT IS402 HYPOTHETICAL 24 KD PROTEIN	Contains protein domain (PF01675) - Transposase		22278996, 264602
147	94320368 (293, 294)	Novel Protein sim. GBank gij2827608[embjCAA16863] - (AL021848) uvrD2 [Mycobacterium tuberculosis]		helicase	264905, 264906, 264909, 264510, 265009, 60433356, 264600, 264601, 264604, 264605, 264687, 264769, 18108365, 65274791, 18108387
148	80248804 (295, 296)	Novel Protein sim. GBank gij2916947[embjCAA17585] - (AL021999) hypothetical protein Rv0986 [Mycobacterium tuberculosis]		transport	265009, 265010, 264600, 264602, 264603, 264604, 264605, 264693, 33657109, 264636

149	80249373 (287, 298)	Novel Protein sim. GBank gi 1723073 sp Q11040 Y081_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.01	Contains protein domain (PF00005) - transport ABC transporter	265010, 264600, 264601, 264603, 264604, 27486265, 264636
150	20294748 (299, 300)	Novel Protein sim. GBank gi 3724125 emb CAA11905  - (AJ224340) maltose phosphorylase [Lactobacillus sanfrancisco]		264600
151	20726398 (301, 302)	Novel Protein sim. GBank gi 729312 sp P07651 DEOB_ECOLI - PHOSPHOPENTOMUTASE (PHOSPHODEOXYRIBOMUTASE)	Contains protein domain (PF01676) - UNCLASSIFIED Metalloenzyme superfamily	264602
152	95002877 (303, 304)	Novel Protein sim. GBank gi 2497952 sp P55667 Y4TM_RHISN - HYPOTHETICAL HYDROLASE/PEPTIDASE Y4TM	peptidase	264602
153	80258665 (305, 306)	Novel Protein sim. GBank gi 3123021 sp Q90508 VT1_FUNHE - VITELLOGENIN 1 PRECURSOR (VTG I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2))	UNCLASSIFIED	264593
154	82305968 (307, 308)	Novel Protein sim. GBank gi 419897 pir JUN0443 - transcription initiation factor sigma homolog hrdB - Streptomyces aureofaciens	Contains protein domain (PF00140) - Sigma-70 factor	264910, 264762, 264691, 264634 264605
155	20429859 (309, 310)	Novel Protein sim. GBank gi 628710 pir J541739 - hypothetical protein - Escherichia coli	UNCLASSIFIED	264565
156	39564742 (311, 312)	Novel Protein sim. GBank gi 3695013 (AF052566) - Cua (Pseudomonas aeruginosa)	Contains protein domain (PF00142) - 4Fe-4S iron sulfur cluster binding proteins, NifH/HrcC family	264691
157	10358887 (313, 314)	Novel Protein sim. GBank gi 1073072 pir J55543 - cnaU protein - Pseudomonas syringae pv. syringae	UNCLASSIFIED	264905
158	79761936 (315, 316)	Novel Protein sim. GBank gi 1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	Contains protein domain (PF00400) - WD domain, G-beta repeat	265008 264605
159	78890376 (317, 318)	Novel Protein sim. GBank gi 5304869 emb CAB46028.1  - (AL031685) dJ963K23.2 (novel protein) [Homo sapiens]	Contains protein domain (PF00327) - Ribosomal protein L30pL7e	22278996, 264600, 264603, 35695917, 32833986, 35696423, 264638
160	11075119 (319, 320)	Novel Protein sim. GBank gi 1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	264112, 264532, 22279002
161	80055007 (321, 322)	Novel Protein sim. GBank gi 1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	UNCLASSIFIED	264639
162	80016371 (323, 324)	Novel Protein sim. GBank gi 1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	UNCLASSIFIED	264605, 264907, 264600
163	11692308 (325, 326)	Novel Protein sim. GBank gi 1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	UNCLASSIFIED	264691
164	80077902 (327, 328)	Novel Protein sim. GBank gi 1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	UNCLASSIFIED	264605, 264486
165	10856067 (329, 330)	Novel Protein sim. GBank gi 1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	UNCLASSIFIED	265010
166	88095003 (331, 332)	Novel Protein sim. GBank gi 1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	UNCLASSIFIED	264600
167	16395460 (333, 334)	Novel Protein sim. GBank gi 1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	UNCLASSIFIED	264556, 264557, 264558, 264559
168	80078362 (335, 336)	Novel Protein sim. GBank gi 1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	UNCLASSIFIED	
169	80239581 (337, 338)	Novel Protein sim. GBank gi 1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	UNCLASSIFIED	

170	78612364 (339, 340)	Novel Protein sim. GBank gij140888[sp]P27847[YIGK_ECOLI - HYPOTHETICAL 15.4 KD PROTEIN IN RECQ-PLDB INTERGENIC REGION (F138)]	Contains protein domain (PF01810) - LysE type translocator		264908 264595, 264604
171	95293073 (341, 342)				
172	37797007 (343, 344)	Novel Protein sim. GBank gij4210905[gjb]AAD12048.1] - (AF045609) AgtG [Sinorhizobium meliloti]	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	264769
173	57529660 (345, 346)	Novel Protein sim. GBank gij132854[sp]P02387[RL2_ECOLI - 50S RIBOSOMAL PROTEIN L2]	Contains protein domain (PF00181) - Ribosomal Proteins L2	ribosomal prot	264769
174	95293078 (347, 348)	Novel Protein sim. GBank gij1881350[djb]BAA19377] - (AB001486) PROBABLE TRANSPORT PROTEIN, SIMILAR TO ANTIBIOTIC TRANSPORT-ASSOCIATED PROTEIN ACTII IN STREPTOMYCES COELICOLOR. [Bacillus subtilis]		transport	264510, 264593, 264602, 264603, 264605, 264762, 264693
175	79756270 (349, 350)	Novel Protein sim. GBank gij207272[emb]CAB08326] - (Z95121) manA [Mycobacterium tuberculosis]	isomerase		264565
176	80066888 (351, 352)	Novel Protein sim. GBank gij1055198 (U40187) - similar to PIR:A41724 chicken LD (limb deformity) gene product and to formin; also P-rich region similar to collagen [Caenorhabditis elegans]	UNCLASSIFIED		264907, 264910, 264681, 264558
177	86684852 (353, 354)	Novel Protein sim. GBank gij2326738[emb]CAB10952] - (Z98288) hypothetical protein Rv1695 [Mycobacterium tuberculosis]	Contains protein domain (PF01513) - Domain of unknown function	UNCLASSIFIED	264768, 60424179, 264687, 264688, 264769, 29331826, 60432289, 18108376, 264689, 18108387, 32833986, 22278996, 265020, 264600, 264601, 264602, 264603, 264604, 264605, 264635, 264762, 264636, 264908, 264564, 264637, 264638, 264486, 60433356, 264768
178	79559526 (355, 356)	Novel Protein sim. GBank gij1906596 (U81788) - kinesin-73 [Drosophila melanogaster]	struct		264693, 33657109, 264635
179	20263112 (357, 358)		UNCLASSIFIED		264563
180	80488958 (359, 360)	Novel Protein sim. GBank gij1169367[sp]P45256[DNAB_HAEIN - REPLICATIVE DNA HELICASE]	helicase		264769
181	79585369 (361, 362)	Novel Protein sim. GBank gij3170615 (AF059485) - DOC4 [Mus musculus]	UNCLASSIFIED		21808767, 264635, 264639, 18108394
182	80577899 (363, 364)		UNCLASSIFIED		264259, 35696052, 56182435, 264511, 265018, 33657109, 264555, 264568
183	11614017 (365, 366)	Novel Protein sim. GBank gij1076627[pir]S54172 - inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco	UNCLASSIFIED		264690
184	10174167 (367, 368)	Novel Protein sim. GBank gij4371280[gjb]AAD18138] - (AC006260) hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED		264510

185	21660822 (369, 370)	Novel Protein sim. GBank gij3008178[emb]CAA18398.1] - (AL022304) putative mma transport regulator [Schizosaccharomyces pombe]		UNCLASSIFIED	264604
186	80070329 (371, 372)	Novel Protein sim. GBank gij2829802[sp]P94408[YCLF_BACSU - HYPOTHETICAL 53.3 KD PROTEIN IN SFP-GERKA INTERGENIC REGION]		transport	264595
187	80186611 (373, 374)	Novel Protein sim. GBank gij3150260[emb]CAA19179] - (AL023634) cydin [Schizosaccharomyces pombe]		UNCLASSIFIED	264369
188	20464942 (375, 376)	Novel Protein sim. GBank gij2145853[pi]j572938 - nix protein - Mycobacterium leprae		kinase	264605
189	82338215 (377, 378)	Novel Protein sim. GBank gij1881244[db]BAA19271] - (AB001488) SIMILAR TO PYRUVATE OXIDASE AND ACETOLACTATE SYNTHASE. [Bacillus subtilis]	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	UNCLASSIFIED	35696032, 264602, 264605, 264762, 264689, 35695917, 18108370, 18108372, 264638, 264565
190	80086821 (379, 380)	Novel Protein sim. GBank gij120226[sp]P28725[FKBP_STROCH - FK506-BINDING PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE)]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	synthase	264563
191	88095012 (381, 382)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]		isomerase	264508, 264604, 264605, 264769, 264555
192	16333379 (383, 384)	Novel Protein sim. GBank gij4980892[gb]AAD35474.1[AE00171] - (AE001718) ABC transporter, ATP-binding protein [Thermotoga maritima]			264567
193	78910127 (385, 386)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]			264908, 264693
194	20464949 (387, 388)	Novel Protein sim. GBank gij4980892[gb]AAD35474.1[AE00171] - (AE001718) ABC transporter, ATP-binding protein [Thermotoga maritima]			264805
195	13518389 (389, 390)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]		transport	264636
196	95005569 (391, 392)	Novel Protein sim. GBank gij3122305[sp]Q27778[K6PF_SCHMA - 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE)]	Contains protein domain (PF00202) - Amino transferases class-III pyridoxal phosphate		264600, 264689, 264638
197	80248665 (393, 394)	Novel Protein sim. GBank gij3122305[sp]Q27778[K6PF_SCHMA - 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE)]	Contains protein domain (PF00365) - Phosphofructokinase		264602, 264682, 264692, 18108374
198	78163635 (395, 396)	Novel Protein sim. GBank gij1781203[emb]CAB06110] - (Z83859) gnd [Mycobacterium tuberculosis]			264636
199	78890715 (397, 398)	Novel Protein sim. GBank gij2642222 (AF030885) - telomere-associated recQ-like helicase [Ustilago maydis]	Contains protein domain (PF00393) - 6-phosphogluconate dehydrogenases		265008
200	79413849 (399, 400)	Novel Protein sim. GBank gij2642222 (AF030885) - telomere-associated recQ-like helicase [Ustilago maydis]		UNCLASSIFIED	264595, 264596
201	86945924 (401, 402)	Novel Protein sim. GBank gij2894379[emb]CAA74911.1] - (Y14573) ring finger protein [Hordeum vulgare]		UNCLASSIFIED	29331826, 265007, 264512, 33657402, 264596, 265017, 18108351, 264682, 264683, 264787, 264629, 55810764, 264634, 264635, 58182323, 80432113, 22279000



202	7958046 (403, 404)	Novel Protein sim. GBank gi231772 sp P30599 CHS1_1 (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 1)	Contains protein domain (PF01644) - synthase Chitin synthase	264600	
203	79843927 (405, 406)	Novel Protein sim. GBank gi1504042 dbj BAA132201 - (D86984) similar to yeast adenylate cyclase (S56776) [Homo sapiens]		22278995, 29331822, 29331825, 29331827, 264906, 21908754, 264683, 21908766, 21908769, 35696423, 264556	
204	79855186 (407, 408)		UNCLASSIFIED	264809	
205	10090583 (409, 410)	Novel Protein sim. GBank gi2633808 emb CAB133101 - (Z99111) similar to hypothetical proteins [Bacillus subtilis]	transport	264909	
206	8758473 (411, 412)		UNCLASSIFIED	264604	
207	20754522 (413, 414)	Novel Protein sim. GBank gi2134381 pir S60678 - polybramo 1 protein - chicken	UNCLASSIFIED	264556	
208	20289281 (415, 416)			264605	
209	80071069 (417, 418)	Novel Protein sim. GBank gi2501040 sp O5814 SYP_MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LIGASE) (PRORS)		264605, 264689	
210	80168800 (419, 420)			264905, 264907, 264909, 264766, 264687, 264691, 264629, 18108374, 264638	
211	80034539 (421, 422)			263978	
212	82442474 (423, 424)	Novel Protein sim. GBank gi15031809 ref NP_005536.1 p SLR - immunoglobulin superfamily containing leucine-rich repeat	UNCLASSIFIED	264508, 264905, 264906, 264907, 264908, 264600, 264762, 264534, 264632, 264634, 264635, 264639, 264486	
213	80249562 (425, 426)	Novel Protein sim. GBank gi3123359 sp O33123 LEU2_MYCLE - 3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)	Contains protein domain (PF00330) - isomerase Aconitase family (aconitate hydratase)	22278996, 264508, 264600, 264602, 264603, 264605, 33657023, 264565, 264486	
214	80079381 (427, 428)	Novel Protein sim. GBank gi116236 sp P19421 CH60_COXBU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (HEAT SHOCK PROTEIN B)	Contains protein domain (PF00118) - eph TCP-1/cpn60 chaperonin family	264600, 264693	
215	14973283 (429, 430)		UNCLASSIFIED	264629	
216	80177716 (431, 432)	Novel Protein sim. GBank gi3417287 (AC002310) - Unknown gene product [Homo sapiens]	Contains protein domain (PF00096) - dna_ma_bind Zinc finger, C2H2 type	264448	
217	79603634 (433, 434)	Novel Protein sim. GBank gi2506924 sp P49754 VP41_HUMAN - VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG (S53)		264508	
218	80258475 (435, 436)	Novel Protein sim. GBank gi1173288 sp P38106 RSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN	mapolymerase	264594	
219	20438797 (437, 438)	Novel Protein sim. GBank gi1781097 emb CAB062311 - (Z83864) gi1B [Mycobacterium tuberculosis]	synthase	264604	
220	13489572 (439, 440)	Novel Protein sim. GBank gi2984703 (AF052427) - unknown [Trypanosoma cruzi]	nucleaseinhib	264689	
221	11287498 (441, 442)	Novel Protein sim. GBank gi4587313 dbj BAA76709.1 - (AB025248) alpha-1,2-mannosidase [Bacillus sp. M-90]	UNCLASSIFIED	264555	

222	79862802 (443, 444)	Novel Protein sim. GBank gij1877268[emb]CAB07049] - (Z92770) hypothetical protein Rv0143c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605, 264769, 35698423
223	83053868 (445, 446)			UNCLASSIFIED	264908, 264907, 264603
224	79557920 (447, 448)			UNCLASSIFIED	264684, 264693
225	79559541 (449, 450)	Novel Protein sim. GBank gij2274851[jb]BAA21515] - (D64159) 3-7 gene product [Homo sapiens]		UNCLASSIFIED	264692
226	79172397 (451, 452)	Novel Protein sim. GBank gij868245 (U29488) - C56C10.7 gene product [Caenorhabditis elegans]		UNCLASSIFIED	22278998, 264112, 33657023, 263981
227	81777186 (453, 454)			UNCLASSIFIED	35695917, 264636, 264907
228	79872285 (455, 456)				264768, 264907, 264908, 264692, 264593, 264639
229	79838266 (457, 458)				264908, 264910
230	11013209 (459, 460)			UNCLASSIFIED	264631
231	20822207 (461, 462)	Novel Protein sim. GBank gij1835114[emb]CAA71733] - (Y10744) homoserine O-acetyltransferase [Leptospira meyeri]			264806, 264600, 264603, 264692
232	80055035 (463, 464)			UNCLASSIFIED	264600, 264603, 264605, 264687, 264769
233	80063054 (465, 466)	Novel Protein sim. GBank gij2642340 (AF032970) - imidazolone propionate hydrolase [Pseudomonas putida]	Contains protein domain (PF00449) - Urease	hydrolase	264604
234	7523998 (467, 468)	Novel Protein sim. GBank gij3510505 (AF030881) - polypeptide [Fugu rubripes]		UNCLASSIFIED	264369
235	80203671 (469, 470)			UNCLASSIFIED	264106
236	78940001 (471, 472)	Novel Protein sim. GBank gij2104609[emb]CAB08805] - (Z95398) PckA [Mycobacterium leprae]		carboxylase	264905
237	11755273 (473, 474)				264681
238	79461401 (475, 476)			UNCLASSIFIED	264639
239	82435190 (477, 478)	Novel Protein sim. GBank gij2495617[sp]Q57252[YDJJ_HAEIN - HYPOTHETICAL PROTEIN H11163	Contains protein domain (PF00037) - 4Fe-4S ferredoxins and related iron-sulfur cluster binding domains.		264908, 265010, 264603, 264762, 264682, 264636, 264638, 264486
240	21635575 (479, 480)	Novel Protein sim. GBank gij3183458[sp]P75796[YLIA_ECOLI - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YLIA		transport	264259, 264769
241	80377307 (481, 482)	Novel Protein sim. GBank gij3875920[emb]CAB0411] - (Z81503) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D65450 comes from this gene; cDNA EST EMBL:D68888 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	264908, 264909, 264784, 264639
242	82148454 (483, 484)			UNCLASSIFIED	264489, 264907, 264908, 264511, 264760, 264784, 264692, 264635, 264637
243	79633207 (485, 486)	Novel Protein sim. GBank gij2624302[emb]CAA15575] - (AL008987) aid [Mycobacterium tuberculosis]		UNCLASSIFIED	264908
244	80248662 (487, 488)	Novel Protein sim. GBank gij2920625 (AF044499) - vgrE protein [Escherichia coli]		dehydrogenase	264600, 264602, 264605, 264769, 264689
245	79863543 (489, 490)			UNCLASSIFIED	264907, 264758
246	79162928 (491, 492)	Novel Protein sim. GBank gij5420387[emb]CAB46678.1] - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01106) - NIT-like domain		264637, 18108381, 18108387, 264565

247	79873185 (493, 494)	Novel Protein sim. GBank gii1639000[embj CAA08648] - (Z85982) argB [Mycobacterium tuberculosis]		kinase	284909, 284691, 35696423, 18108387
248	80488983 (495, 496)	Novel Protein sim. GBank gii168574[spIP24264]ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	35698286, 284907, 284511, 284602, 284788, 284688, 285021, 35695855, 18108385
249	79764645 (497, 498)			UNCLASSIFIED	284907, 284910, 285011, 284782, 284638
250	79519980 (499, 500)				21906768, 284692
251	84359488 (501, 502)			UNCLASSIFIED	52645156, 29331822, 29331824, 52644045, 285018, 21906765, 21906768, 285020, 27486261, 27486265, 35695763, 18108376, 284556, 284559, 284565
252	79737756 (503, 504)	Novel Protein sim. GBank gii3327166[dbj BAA31651] - (AB014576) KIAA0876 protein [Homo sapiens]			284685, 284687, 284632
253	20443124 (505, 506)	Novel Protein sim. GBank gii3036880[embj CAA18513] - (AL022374) putative ATP-dependent DNA helicase [Streptomyces coelicolor]		helicase	284604
254	80027421 (507, 508)	Novel Protein sim. GBank gii3915488[spjO34881]YJMB_BACSU - HYPOTHETICAL SYMPORTER IN COTT-RAPA INTERGENIC REGION		UNCLASSIFIED	284508, 284906, 284602, 284687, 285021, 284486
255	11398315 (509, 510)	Novel Protein sim. GBank gii1665720[dbj BAA04134] - (D17312) diarrheal toxin [Bacillus cereus]		UNCLASSIFIED	284593
256	80028158 (511, 512)	Novel Protein sim. GBank gii465787[spjP34422]YL31_CAEEL - HYPOTHETICAL 86.0 KD PROTEIN F4488.1 IN CHROMOSOME III	Contains protein domain (PF003326) - Prolyl oligopeptidase family	peptidase	284602, 284692
257	20289282 (513, 514)	Novel Protein sim. GBank gii1172039[spjP42315]SCOA_BACSU - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE SUBUNIT A (SUCCINYL COA:3-OXOACID COA-TRANSFERASE) (OXCT A)	Contains protein domain (PF01144) - Coenzyme A transferase	transferase	284605
258	20459464 (515, 516)	Novel Protein sim. GBank gii3127838[embj CAA18902] - (AL023496) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	284604
259	79910152 (517, 518)			collagen	284681, 284686, 284692
260	20379437 (519, 520)			UNCLASSIFIED	284692, 284556
261	20285883 (521, 522)	Novel Protein sim. GBank gii123761[spjP24221]HUTH_STRGR - HISTIDINE AMMONIA-LYASE (HISTIDASE)	Contains protein domain (PF00221) - Phenylalanine and histidine ammonia lyases	UNCLASSIFIED	284600
262	80189317 (523, 524)			UNCLASSIFIED	285017, 284369
263	88095045 (525, 526)	Novel Protein sim. GBank gii3924708[embj CAA84646] - (Z35587) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL: T02089 comes from this gene; cDNA EST EMBL: D76135 comes from this gene; cDNA EST EMBL: D73147 comes from this gene; cDNA EST EMBL: ...		UNCLASSIFIED	284488, 284905, 284806, 284907, 284908, 284909, 284512, 284910, 284758, 284596, 284604, 285019, 284605, 284760, 18108351, 284763, 284764, 284288, 284766, 284768, 284769, 284691, 284692, 284693, 284628, 284634, 284635, 284555, 284636, 284638, 284639
264	87370826 (527, 528)	Novel Protein sim. GBank gii3043734[dbj BAA25531] - (AB011177) KIAA0605 protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	protease	284259, 284908, 21906754, 285018, 285019, 285020

265	95355846 (528, 530)	Novel Protein sim. GBank gll4569624[db][BAA76034.1] - (AB023207) KIAA0990 protein [Homo sapiens]		kinase	264488, 35696286, 29331824, 56182181, 35696052, 264508, 284905, 264908, 284907, 66712502, 264908, 284908, 284511, 284512, 284910, 264592, 264595, 264758, 264596, 55811386, 264600, 285017, 284603, 284604, 264805, 264760, 18108351, 284782, 284681, 264784, 264288, 284788, 264788, 264789, 21906765, 21906767, 21906769, 265020, 284691, 33657023, 33657109, 33657182, 284628, 35696423, 35695855, 284630, 284631, 264632, 264634, 264635, 284636, 284555, 264838, 83373044, 56328486, 87168518, 264564, 264586, 264486, 284600
266	79588075 (531, 532)			UNCLASSIFIED	284828
267	11362222 (533, 534)			UNCLASSIFIED	264687, 264769, 264689
268	78909566 (535, 536)			UNCLASSIFIED	284802
269	80025810 (537, 538)			UNCLASSIFIED	264693
270	84361144 (539, 540)	Novel Protein sim. GBank gll4507367[ref]NP_003182.1pTARS - lhronyl-tRNA synthetase		UNCLASSIFIED	
271	79552301 (541, 542)			UNCLASSIFIED	284909, 264693
272	9674778 (543, 544)	Novel Protein sim. GBank gll4980738[gbl]AAD35331.1(AE00170) glucose-1-phosphate adenylyltransferase [Thermotoga maritima]		synthase	264908
273	12840694 (545, 546)	Novel Protein sim. GBank gll1168224[sp]P44569[5NTD_HAEN - PROBABLE 5' NUCLEOTIDASE PRECURSOR		UNCLASSIFIED	284688
274	38524246 (547, 548)				264564
275	82787041 (549, 550)	Novel Protein sim. GBank gll3253159 (AF005355) - translation initiation factor eIF2C [Oryctolagus cuniculus]		UNCLASSIFIED	284907, 284908, 264909, 264766, 284768, 284691, 264632, 264636
276	86671073 (551, 552)	Novel Protein sim. GBank gll134920[sp]P21997[SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			265008, 60432229
277	80078735 (553, 554)	Novel Protein sim. GBank gll128021[sp]P20984[OBG_BACSU - SPO0B-ASSOCIATED GTP-BINDING PROTEIN		ribosomal prot	284600, 18108387
278	12866947 (555, 556)			UNCLASSIFIED	264689
279	95292718 (557, 558)	Novel Protein sim. GBank gll79839[pir][S03812 - uwrB protein - Micrococcus luteus		nuclease	264508, 264604, 21906764, 284638, 264557, 264404
280	5603617 (559, 560)				284259
281	80249599 (561, 562)	Novel Protein sim. GBank gll3123180[sp]Q18964[YLN2_CAEEL - HYPOTHETICAL 46.2 KO TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II			18108392, 284634, 284555, 284556, 284557, 284558
282	18598682 (563, 564)			UNCLASSIFIED	265019
283	20614211 (565, 566)			UNCLASSIFIED	284555

284	91212160 (567, 568)	Novel Protein sim. GBank gij2428094 (U58632) - acetyl xylan esterase; AxeA [Thermotoga neapolitana]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	UNCLASSIFIED	35696052, 29331828, 264508, 264905, 264600, 264602, 264605, 264682, 264764, 56181562, 21906764, 18108376, 264636, 264559, 18108387
285	8757940 (569, 570)			UNCLASSIFIED	264803
286	80503235 (571, 572)	Novel Protein sim. GBank gij2072674 [embjCAB08305] - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	35696052, 264769, 264638
287	12745521 (573, 574)			UNCLASSIFIED	264689
288	20756502 (575, 576)	Novel Protein sim. GBank gij765323 [bbs]157676 - (S74439) silk fibroin heavy chain (C-terminal) [Bombyx mori]; silk fibroin heavy chain (C-terminal) [Bombyx mori]; mori=silkworms, Peptide Partial, 633 aa [Bombyx mori]		UNCLASSIFIED	264557
289	80043804 (577, 578)	Novel Protein sim. GBank gij1870009 [embjCAB06860] - (Z92539) hypothetical protein Rv1019 [Mycobacterium tuberculosis]	Contains protein domain (PF00440) - Bacterial regulatory proteins, telR family		264593, 264600
290	80430175 (579, 580)			UNCLASSIFIED	264768
291	20747431 (581, 582)	Novel Protein sim. GBank gij2506684 [spP40120] YDCG_ECOLI - 59.4. PROTEIN IN TRG-RIML INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264601
292	80052555 (583, 584)	Novel Protein sim. GBank gij625182 (L39015) - mitochondrial glutamyl-tRNA synthetase [Saccharomyces cerevisiae]		UNCLASSIFIED	264605
293	80062519 (585, 586)	Novel Protein sim. GBank gij1718065 [spP53528] UVRD_MYCLE - PUTATIVE DNA HELICASE II HOMOLOG	helicase		264909, 264605, 284687, 264689, 264692
294	79830303 (587, 588)	Novel Protein sim. GBank gij117422 [spP10040] CRB_DROME - CRUMBS PROTEIN PRECURSOR (95F)	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696052, 264906, 265011, 264628, 55811576
295	79444180 (589, 590)	Novel Protein sim. GBank gij1181619 [dbjBAA11585] - (D82384) a variant of TSC-22 [Gallus gallus]			52644507, 29331822, 264592, 265020, 264639
296	79607076 (591, 592)	Novel Protein sim. GBank gij3649789 [dbjBAA33403] - (AB012228) SecA [Vibrio alginolyticus]		synthase	264508
297	79631297 (593, 594)	Novel Protein sim. GBank gij5689967 [embjCAB52004.1] - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264905, 264687, 264638
298	80418898 (595, 596)			UNCLASSIFIED	264905, 264691, 264639, 264766

299	95293298 (597, 598)	Novel Protein sim. GBank gij1220637[dbj]BAA014771 - (D10627) zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	264488, 263994, 56994075, 22278997, 22278998, 22278999, 20281089, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264906, 264907, 264908, 52644045, 264909, 264511, 265008, 264910, 264595, 264598, 264758, 33657084, 87168559, 265018, 265019, 264784, 264288, 264766, 264687, 56181582, 264769, 21906765, 21906768, 21906769, 33657023, 264692, 33657109, 27486281, 18108370, 264628, 264629, 55811576, 35695855, 264631, 264634, 264635, 264638, 264639, 83373044, 18108387, 87168518, 22278000, 22278002, 264565, 264568, 264567
300	20711340 (599, 600)	Novel Protein sim. GBank gij145922 (M20981) - Iron diclrate transport protein precursor [Escherichia coli]	UNCLASSIFIED	264602
301	13511332 (601, 602)	Novel Protein sim. GBank gij1174661[sp]P44594[GTG]_HAEIN - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)	transport	264687
302	9875260 (603, 604)	Novel Protein sim. GBank gij1174661[sp]P44594[GTG]_HAEIN - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)		264908
303	79574895 (605, 606)	Novel Protein sim. GBank gij67985[pil]HJNVAV - helicase (EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus	helicase	264689
304	20711344 (607, 608)	Novel Protein sim. GBank gij728867[sp]P40602[APG]_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		264602
305	80412520 (609, 610)	Novel Protein sim. GBank gij728867[sp]P40602[APG]_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		264763
306	8515876 (611, 612)	Novel Protein sim. GBank gij7657554[sp]AAB18082.1] - (U73857) hypothetical protein [Escherichia coli]	UNCLASSIFIED	263978
307	80222801 (613, 614)	Novel Protein sim. GBank gij170612[sp]Q10793[RNH2]_MYCTU - PROBABLE RIBONUCLEASE HI (RNASE HI)	UNCLASSIFIED	265010, 21906768, 265020, 18108374, 263977
308	80064305 (615, 616)	Novel Protein sim. GBank gij170612[sp]Q10793[RNH2]_MYCTU - PROBABLE RIBONUCLEASE HI (RNASE HI)	Contains protein domain (PF01351) - Ribonuclease HI	264910, 264600, 264605, 264687, 264689, 264638, 18108387
309	80504138 (617, 618)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		264769
310	80053818 (619, 620)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]	synthase	264603
311	11090658 (621, 622)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]		264602
312	80054347 (623, 624)		UNCLASSIFIED	264566
313	80046168 (625, 626)			264603, 264567

314	87645112 (627, 628)	Novel Protein sim. GBank gj13661583 (AF092175) - Ikaros [Danio rerio]	Contains protein domain (PF00320) - GATA zinc finger	dna_rna_bind	264259, 60432289, 29331828, 264905, 264906, 264908, 264909, 265008, 264910, 60432229, 33657402, 60433438, 33109954, 265011, 265017, 264603, 265018, 264288, 264768, 264682, 35693783, 264628, 264629, 264639, 60170394, 22279002, 264568
315	82356091 (629, 630)	Novel Protein sim. GBank gj11652620dbj[BAA17540] - (D90907) pyridine nucleotide transhydrogenase beta subunit [Synectocystis sp.]			264508, 264600, 264762, 264687, 264768, 52644229, 264769, 264689, 264635, 264636, 264638, 264486
316	79911071 (631, 632)	Novel Protein sim. GBank		UNCLASSIFIED	264693
317	20466944 (633, 634)	Novel Protein sim. GBank gj11182441spP24176[DAPE_ECOLI - SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (SDAP)]		UNCLASSIFIED	264605
318	94141836 (635, 636)	Novel Protein sim. GBank gj14680229gbAAD27583.1[AF118274] DNB-5 [Homo sapiens]	Contains protein domain (PF00526) - Dictyostellium (slime mold) repeats	transport	264908, 264909, 264910, 264593, 264594, 264760, 264288, 264788, 264789, 21908769, 264691, 264693, 264628, 65274791, 264635, 264636, 264638, 83373044, 22279002, 264566
319	17289380 (637, 638)	Novel Protein sim. GBank gj1149693jembj[CAA60220] - (X86499) rbsC [Clostridium perfringens]		transport	265018
320	13527675 (639, 640)	Novel Protein sim. GBank gj12811033jspIO05314[GLGC_MYCTU - GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE)]		synthase	264687
321	84134387 (641, 642)	Novel Protein sim. GBank gj11680716 (U68234) - all-trans-retinoic acid 4-hydroxylase [Danio rerio]		cyto450	264509, 264906, 264907, 264908, 265009, 264596, 264764, 264628, 264634, 264635, 264638, 264639, 83373044, 264567
322	66489053 (643, 644)	Novel Protein sim. GBank gj1160355 (U33058) - UNC-89 [Caenorhabditis elegans]		UNCLASSIFIED	55811150, 264691, 60431528, 55810764
323	94653725 (645, 646)			UNCLASSIFIED	264488, 265009, 264593, 264628, 264635
324	79174383 (647, 648)				264687
325	79862691 (649, 650)			UNCLASSIFIED	264693
326	28774974 (651, 652)			UNCLASSIFIED	264288, 18108385
327	79776267 (653, 654)	Novel Protein sim. GBank gj1451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]			264488, 264905, 264509, 264910
328	80263202 (655, 656)			UNCLASSIFIED	264592
329	10173821 (657, 658)			UNCLASSIFIED	264510
330	86597767 (659, 660)			UNCLASSIFIED	264259, 264908
331	79754888 (661, 662)	Novel Protein sim. GBank gj14191358 (AF087825) - claudin-7 [Mus musculus]		transcriptfactor	264910, 264687, 264688, 264636, 264567
332	80071440 (663, 664)	Novel Protein sim. GBank gj114049jspP19480[AHPF_SALTY - ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F (ALKYL HYDROPEROXIDE REDUCTASE F52A PROTEIN)]		reductase	35696423, 264636, 264638, 264565
333	13009555 (685, 686)				264687

334	80230771 (667, 668)	Novel Protein sim. GBank glj3222228ipj[S32227 - glutamate dehydrogenase (NADP+)] (EC 1.4.1.4) - Corynebacterium glutamicum	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	264805, 264800, 264604, 264486
335	80057028 (668, 670)	Novel Protein sim. GBank glj2193938jemb[CAB09602] - (Z96800) glpQ2 [Mycobacterium tuberculosis]		esterase	264907, 264603, 264693, 18108374, 264638, 18108387
336	80414319 (671, 672)			UNCLASSIFIED	265009, 264766, 264686
337	11090829 (673, 674)				264602
338	95413134 (675, 678)	Novel Protein sim. GBank glj545074jref[NP_006303.1]pSMRT - silencing mediator for retinoid and thyroid hormone receptors	Contains protein domain (PF00249) - Myb-like DNA-binding domain	nuc_recp	264368, 18108397, 22278998, 29331822, 20281099, 29331824, 56182181, 68714117, 29331825, 35696052, 29331828, 264508, 29331825, 35696052, 29331828, 264508, 264509, 264905, 264906, 264807, 264908, 264909, 265008, 265008, 264910, 265008, 264758, 55812038, 65274444, 265011, 87168559, 265017, 265018, 265019, 264760, 55811150, 264681, 264762, 18108351, 264682, 264764, 264765, 264685, 264686, 264768, 52644229, 264689, 55811957, 35895917, 264692, 264693, 264628, 18108370, 18108374, 55811578, 35696423, 35695855, 264635, 264555, 264638, 264556, 264637, 264557, 18108380, 264638, 264558, 264639, 18108381, 83373044, 18108385, 87168518, 60432113
339	11398513 (677, 678)	Novel Protein sim. GBank glj4001713jcbj[BAA35087.1] - (AB015879) DnaK [Porphyrromonas gingivalis]		eph	264593
340	80504149 (679, 680)	Novel Protein sim. GBank glj2842699jsgjQ92353jUBPC_SCHPO - PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE CGG9.08 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)		ubiquitin	264905, 265019, 264769, 18108374
341	11075198 (681, 682)	Novel Protein sim. GBank glj2688580 (AE001166) - conserved hypothetical protein [Borrelia burgdorferi]	Contains protein domain (PF00280) - Trypophan synthase alpha chain	isomerase	264605
342	80054186 (683, 684)	Novel Protein sim. GBank glj1684739jembj[CAA70601] - (Y09452) Yed j hypothetical protein [Pseudomonas syringae]			264603, 264604
343	20466792 (685, 686)				264605
344	80428870 (687, 688)	Novel Protein sim. GBank glj2117279jembj[CAB09104] - (Z95818) hypothetical protein Rv0807 [Mycobacterium tuberculosis]		UNCLASSIFIED	264600, 264605, 264768, 18108370, 18108374, 35695855
345	80258853 (689, 690)	Novel Protein sim. GBank glj3023317jsgjQ48935jAPHA_MYCRA - ACETYL POLYAMINE AMINOHYDROLASE		histone	264593
346	79831058 (691, 692)	Novel Protein sim. GBank glj4239787jembj[CAA75437] - (Y15166) NADP-glutamate dehydrogenase [Pseudomonas aeruginosa]	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	264905



347	79158195 (693, 694)	Novel Protein sim. GBank gi 731675 sp P38795 YHN4_YEAST - HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION		UNCLASSIFIED	265006, 265008, 265010, 265018, 263967, 263981
348	80020208 (695, 696)	Novel Protein sim. GBank gi 1073610 pir S47672 - upgB protein - Escherichia coli		transport	264602, 18108351, 18108387
349	17282112 (697, 698)	Novel Protein sim. GBank gi 3261599 emb CAB009171 - (Z77137) hypothetical protein Rv1277 [Mycobacterium tuberculosis]		nuclease	265007 265009, 264769, 264689, 18108370
350	80502370 (699, 700)	Novel Protein sim. GBank gi 2959387 emb CAA179211 - (AL022117) hypothetical protein [Schizosaccharomyces pombe]		glycoprotein	264769, 264905, 264908
351	80501805 (701, 702)	Novel Protein sim. GBank gi 4416302 gb AAD203071 - (AF105716) copia-type pol polyprotein [Zea mays]		protease	264595
352	11611585 (703, 704)	Novel Protein sim. GBank gi 1174887 sp P42873 URE1_STAXY - UREASE ALPHA SUBUNIT [UREA AMIDOHYDROLASE]	Contains protein domain (PF00449) - Urease	UNCLASSIFIED	264604
353	80081653 (705, 706)	Novel Protein sim. GBank gi 115157 sp P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA		UNCLASSIFIED	264628
354	56626130 (707, 708)	Novel Protein sim. GBank gi 115157 sp P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA	Contains protein domain (PF00072) - Response regulator receiver domain	UNCLASSIFIED	264909, 264595, 264683, 22279002
355	80046344 (709, 710)	Novel Protein sim. GBank gi 115157 sp P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA		transcriptfactor	264909, 264591, 264592
356	80043835 (711, 712)	Novel Protein sim. GBank gi 497637 (J03939) - cytochrome oxidase d subunit I [Escherichia coli]		oxidase	264605
357	80070568 (713, 714)	Novel Protein sim. GBank gi 2290990 (AF060000) - Brg1 [Bordetella pertussis]		UNCLASSIFIED	264768
358	37032756 (715, 716)	Novel Protein sim. GBank gi 3510639 (AF049344) - UDP- GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 [Rattus norvegicus]		UNCLASSIFIED	264604, 264769
359	80501488 (717, 718)	Novel Protein sim. GBank gi 113784 sp P25718 AMY1_ECOLI - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)		UNCLASSIFIED	264594
360	80026748 (719, 720)	Novel Protein sim. GBank gi 113784 sp P25718 AMY1_ECOLI - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)		transferase	22278996, 264259, 29331822, 29331824, 264605, 55811957, 265022
361	80584075 (721, 722)	Novel Protein sim. GBank gi 113784 sp P25718 AMY1_ECOLI - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)		amylase	264688
362	13089485 (723, 724)	Novel Protein sim. GBank gi 2829818 sp P95171 NUOK_MYCTU - NADH DEHYDROGENASE I CHAIN K (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11) (NUO11)			
383	76750145 (725, 726)	Novel Protein sim. GBank gi 2829818 sp P95171 NUOK_MYCTU - NADH DEHYDROGENASE I CHAIN K (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11) (NUO11)	Contains protein domain (PF00420) - NADH-ubiquinone/plastoquinone oxidoreductase chain 4L	dehydrogenase	264568 264769, 264602, 264604, 264508, 264762, 264638, 264486
384	82443593 (727, 728)	Novel Protein sim. GBank gi 2829818 sp P95171 NUOK_MYCTU - NADH DEHYDROGENASE I CHAIN K (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11) (NUO11)			

365	88040288 (729, 730)	Novel Protein sim. GBank gij4929268[gb AAD33924.1] - (AF144237) LOMP protein [Homo sapiens]	Contains protein domain (PF00412) - LIM domain containing proteins	264488, 21906766, 21906767, 55811576, 21906769, 29148629, 22278995, 22278996, 265020, 265022, 264634, 264691, 264593, 33657023, 33657402, 264693, 264639, 264594, 29331824, 264768, 18108365, 29331827, 87168559, 265016, 22278000, 265019, 264482, 264761, 264681, 18108351, 265017, 264757
366	81821638 (731, 732)	Novel Protein sim. GBank gij4503843[re NP_003908.1pG2AD - UNKNOWN]	Contains protein domain (PF01602) - Adaplin N terminal region	60424179, 65274572, 56182575, 22278994, 56994075, 22278998, 264259, 29331822, 29331824, 56182181, 60424269, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264905, 264828, 56182435, 265006, 264512, 265008, 264591, 55812038, 55811386, 285010, 87188559, 265017, 285018, 264804, 265019, 55811150, 264448, 264369, 264288, 264888, 264768, 56181562, 21908768, 21906769, 55811957, 35695917, 265022, 60170815, 33657023, 65274620, 18108365, 263967, 33657109, 33657349, 35695783, 264828, 18108378, 55811576, 65274791, 35695855, 56182323, 83373044, 60432113, 264563, 264564, 264567, 264509
367	95357471 (733, 734)	Novel Protein sim. GBank gij3913029[sp P94967 ALR_MYCSM - ALANINE RACEMASE]	UNCLASSIFIED	264508, 264604, 264605, 264636
370	88090968 (739, 740)	Novel Protein sim. GBank gij3249559 (AF018261) - EH domain binding protein Epsin [Rattus norvegicus]	Contains protein domain (PF01715) - IPP transferase	264805, 264592, 264605, 264766, 264691
371	95292598 (741, 742)	Novel Protein sim. GBank gij2995289[emb CAA18328] - (AL022268) putative IRNA delta(2)-isopentenylpyrophosphate transferase [Streptomyces coelicolor]	transferase	264905, 264908, 264510, 264600, 264601, 264802, 264603, 265018, 264804, 264605, 265021, 264692, 264636, 264584
372	80021107 (743, 744)	Novel Protein sim. GBank gij2506393[sp P31576 FIXX_ECOLI - FERREDOXIN LIKE PROTEIN]		264564
373	79863768 (745, 746)	Novel Protein sim. GBank gij3341640[emb CAA13164] - (AJ231122) z61f [Vibrio cholerae]	UNCLASSIFIED	264909
374	79847568 (747, 748)	Novel Protein sim. GBank gij5456934[gb AAD43716.1] - (AF152322) protocadherin gamma A2 [Homo sapiens]	UNCLASSIFIED	264905, 264806
375	91230181 (749, 750)	Novel Protein sim. GBank gij1805408[dbj BAA08970] - (D50463) homologues to nitrile hydratase region 3'-hypothetical protein P47K of P. chlororaphis [Bacillus subtilis]	cadherin	65274572, 264259, 29331826, 56182435, 60433356, 60433438, 264757, 55812038, 264758, 55811957, 264690, 33657023, 264768
376	80505214 (751, 752)	Novel Protein sim. GBank gij1805408[dbj BAA08970] - (D50463) homologues to nitrile hydratase region 3'-hypothetical protein P47K of P. chlororaphis [Bacillus subtilis]	UNCLASSIFIED	
377	10339083 (753, 754)			264906

376	80056153 (755, 756)	Novel Protein sim. GBank gij1076013[pir]A49930 - carB protein homolog - Mycobacterium bovis (strain BCG) (fragment)	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase [CPSase]	UNCLASSIFIED	265008, 264555
379	80503437 (757, 758)	Novel Protein sim. GBank gij216556[dbj]BAA02174 - (D12651) glucose dehydrogenase [Escherichia coli]	Contains protein domain (PF01011) - PQQ enzyme repeat	dehydrogenase	264789
380	80060937 (759, 760)				264604
381	11769027 (761, 762)			UNCLASSIFIED	264684
382	80054377 (763, 764)				264592
383	83259025 (765, 766)	Novel Protein sim. GBank gij3327136[dbj]BAA31636 - (AB014561) KIAA0661 protein [Homo sapiens]			264595, 265017, 265021, 264638, 87168518, 22279002
384	95314255 (767, 768)			UNCLASSIFIED	264259, 26331822, 60432289, 29331827, 264288, 264766, 263967, 65274791, 35895855, 263981, 83373044, 264567
385	10237678 (769, 770)	Novel Protein sim. GBank gij1073456[pir]S47810 - probable alcohol dehydrogenase (EC 1.1.1.1) - Escherichia coli	Contains protein domain (PF00465) - Iron-containing alcohol dehydrogenases	dehydrogenase	264692
386	79633434 (771, 772)				264906
387	17860637 (773, 774)	Novel Protein sim. GBank gij1460074[emb]CAB01049 - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]	Contains protein domain (PF01841) - Transglutaminase-like superfamily	UNCLASSIFIED	264760
388	87741376 (775, 776)	Novel Protein sim. GBank gij4240169[dbj]BAA74863.1 - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	homeobox	35896286, 264905, 68712502, 60432229, 264593, 60433356, 264688, 264688, 21908765, 264891, 22279000, 264482
389	79316971 (777, 778)			UNCLASSIFIED	18108394, 22278996, 264630, 264556, 22279002
390	80079949 (779, 780)	Novel Protein sim. GBank gij854065[emb]CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264600
391	7657302 (781, 782)				264482
392	79796056 (783, 784)	Novel Protein sim. GBank gij3378523[emb]CAA08867 - (AJ009832) cyclomaltodextrinase glucanotransferase [Thermotoga neapolitana]		UNCLASSIFIED	264508
393	33206031 (785, 786)			synthase	264502, 21906764
394	10104463 (787, 788)				264683
395	80229010 (789, 790)			UNCLASSIFIED	264508, 264563
396	20436224 (791, 792)	Novel Protein sim. GBank gij2677780 (U70327) - unknown [Pareitropus polyacis]	Contains protein domain (PF00047) - strud		264556
397	80417014 (793, 794)	Novel Protein sim. GBank gij4507809[ref]NP_000368.1[pWAS] - Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	Immunoglobulin domain		265007, 265009, 264508, 264556, 264629, 264786
398	91230517 (795, 796)	Novel Protein sim. GBank gij1518458 (U45998) - mitochondrial solute carrier [Onchocerca volvulus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	18108398, 22278995, 22278996, 56994075, 22278999, 264259, 29331824, 29331826, 264905, 264908, 265007, 265008, 265009, 21906754, 33657084, 265017, 264448, 264288, 264768, 21906765, 21906766, 21906767, 265020, 265021, 33657023, 33657109, 264628, 35896423, 35895855, 264952, 18108390, 264587, 18108391

399	60055278 (797, 786)	Novel Protein sim. GBank gl 335809 dbj BAA31995  - (AB015974) glycerol kinase [Pseudomonas tolaasii]	Contains protein domain (PF00370) - Kinase FGGY family of carbohydrate kinases	284592, 264595	
400	94117490 (799, 800)	Novel Protein sim. GBank gl 728835 sp P39192 ALU5_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY IIII	Contains protein domain (PF00560) - cadherin Leucine Rich Repeat	18108394, 56182575, 22278995, 22278997, 22278999, 264259, 28331824, 265006, 265007, 265009, 60432228, 33657402, 21906754, 285010, 285017, 285018, 285019, 18108351, 18108357, 21906765, 285021, 285022, 264691, 264692, 33657023, 18108370, 85274791, 284634, 284636, 60170394, 56182323	
401	11397491 (801, 802)	Novel Protein sim. GBank gl 4928292 gb AAD33527.1 AF13211 - (AF132117) FhuA [Staphylococcus aureus]	transport	284594	
402	95420284 (803, 804)	Novel Protein sim. GBank gl 5689487 dbj BAA83027.1  - (AB028998) KIAA1075 protein [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	65274572, 56182575, 35696286, 22278998, 22278999, 264093, 264259, 28331822, 29331824, 28331825, 28331826, 60432289, 29331827, 28331828, 264906, 264907, 264909, 265006, 264511, 265007, 265008, 264910, 264591, 33657402, 60433356, 60433438, 264596, 21906754, 52644296, 265010, 285011, 87168559, 265017, 265018, 265019, 284681, 18108351, 264682, 264448, 264288, 264684, 264766, 264767, 284686, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 264690, 264693, 85274620, 35695763, 264628, 18108370, 264629, 18108378, 35696423, 55811576, 264635, 264636, 264557, 284639, 18108385, 22279002, 284563, 284564, 284565, 284566, 284768, 284632, 284639, 264563	
403	80438913 (805, 806)		UNCLASSIFIED	264682	
404	11809865 (807, 808)		polymerase	265009, 264682	
405	78471260 (809, 810)	Novel Protein sim. GBank gl 266164 emb CAA15755  - (AL009198) dnaE2 [Mycobacterium tuberculosis]	Contains protein domain (PF00159) - Pancreatic hormone peptides	18108357, 264693	
406	78634172 (811, 812)		UNCLASSIFIED		
407	80478229 (813, 814)		UNCLASSIFIED	264769	
408	80079958 (815, 816)		UNCLASSIFIED	284600	
409	5640527 (817, 818)	Novel Protein sim. GBank gl 3047117 (AF058919) - similar to ATP-dependent RNA helicases [Arabidopsis thaliana]	UNCLASSIFIED helicase	284259	

410	95357496 (819, 820)	Novel Protein sim. GBank gi 475016 dbj BAA06184  - (D29801) Unknown [Mus musculus]		UNCLASSIFIED	264489, 52646365, 52646842, 56181886, 35696286, 52645080, 29331822, 29331824, 56182181, 29331825, 60424289, 35698052, 33656970, 264508, 264509, 264905, 264906, 264907, 264908, 52644045, 264909, 264510, 265007, 264512, 265008, 264910, 33657402, 264758, 52646317, 55811388, 265010, 265011, 265017, 264604, 265018, 55811150, 264782, 264764, 264768, 264687, 264768, 264769, 52644229, 21906768, 265020, 265021, 264534, 52644150, 264892, 33657023, 65274820, 33657109, 33657182, 27486281, 35695763, 264628, 264628, 60431528, 18108376, 263978, 35698423, 35698955, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 56182323, 264559, 60432113, 22279002, 264563, 264565, 264486
411	80501670 (821, 822)			UNCLASSIFIED	264769
412	80241662 (823, 824)				264907, 264910, 263973, 22279002
413	11076446 (825, 826)	Novel Protein sim. GBank gi 3261784 emb CAB08997  - (Z95558) htpX [Mycobacterium tuberculosis]		eph	264605
414	82050554 (827, 828)	Novel Protein sim. GBank gi 129036 sp P20707 OD01_AZOVI - 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (ALPHA-KETOGLUTARATE DEHYDROGENASE)		dehydrogenase	18108374, 264760, 264769, 264602, 264638, 264603, 264909, 264605
415	84453144 (829, 830)	Novel Protein sim. GBank gi 4668350 gb AAD31273.1 AF13202 - (AF132025) rhophilin [Drosophila melanogaster]		UNCLASSIFIED	264908, 87168518
416	80402775 (831, 832)	Novel Protein sim. GBank gi 2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium etli]		kinase	264488, 264600, 264602, 264764, 264636
417	20153787 (833, 834)	Novel Protein sim. GBank gi 1709171 sp P52311 MTX2_XANOR - MODIFICATION METHYLASE XORII (CYTOSINE-SPECIFIC METHYLTRANSFERASE XORII) (M.XORII)	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase		264605
418	94125841 (835, 836)			UNCLASSIFIED	264889, 264693
419	95314273 (837, 838)			collagen	264908, 264910, 264764, 264639
420	37036349 (839, 840)	Novel Protein sim. GBank gi 3261659 emb CAB03751  - (Z81368) hypothetical protein Rv2419c [Mycobacterium tuberculosis]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	phosphatase	264769
421	95292942 (841, 842)	Novel Protein sim. GBank gi 2916942 emb CAA17580  - (AL021999) hypothetical protein Rv0981 [Mycobacterium tuberculosis]	Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase	264906, 264600, 264601, 264603, 264604, 264760, 264769
422	79471293 (843, 844)	Novel Protein sim. GBank gi 231752 sp Q00787 CH61_STRAL - 60 KD CHAPERONIN 1 (PROTEIN CPN60 1) (HSP58)	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	eph	22278996, 264682, 18108376, 18108387
423	79604948 (845, 846)			UNCLASSIFIED	264509

424	78966557 (847, 848)	Novel Protein sim. GBank gi 4826814 ref NP_004977.1 pKTN1 - kinesin 1 (kinesin receptor)			265019	
425	80431450 (849, 850)	Novel Protein sim. GBank gi 1703701 bbs 178462 - KRP5=kinesin-related protein [rats, testes, Peptide Partial, 167 aa]	Contains protein domain (PF00225) - Kinesin motor domain		264909, 265007, 55811388, 264768, 55810764	
426	80064522 (851, 852)	Novel Protein sim. GBank		UNCLASSIFIED	264605, 264559	
427	80057232 (853, 854)	gi 231829 sp P29929 COBN_PSEDE - COBN PROTEIN			264603, 264636	
428	79487788 (855, 856)	Novel Protein sim. GBank gi 81286 pir S22697 - extensin - Volvox carter (fragment)		UNCLASSIFIED	264683	
429	80091252 (857, 858)	Novel Protein sim. GBank gi 1806154 emb CAB06451  - (Z84395) hypothetical protein Rv0688 [Mycobacterium tuberculosis]		UNCLASSIFIED	35698423, 35695763, 35695855, 265017, 264564, 264762	
430	80504192 (859, 860)	Novel Protein sim. GBank gi 1806154 emb CAB06451  - (Z84395) hypothetical protein Rv0688 [Mycobacterium tuberculosis]		reductase	264508, 264905, 264508, 264908, 264809, 265008, 264600, 264887, 264789, 264889, 264636, 264638, 18108385, 264486	
431	20624249 (861, 862)				264566	
432	16525372 (863, 864)				265020	
433	81494303 (865, 866)	Novel Protein sim. GBank gi 3123552 emb CAA18609  - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) Homo sapiens]		UNCLASSIFIED	264907, 264908, 264909, 264910, 264592, 264595, 264758, 264804, 264760, 264782, 264763, 264636, 264637, 22279002	
434	94326323 (867, 868)	Novel Protein sim. GBank gi 2495272 sp Q99626 CDX2_HUMAN - HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3)	Contains protein domain (PF00169) - PH domain	UNCLASSIFIED	55812038, 56182181, 56181562, 28331828, 35696052, 55810784, 55811578, 65274791, 35695855, 60432113, 55811150, 264636, 264768	
435	80502738 (869, 870)	Novel Protein sim. GBank gi 114105 sp P08532 ARAH, ECOLI - L-ARABINOSE TRANSPORT SYSTEM PERMEASE PROTEIN ARAH		transport	264595, 264769	
436	41085953 (871, 872)			UNCLASSIFIED	265020, 22279002	
437	11399281 (873, 874)			UNCLASSIFIED	264593	
438	11773835 (875, 876)			UNCLASSIFIED	264686	
439	80018495 (877, 878)	Novel Protein sim. GBank gi 3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana]			264905, 264600, 264602, 264604	
440	78841062 (879, 880)	Novel Protein sim. GBank gi 2281232 gb AA06535.1  - (AF016427) Contains similarity to Pfam domain: PF00004 (AAA). Score=288.1, E-value=3.7e-77, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00004) - ATPases associated with various cellular activities (AAA)		35696052, 264905, 284908, 264909, 265011, 35698423	
441	20396935 (881, 882)	Novel Protein sim. GBank gi 5639946 gb AA045904.1 AF16132 - (AF161328) histidine kinase CstS [Corynebacterium diphtheriae]			264805	
442	85281058 (883, 884)	Novel Protein sim. GBank gi 1184780 (U46068) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 264809	
443	82456427 (885, 886)	Novel Protein sim. GBank gi 5689893 emb CAB52056.1  - (AL109732) putative ATP-binding RNA helicase [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	35696052, 264508, 264908, 264512, 264604, 264762, 264769, 264889, 264636	
444	11395897 (887, 888)	Novel Protein sim. GBank gi 1783249 dbj BAA11726  - (D83026) homologous to citrate-sodium symport (citrate transporters); hypothetical [Bacillus subtilis]		UNCLASSIFIED	264591	

445	79552709 (889, 890)	Novel Protein sim. GBank gij5531272[embjCAB50897.1] - (AJ243800) WSC4 homologue [Kuyveromyces lactis]		UNCLASSIFIED	264893
446	79810937 (891, 892)	Novel Protein sim. GBank gij538413 (L36315) - zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type		264509
447	80438888 (893, 894)	Novel Protein sim. GBank gij1542914[embjCAB02185] - (Z80108) fnt [Mycobacterium tuberculosis]	Contains protein domain (PF00551) - Formyl transferase	transcript factor	264768, 55811576
448	80238110 (895, 896)	Novel Protein sim. GBank gij118794[spIP10443]DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		dehydrogenase	264508, 264600, 264603, 264605, 264682, 264769, 18108362, 264634, 18108387
449	20460634 (897, 898)	Novel Protein sim. GBank gij118794[spIP10443]DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	264605, 264559
450	94631210 (899, 900)	Novel Protein sim. GBank gij4589508[dbjBAA76775.1] - (AB023148) KIAA0931 protein [Homo sapiens]	Contains protein domain (PF00481) - Protein phosphatase 2C	phosphatase	55274572, 22278998, 29331824, 29331826, 264908, 264910, 264592, 52646317, 265017, 21908767, 55811957, 56528486, 22279002
451	21433609 (901, 902)	Novel Protein sim. GBank gij2850814 (AE001104) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	264486
452	10287278 (903, 904)	Novel Protein sim. GBank gij2493000[spIQ09450]SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-TRANSFERASE)		UNCLASSIFIED	264892
453	52560096 (905, 906)	Novel Protein sim. GBank gij2493000[spIQ09450]SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-TRANSFERASE)		UNCLASSIFIED	264907, 264600
454	39523922 (907, 908)	Novel Protein sim. GBank gij2493000[spIQ09450]SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-TRANSFERASE)		transferase	264603
455	13088692 (909, 910)	Novel Protein sim. GBank gij4468699[embjCAB38153.1] - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]		UNCLASSIFIED	264687
456	79563081 (911, 912)	Novel Protein sim. GBank gij4468699[embjCAB38153.1] - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]		UNCLASSIFIED	264691
457	79831273 (913, 914)	Novel Protein sim. GBank gij3411053 (AF034863) - synaptic scaffolding molecule [Rattus norvegicus]			264805
458	79581227 (915, 916)	Novel Protein sim. GBank gij4506075[refNP_002733.1]pPRKC - protein kinase C, mu	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	kinase	55812038, 265010, 265018, 264681
459	80567359 (917, 918)	Novel Protein sim. GBank gij4506075[refNP_002733.1]pPRKC - protein kinase C, mu	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	22278997, 264259, 29331826, 265018, 264448, 264369, 21908765, 35696423
460	79245880 (919, 920)	Novel Protein sim. GBank gij113158[spIP25516]ACO1_ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDRO-LYASE 1) (ACONITASE 1)		UNCLASSIFIED	264806
461	95287618 (921, 922)	Novel Protein sim. GBank gij1168574[spIP42464]ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	264602, 264605, 264768, 264769, 265021, 33857023, 264559

462	79606589 (923, 924)	Novel Protein sim. GBank gij1346891[sp]P45597[PTF1_XANCP - MULTIPHOSPHORYL TRANSFER PROTEIN (MTP) (CONTAINS: PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I); PHOSPHOCARRIER PROTEIN HPR (PROTEIN H); PTS SYSTEM, FRUCTOSE-SPECIFIC IIA COMPONENT ...	Contains protein domain (PF00391) - PEP-utilizing enzymes	UNCLASSIFIED	264907
463	79796417 (925, 926)	Novel Protein sim. GBank gij854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264905, 264906, 264908, 264909, 264910, 264991, 264995, 265011, 264932, 264935, 264936, 264937, 264938, 264939 264934
464	82340151 (927, 928)			UNCLASSIFIED	265017, 21906764, 265020
465	83005730 (929, 930)	Novel Protein sim. GBank gij5689776[emb]CAB52137.1] - (AJ242832) calpain [Homo sapiens]	Contains protein domain (PF00648) - Calpain family cysteine protease		
466	20460645 (931, 932)	Novel Protein sim. GBank gij1806175[emb]CAB06470] - (Z64395) rpsC [Mycobacterium tuberculosis]	Contains protein domain (PF00417) - Ribosomal protein S3, N-terminal domain.		264605, 264559
467	80409035 (933, 934)	Novel Protein sim. GBank gij548705[sp]P36949[RBSB_BACSU - D-RIBOSE-BINDING PROTEIN PRECURSOR		UNCLASSIFIED	264764
468	52562208 (935, 936)				
469	19520527 (937, 938)	Novel Protein sim. GBank gij2114024[emb]CAB08957] - (Z95558) grcC1 [Mycobacterium tuberculosis]		UNCLASSIFIED	264692
470	80502756 (939, 940)	Novel Protein sim. GBank gij2909459[emb]CAA17347] - (AL021929) cobQ [Mycobacterium tuberculosis]		UNCLASSIFIED	264488
471	17837351 (941, 942)	Novel Protein sim. GBank gij114921[sp]P17447[BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN		synthase	264602, 264769
472	80047458 (943, 944)			transport	265019
473	20558793 (945, 946)	Novel Protein sim. GBank gij862343 (L10908) - Gcap1 gene product [Mus musculus]			264596, 264685, 264557
474	80593365 (947, 948)			UNCLASSIFIED	264369
475	82454665 (949, 950)			UNCLASSIFIED	22278997, 264692, 264288
476	94143857 (951, 952)	Novel Protein sim. GBank gij5453656[ref]NP_006329.1[pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264907, 264908, 264511, 265009, 264762, 264448, 264638, 264638
477	79175833 (953, 954)				65274572, 60432049, 264259, 264508, 52644045, 55812038, 264758, 265011, 264288, 264686, 52644229, 65274791, 264638, 264586
478	79633463 (955, 956)			UNCLASSIFIED	264636
479	80189746 (957, 958)			UNCLASSIFIED	264690, 264693
480	79390729 (959, 960)	Novel Protein sim. GBank gij1127551 (U18939) - orf2 [Batrachococcus baikalensis]	collagen		264686, 35695855, 265008, 264631, 264910, 264632, 264638, 265018, 264369, 264909
481	79624578 (961, 962)			mapolymerase	264369
482	83050611 (963, 964)	Novel Protein sim. GBank gij4083042 (AF068065) - GP900; mucin-like glycoprotein [Cryptosporidium parvum]		UNCLASSIFIED	264693
				UNCLASSIFIED	264909, 264686, 264768, 264693, 55811576, 56182323, 18108385



483	20293306 (865, 866)	Novel Protein sim. GBank gij2104303[emb]CAB08632] - (Z95387) hypothetical protein Rv2610c [Mycobacterium tuberculosis]	Contains protein domain (PF00534) - Glycosyl transferases group 1	264600	
484	11618046 (867, 868)	Novel Protein sim. GBank gij3450883 (AF083334) - fibrin [Antheraea pernyi]		UNCLASSIFIED	264594
485	80181234 (869, 970)	Novel Protein sim. GBank gij5042272[emb]CAB44526.1] - (AL078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]		UNCLASSIFIED	264604
486	80059042 (871, 972)	Novel Protein sim. GBank gij5042272[emb]CAB44526.1] - (AL078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]		dehydrogenase	264604
487	11813338 (873, 974)	Novel Protein sim. GBank gij5724779[gb]AAC53522.2] - (AF012273) rho-type GTPase-activating protein rhoGAPX-1 [Mus musculus]	Contains protein domain (PF00620) - RhoGAP domain		264638
488	91222383 (875, 976)	Novel Protein sim. GBank gij5724779[gb]AAC53522.2] - (AF012273) rho-type GTPase-activating protein rhoGAPX-1 [Mus musculus]			264686, 66714117, 264768, 18108385, 55811576, 265006, 265008, 265009, 265019, 22279002, 264259, 18108370, 264907, 254764, 56182323, 264288, 264693
489	10867710 (877, 978)	Novel Protein sim. GBank gij3882223[gb]BAA34471.1] - (AB018294) KIAA0751 protein [Homo sapiens]	kinase		264639
490	95361124 (879, 980)	Novel Protein sim. GBank gij82091[pt]A25484 - hydroxyproline-rich glycoprotein - tomato (fragment)	collagen		22278996, 29331822, 29331828, 264107, 264909, 264110, 265009, 264592, 264993, 60433356, 264288, 264693, 263974, 263976, 20281071, 60432113
491	80496412 (881, 982)	Novel Protein sim. GBank gij2894208[emb]CAA17072] - (AL021840) hypothetical protein Rv3258c [Mycobacterium tuberculosis]	UNCLASSIFIED		264769
492	87421264 (883, 984)	Novel Protein sim. GBank gij5262603[emb]CAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264600
493	11692942 (885, 986)	Novel Protein sim. GBank gij5262603[emb]CAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264638
494	87726604 (887, 988)	Novel Protein sim. GBank gij5262603[emb]CAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]			264489, 35696286, 60432289, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 33657402, 264762, 264764, 264768, 264769, 264688, 21908765, 21908769, 35695917, 265020, 264693, 33657109, 264629, 35696423, 35695855, 264634, 264638
495	80028599 (889, 990)	Novel Protein sim. GBank gij2791517[emb]CAA16054] - (AL021248) hypothetical protein Rv2477c [Mycobacterium tuberculosis]	Contains protein domain (PF00005) - ABC transporter	transport	264602, 264682, 264638
496	78985624 (891, 992)	Novel Protein sim. GBank gij230281[pt]R69] - 434 Repressor (Amino-Terminal Domain) (R1-69)	Contains protein domain (PF01381) - Helix-turn-helix		264601, 265021
497	78949661 (893, 994)	Novel Protein sim. GBank gij129736[pt]P28225[PDXH_ECOLI - PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP OXIDASE)]	oxidase		265006

498	88095488 (995, 998)	Novel Protein sim. GBank gi 1145789 (U41662) - neuroligin 2 [Rattus norvegicus]	Contains protein domain (PF00135) - Carboxylesterases	- esterase	264259, 29331826, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264991, 33657402, 264758, 265010, 265011, 264800, 264601, 264605, 264683, 264764, 264766, 264767, 264768, 264687, 264769, 21806767, 33657023, 264693, 264628, 264629, 35696423, 264630, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 18108385, 264563, 264584, 264565, 264566, 264567
499	20438222 (987, 998)	Novel Protein sim. GBank gi 97480 pir S19739 - Integral membrane protein - Rhodobacter capsulatus		UNCLASSIFIED	264605
500	11076810 (999, 1000)				264605
501	13418034 (1001, 1002)	Novel Protein sim. GBank gi 5708250 emb CAB52363.1  - (AL109747) putative integral membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264688
502	80021176 (1003, 1004)	Novel Protein sim. GBank gi 4468678 emb CAB38132.1  - (AL035591) glucose-6-phosphate isomerase [Streptomyces coelicolor]	Contains protein domain (PF00342) - Phosphoglucose isomerase	- isomerase	22278996, 265011, 264602, 264605, 264635
503	20264483 (1005, 1006)			UNCLASSIFIED	264564
504	10887321 (1007, 1008)			UNCLASSIFIED	264687
505	95003068 (1009, 1010)			UNCLASSIFIED	264369
506	16454292 (1011, 1012)	Novel Protein sim. GBank gi 4033509 sp P02598 CALM_TETPY - CALMODULIN	Contains protein domain (PF00036) - EF hand	- struct	265010
507	20451598 (1013, 1014)	Novel Protein sim. GBank gi 2501069 sp Q46127 SYW_CLOLO - TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN--TRNA LIGASE) (TRPRS)		UNCLASSIFIED	264604
508	78841424 (1015, 1016)	Novel Protein sim. GBank gi 466068 sp P34618 YO82_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN ZK1236.2 IN CHROMOSOME III		UNCLASSIFIED	264908
509	11776386 (1017, 1018)				264638
510	83373465 (1019, 1020)			UNCLASSIFIED	264687, 264639
511	16525578 (1021, 1022)				265007
512	20399484 (1023, 1024)	Novel Protein sim. GBank gi 2497419 sp P55635 Y4RB_RHISN - PUTATIVE INTEGRASE/RECOMBINASE Y4RB		UNCLASSIFIED	264565
513	78457404 (1025, 1026)	Novel Protein sim. GBank gi 1276897 (U41809) - cyclin J [Drosophila melanogaster]	Contains protein domain (PF00134) - Cyclin	- cyclin	264683, 264689, 35696423, 264639
514	79813805 (1027, 1028)	Novel Protein sim. GBank gi 1184780 (U46068) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 264909
515	79462591 (1029, 1030)				22278998, 264690
516	9862020 (1031, 1032)	Novel Protein sim. GBank gi 2127400 pir S65770 - maltotriose trehalase [Arthrobacter sp. (strain Q38)]		- amylase	264910

517	95292994 (1033, 1034)	Novel Protein sim. GBank gij2983605 (AE000725) - ribose 5 phosphate isomerase B [Aquilifex aeolicus]		isomerase	265018, 264605, 264764, 264766, 264687, 264691, 264565
518	8491831 (1035, 1036)	Novel Protein sim. GBank gij854065[emb]CAA563371 - (X03413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264487
519	91677888 (1037, 1038)	Novel Protein sim. GBank gij5689365[dbj]BAA83073.1 - (AB024075) B120 [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	dna_rna_bind	52644507, 22278997, 22278998, 60432049, 264259, 52845080, 29331824, 66714117, 60424269, 29331826, 35696052, 264905, 29331830, 66712502, 264511, 265007, 264591, 60432229, 33657402, 60433438, 21906754, 33109954, 52844296, 87168474, 87168559, 285017, 285018, 284604, 285019, 284681, 264448, 264369, 264288, 264685, 21906765, 21906766, 21906767, 21906769, 285021, 60170615, 33657023, 264692, 52645129, 33657109, 27486262, 27486264, 35695763, 18108370, 264629, 52844332, 56182323, 264639, 83373044, 18108385, 56528486, 60432113
520	78869188 (1039, 1040)				264769
521	11076821 (1041, 1042)	Novel Protein sim. GBank gij1169128[sp]P46839[CTPA_MYCLE - CATION-TRANSPORTING P-TYPE ATPASE A		transport	264605
522	80435060 (1043, 1044)	Novel Protein sim. GBank gij1172869[sp]P44331[RBSK_HAEIN - RIBOKINASE	Contains protein domain (PF00294) - pfkB family carbohydrate kinase	kinase	284905, 264768
523	18356013 (1045, 1046)	Novel Protein sim. GBank gij213224[pir]S61028 - hypothetical protein YPL236c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	264629
524	80261805 (1047, 1048)	Novel Protein sim. GBank gij4033608[dbj]BAA351361 - (AB012308) B2HC [Anthracidaris crassispina]		ATPase, associated	264092, 264596, 265011
525	79610046 (1049, 1050)				264907
526	36827630 (1051, 1052)	Novel Protein sim. GBank gij4106610[emb]CAA213651 - (AL031868) ORF42, len=386 aa, similarity to an aminotransferase, in P95957 Sulfolobus solfataricus, (401 aa), 33.1% identity in 393 aa overlap. Fasta scores: opt-468, E(): 8.5e-24, in Q84602 R. norvegicus, (425 aa), 28.6% ident...		UNCLASSIFIED	264758
527	80504729 (1053, 1054)			UNCLASSIFIED	264769
528	85484134 (1055, 1056)			UNCLASSIFIED	56182575, 265017, 265018
529	17938810 (1057, 1058)	Novel Protein sim. GBank gij731088[sp]P24215[JUXUA_ECOLI - MANNONATE DEHYDRATASE (D-MANNONATE HYDROLASE)		hydrolase	265019
530	10887336 (1059, 1060)	Novel Protein sim. GBank gij42144[emb]CAA252001 - (X00513) NusA protein (nusA) [Escherichia coli]		UNCLASSIFIED	264687
531	80226576 (1061, 1062)			UNCLASSIFIED	264555, 264556, 264557, 264558, 18108385
532	90933444 (1063, 1064)	Novel Protein sim. GBank gij5262640[emb]CAB45758.1 - (AL080170) hypothetical protein [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	264488, 264490, 264259, 264592, 264760, 265021, 264690, 263976, 264558

533	87761531 (1085, 1086)	Novel Protein sim. GBank gi 4883636 gb AAD31593.1 AF11229 - (AF11229) Integral inner nuclear membrane protein MAN1 [Homo sapiens]				264907, 264908, 264768, 35695917, 264630, 264555
534	82368284 (1087, 1088)	Novel Protein sim. GBank gi 2995352 emb CAA04606.1  - (AJ001206) pep1 [Streptomyces coelicolor]		UNCLASSIFIED		264905, 265011, 264601, 264602, 264605, 264762, 264768, 265020, 264693, 264636 264908
535	79641850 (1088, 1070)	Novel Protein sim. GBank gi 3878636 emb CAA88953  - (Z49128) similar to cAMP-dependant protein kinase; cDNA EST EMBL: T00719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk49214.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	ATPase-associated		
536	79907207 (1071, 1072)	Novel Protein sim. GBank gi 2495828 sp P55757 YOH1_SERMA - HYPOTHETICAL 10.1 KD PROTEIN IN BIOA 5 REGION		reductase		18108376, 264905, 264906, 264907, 264909
537	84147448 (1073, 1074)	Novel Protein sim. GBank				265008, 264605, 85274781
538	87821863 (1075, 1076)	Novel Protein sim. GBank gi 134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	collagen		29331822, 29331824, 29331825, 29331826, 29331827, 264908, 52844045, 33657402, 265017, 264762, 264683, 264288, 264685, 21906765, 35695763, 264558, 60170394, 264559, 22279002 264602, 265019
539	28396269 (1077, 1078)	Novel Protein sim. GBank gi 2498433 sp Q12341 HAT1_YEAST - HISTONE ACETYLTRANSFERASE		histone		
540	79637077 (1079, 1080)	Novel Protein sim. GBank				264693
541	87762268 (1081, 1082)	Novel Protein sim. GBank gi 3682241 db BAA34480.1  - (AB018303) KIAA0760 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor		18108394, 22278997, 22278998, 264259, 264112, 265009, 33657402, 55812038, 52846317, 265017, 21906765, 264693, 55811576, 264635, 56528486, 264568 264910, 265018, 264689, 264638, 264486
542	95295836 (1083, 1084)	Novel Protein sim. GBank gi 5042272 emb CAB44526.1  - (AL078818) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]		dehydrogenase		
543	79786290 (1085, 1086)	Novel Protein sim. GBank		UNCLASSIFIED		264602, 264908
544	20437191 (1087, 1088)	Novel Protein sim. GBank gi 2791398 emb CAA15984  - (AL021184) hypothetical protein Rv1464 [Mycobacterium tuberculosis]		UNCLASSIFIED		264605
545	80434504 (1089, 1090)	Novel Protein sim. GBank				264768, 264634, 264907, 264592, 264909
546	80249016 (1091, 1092)	Novel Protein sim. GBank gi 4887211 gb AAD32237.1 AF14744 - (AF14744) penicillin binding protein 1B [Pseudomonas aeruginosa]				264600, 264602, 21908765
547	11077563 (1093, 1094)	Novel Protein sim. GBank gi 1350855 sp P19176 IRPOC_PSEPU - DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT)		mapolymerase		264604
548	82114938 (1095, 1096)	Novel Protein sim. GBank gi 2330021 AF019250  - kinesin- related protein; KRP; Costal2 [Drosophila melanogaster]		UNCLASSIFIED		264488, 264905, 264810, 264760, 264693, 284639, 264583, 264564

549	95421904 (1097, 1098)	Novel Protein sim. GBank gi 4337460 gb AAD18133  - (AF056195) neuroblastoma-amplified protein [Homo sapiens]		UNCLASSIFIED	264488, 65274572, 18108398, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 29331826, 35696052, 265007, 265008, 264910, 264592, 33857402, 33109954, 265017, 265018, 265019, 18108351, 264448, 264764, 264369, 264288, 264766, 264688, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264691, 33657023, 264692, 264693, 65274620, 52845129, 33857109, 27486261, 27486262, 27486264, 33857349, 55811576, 18108387, 60432113, 22279002
550	10886616 (1099, 1100)				264688
551	80439990 (1101, 1102)	Novel Protein sim. GBank gi 3122893 sp P94985 SYFB_MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)		UNCLASSIFIED	264908, 264909, 264768
552	94872870 (1103, 1104)	Novel Protein sim. GBank gi 552087 (M33753) - crumbs protein [Drosophila melanogaster]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264689, 264639, 264563
553	80106002 (1105, 1106)	Novel Protein sim. GBank gi 501977 gb AAD37857.1 AF133263 histidine protein kinase-response regulator hybrid protein CvgSY [Pseudomonas syringae pv. syringae]		UNCLASSIFIED	55811957, 284628
554	78618378 (1107, 1108)	Novel Protein sim. GBank gi 131515 sp P02908 PTGA_SALTY - PTS SYSTEM, GLUCOSE-SPECIFIC IIA COMPONENT (EIIA-GLC) (GLUCOSE-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIIA-GLC)	Contains protein domain (PF00356) - transport phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1	kinase	264906
555	78996347 (1109, 1110)	Novel Protein sim. GBank gi 3914014 sp P96380 MFD_MYCTU - TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)		transport	264762
556	20457127 (1111, 1112)	Novel Protein sim. GBank gi 3914014 sp P96380 MFD_MYCTU - TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)		transcriptfactor	264508, 264605, 264559
557	18523405 (1113, 1114)	Novel Protein sim. GBank gi 5042273 emb CAB44527.1  - (AL078618) nuoE, NADH dehydrogenase subunit [Streptomyces coelicolor]		dehydrogenase	264488
558	20724428 (1115, 1116)	Novel Protein sim. GBank gi 1170933 sp P45331 METE_HAEN - 5-METHYL-TETRAHYDROPTEROYL-TRIGLUTAMATE-HOMOCYSTEINE METHYLTRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE)		UNCLASSIFIED	264602
559	80084353 (1117, 1118)	Novel Protein sim. GBank gi 4980567 gb AAD35173.1 AE001694 iron(III) ABC transporter, permease protein [Thermotoga maritima]		UNCLASSIFIED	264634

560	80066533 (1118, 1120)	Novel Protein sim. GBank gi 2492595 sp Q53193 Y4TR_RHISN - PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TR	Contains protein domain (PF00005) - transport ABC transporter	18108396, 284808, 284602, 284604, 18108374
561	20293187 (1121, 1122)		UNCLASSIFIED	284800
562	11898181 (1123, 1124)		UNCLASSIFIED	284889
563	79761420 (1125, 1126)	Novel Protein sim. GBank gi 4104925 (AF042276) - poly(hydroxycalcinate) granule associated protein GA2 [Pseudomonas putida]	UNCLASSIFIED	284910, 284691
564	56716390 (1127, 1128)	Novel Protein sim. GBank gi 2792310 (AF040570) - unknown [Amycolatopsis mediterranei]	dehydrogenase	284592
565	56465618 (1129, 1130)	Novel Protein sim. GBank gi 3449294 dbj BAA32462  - (AB011532) MEGF9 [Rattus norvegicus]	synthase	285010
566	94323888 (1131, 1132)	Novel Protein sim. GBank gi 4539568 emb CAB38487.1  - (AL035638) putative helicase [Streptomyces coelicolor]	helicase	284809, 284510, 285008, 284910, 284758, 284600, 284602, 284604, 284605, 284788, 284887, 284689, 35695917, 284693, 65274620, 284488
567	79560955 (1133, 1134)		UNCLASSIFIED	284681, 284681, 284593
568	94661793 (1135, 1136)	Novel Protein sim. GBank gi 100506 pir S17455 - Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flavaria trimeria (fragment)	dehydrogenase	284689
569	39506697 (1137, 1138)	Novel Protein sim. GBank gi 3915843 sp Q31212 RS2_STRCO - 30S RIBOSOMAL PROTEIN S2	Contains protein domain (PF00318) - ribosomal prot	284565
570	78375927 (1139, 1140)		UNCLASSIFIED	18108376, 18108387, 284585
571	79783981 (1141, 1142)	Novel Protein sim. GBank gi 115122 sp P21827 BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD	transport	284907, 284909
572	38986038 (1143, 1144)		UNCLASSIFIED	284762
573	20715521 (1145, 1146)	Novel Protein sim. GBank gi 4539223 emb CAB3988.1  - (AL049497) putative integral membrane protein [Streptomyces coelicolor]	UNCLASSIFIED	285007, 284601
574	13521592 (1147, 1148)			284638
575	13076418 (1149, 1150)	Novel Protein sim. GBank gi 118704 sp P10443 DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN	polymerase	284687
576	20482246 (1151, 1152)	Novel Protein sim. GBank gi 5457625 emb CAB49116.1  - (AJ248283) PAB2227 [Pyrococcus abyssi]		284605
577	66727102 (1153, 1154)	Novel Protein sim. GBank gi 5042274 emb CAB44528.1  - (AL078618) nuoD, NADH dehydrogenase subunit [Streptomyces coelicolor]	dehydrogenase	35696052, 284636
578	11804477 (1155, 1156)			284638
579	11794723 (1157, 1158)	Novel Protein sim. GBank gi 1723081 sp Q11046 Y089_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.09	transport	284682, 284556

580	80059417 (1159, 1160)				22278999, 35696052, 264555, 264556, 264558
581	79230833 (1161, 1162)	Novel Protein sim. GBank gii3243131 (AF045777) - tilin	Contains protein domain (PF00047) - struct	UNCLASSIFIED	265008, 264584
582	80049617 (1163, 1164)	[Drosophila melanogaster]	Immunoglobulin domain		265021, 264555, 264557
583	79321382 (1165, 1166)	Novel Protein sim. GBank gii2501162[spP77728]YAJR_ECOLI - HYPOTHETICAL	transport		264594
584	79845024 (1167, 1168)	Novel Protein sim. GBank gii2501162[spP77728]YAJR_ECOLI - HYPOTHETICAL			
585	79581454 (1169, 1170)	49.0 KD PROTEIN IN ABPA-CYOE INTERGENIC REGION		UNCLASSIFIED	264488, 264906, 264766, 264687, 35696423
586	38277486 (1171, 1172)	Novel Protein sim. GBank gii388222[gbjBAA34470.1] -		UNCLASSIFIED	265018, 264684, 21906769
587	80497359 (1173, 1174)	(AB018293) KIAA0750 protein [Homo sapiens]			
588	79557239 (1175, 1176)	Novel Protein sim. GBank gii4467250[emb]CAB37575] -		UNCLASSIFIED	264908, 265007
589	79805828 (1177, 1178)	(AL035569) probable Glu-tRNA Gln amidotransferase	hydrolase		264600, 264602, 264605, 264769, 264680, 264557
590	79815629 (1179, 1180)	subunit [Streptomyces coelicolor]			
591	10313540 (1181, 1182)	Novel Protein sim. GBank gii568951[gbjBAA83043.1] -		UNCLASSIFIED	265020, 264692
592	13889767 (1183, 1184)	(AB029014) KIAA1091 protein [Homo sapiens]			
593	82346699 (1185, 1186)			UNCLASSIFIED	22278996, 264907, 264909, 264510, 265009, 265010, 264687, 264769, 35695917, 18108376, 264634, 264638, 264638
594	20212392 (1187, 1188)	Novel Protein sim. GBank gii2143293[emb]CAB03390] -	mapolymerase		264906, 264909
595	10064064 (1189, 1190)	(Z95972) rpoB [Mycobacterium tuberculosis]			264691
596	13085170 (1191, 1192)	Novel Protein sim. GBank gii4511983[gbjAAD21543.1] -	MHC		263972
597	80259003 (1193, 1194)	(AF088896) electroltransfer ubiquinone oxidoreductase	dehydrogenase		264511, 264762, 264769, 264486
598	94140216 (1195, 1196)	[Zymomonas mobilis]			
599	20385137 (1197, 1198)	Novel Protein sim. GBank gii1272368 (U51896) - LfGE		UNCLASSIFIED	264605
600	10357663 (1199, 1200)	Novel Protein sim. GBank gii131490[spP20966]PTFB_ECOLI - PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIBC-FRU)			264769
601	79610404 (1201, 1202)	(PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EII-FRU)		UNCLASSIFIED	
602	80259003 (1193, 1194)			UNCLASSIFIED	264636
603	94140216 (1195, 1196)			UNCLASSIFIED	264592
604	20385137 (1197, 1198)	Novel Protein sim. GBank gii125328[spP04951]KDSB_ECOLI - 3-DEOXY-MANNO-OCTULONATE CYTIDYLTRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULONIC ACID SYNTHETASE) (CKS)		UNCLASSIFIED	264758, 55810764, 264555, 264556, 264637, 83373044
605	10357663 (1199, 1200)				264603
606	79610404 (1201, 1202)	Novel Protein sim. GBank gii2127414[pir]S60064 -			264906
607		hypothetical protein 2 - Corynebacterium glutamicum		UNCLASSIFIED	264510

602	78250602 (1203, 1204)	Novel Protein sim. GBank gii3522861[gb AAC34243.1] - (AC004411) putative pto kinase [Arabidopsis thaliana]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	285007
603	11466067 (1205, 1208)			UNCLASSIFIED	284595
604	81675420 (1207, 1208)			UNCLASSIFIED	284758
605	20438657 (1209, 1210)	Novel Protein sim. GBank gii175322[sp P44917 Y883_HAEIN - HYPOTHETICAL PROTEIN H0883		UNCLASSIFIED	284605
606	80334582 (1211, 1212)	Novel Protein sim. GBank gii5020284[gb AAD38043.1 AF15136 - (AF151363) Cdc42 GTPase-activating protein [Mus musculus]		UNCLASSIFIED	264784
607	95361506 (1213, 1214)	Novel Protein sim. GBank gii188864 (M74027) - mucin [Homo sapiens]		UNCLASSIFIED	284508, 284908, 85658542, 284682, 284687, 284689, 284534, 18108376, 35898423, 284636, 284555, 284638
608	11810888 (1215, 1216)			UNCLASSIFIED	284682
609	80084775 (1217, 1218)	Novel Protein sim. GBank gii2496701[sp P55552 Y4LL_RHISN - HYPOTHETICAL 91.8 KD PROTEIN Y4LL	Contains protein domain (PF00989) - PAS domain	UNCLASSIFIED	284605
610	78628413 (1219, 1220)				284682
611	87568205 (1221, 1222)				284508, 284905, 284907, 284908, 284909, 284511, 284910, 284758, 284604, 284684, 284766, 284689, 284692, 284628, 284635, 284636, 284637, 284558
612	95287851 (1223, 1224)	Novel Protein sim. GBank gii1877368[emb CAB07118] - (Z92772) recD [Mycobacterium tuberculosis]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	nuclease	284600, 284601, 284604, 284789, 284558, 284565
613	7523475 (1225, 1226)			UNCLASSIFIED	284369
614	79869348 (1227, 1228)	Novel Protein sim. GBank gii5114231[gb AAD40238.1 AF13670 - (AF136709) histidine kinase YycG [Staphylococcus aureus]		kinase	18108372, 284563
615	39586598 (1229, 1230)	Novel Protein sim. GBank gii1339950[dbj BAA12741] - (D85230) large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]		synthase	284600, 284602, 284629
616	20465331 (1231, 1232)	Novel Protein sim. GBank gii544367[sp P35673 GALE_ERWAM - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		isomerase	284605
617	91227222 (1233, 1234)	Novel Protein sim. GBank gii2498087[sp Q60769 TNF3_MOUSE - TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20)	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	Inf	52845156, 21906765, 35898423, 21906768, 21908789, 22278994, 35898286, 22278998, 265020, 265021, 265007, 265008, 284638, 52844150, 33657023, 284692, 284693, 28431822, 29331824, 55812038, 83373044, 56182181, 60424269, 68714117, 29331825, 33657109, 29331826, 33657182, 29331827, 35896052, 29331828, 27486282, 33657349, 56326486, 265018, 265019, 22279002, 284482, 284448, 29331830, 68712502, 284908



618	20632843 (1235, 1236)	Novel Protein sim. GBank gi 5459388 emb CAB50746.1  - (AL096839) putative aminotransferase [Streptomyces coelicolor]		isomerase	264603	
619	91227224 (1237, 1238)					56994075, 29331826, 33656970, 265008, 33657402, 33109954, 87188559, 264448, 18108374, 83373044
620	61183143 (1239, 1240)	Novel Protein sim. GBank gi 464335 sp Q05922 DUS2_MOUSE - DUAL SPECIFICITY PROTEIN PHOSPHATASE 2 (DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1)		phosphatase		29146498, 264758, 264369, 29148627
621	80239251 (1241, 1242)			UNCLASSIFIED	264556, 264558, 264639	
622	20456427 (1243, 1244)	Novel Protein sim. GBank gi 2633557 emb CAB13060  - (Z99110) yJdF [Bacillus subtilis]		UNCLASSIFIED	264605	
623	10131798 (1245, 1246)	Novel Protein sim. GBank gi 1857710 gb AA848482  - (U87224) contactin associated protein [Rattus norvegicus]	Contains protein domain (PF00054) - Laminin G domain	laminin	264906	
624	19534127 (1247, 1248)	Novel Protein sim. GBank gi 1705703 sp P52225 CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK		cytochrome	264596	
625	13084618 (1249, 1250)	Novel Protein sim. GBank gi 2894252 emb CAA17114.1  - (AL021841) hypothetical protein Rv3342 [Mycobacterium tuberculosis]		UNCLASSIFIED	264688	
626	88062603 (1251, 1252)	Novel Protein sim. GBank gi 416592 sp P32323 AGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR		UNCLASSIFIED	29331822, 264905, 264908, 33657023, 33657109, 264558	
627	80255457 (1253, 1254)	Novel Protein sim. GBank gi 3098418  (AF040944) - P140 [Mus musculus]		UNCLASSIFIED	18108394, 264112, 264593, 265022, 264635	
628	80077096 (1255, 1256)	Novel Protein sim. GBank gi 1711543 sp P50526 SSP1_SCHPO - SERINE/THREONINE-PROTEIN KINASE SSP1	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264600	
629	79851602 (1257, 1258)	Novel Protein sim. GBank gi 1143204  (U34305) - ORF2; Method: conceptual translation supplied by author. [Shigella sonnei]		isomerase	264806, 264907	
630	39565156 (1259, 1260)	Novel Protein sim. GBank gi 3236368  (AF064748) - S3-12 [Mus musculus]		UNCLASSIFIED	264490	
631	20598718 (1261, 1262)	Novel Protein sim. GBank gi 140887 sp P11668 YGG8_ECOLI - HYPOTHETICAL 30.9 KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 4) (F286)			263978	
632	27843890 (1263, 1264)			UNCLASSIFIED	264906, 264600, 264605, 264769, 264689, 264486	
633	80477772 (1265, 1266)			UNCLASSIFIED	264769	
634	17938806 (1267, 1268)				265019	
635	79574508 (1269, 1270)			UNCLASSIFIED	264689	
636	79910981 (1271, 1272)			UNCLASSIFIED	264596, 264762, 264693	

637	82455796 (1273, 1274)	Novel Protein sim. GBank gll2326739[emb]CAB10953] : (Z98268) recN [Mycobacterium tuberculosis]		nuclease	264906, 264907, 264510, 264511, 264601, 264602, 264603, 264604, 264605, 18108351, 264782, 264786, 264887, 264788, 264889, 35695917, 264893, 264834, 264638, 264639, 264558, 18108385, 264638
638	14957457 (1275, 1276)	Novel Protein sim. GBank gll4678662[emb]CAB41074.1] - (AL049845) putative large ATP-binding protein [Streptomyces coelicolor]			
639	80204210 (1277, 1278)	Novel Protein sim. GBank gll4589629[emb]BAA76836.1] - (AB023209) KIAA0992 protein [Homo sapiens]	struct		264112, 263974
640	17928579 (1278, 1280)	Novel Protein sim. GBank gll1432083 (U60981) - homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana]	Contains protein domain (PF01466) - Skp1 family	mapolymerase	265009, 265010
641	79636398 (1281, 1282)			UNCLASSIFIED	264693
642	19898737 (1283, 1284)			UNCLASSIFIED	264565
643	81516220 (1285, 1286)			UNCLASSIFIED	264635, 264639, 264564
644	11751367 (1287, 1288)			UNCLASSIFIED	264884
645	95010907 (1289, 1290)			UNCLASSIFIED	264906, 264762, 264693, 264639, 264559
646	80069083 (1291, 1292)			UNCLASSIFIED	264595, 264586
647	80257085 (1293, 1294)	Novel Protein sim. GBank gll4507813[ref]NP_003738.1pTNKS - TANKYRASE	Contains protein domain (PF00023) - Ank repeat	transcriptfactor	264909, 264591
648	80077428 (1295, 1296)	Novel Protein sim. GBank gll1044983[bbas]169646 - protamine [Monodonita turbinata, gonads, Peptide, 106 aa]		UNCLASSIFIED	264600
649	80247447 (1297, 1298)			UNCLASSIFIED	263978
650	11798316 (1299, 1300)			UNCLASSIFIED	264686
651	11776932 (1301, 1302)	Novel Protein sim. GBank gll1346918[sp]P12283[PURA_ECOLI - ADENYLOSUCCINATE SYNTHETASE (IMP--ASPARTATE LIGASE)]			264602, 264638
652	85516704 (1303, 1304)	Novel Protein sim. GBank gll1722977[sp]Q10638[Y03C_MYCTU - HYPOTHETICAL 82.8 KD PROTEIN CY130.12C]		UNCLASSIFIED	264805, 264907, 264909, 263978, 264637
653	82124947 (1305, 1306)			UNCLASSIFIED	22278996, 264510, 264511, 264512, 264593, 21906754, 264603, 264760, 18108376, 264556
654	85010589 (1307, 1308)			UNCLASSIFIED	264906, 264595, 264632
655	78320692 (1309, 1310)	Novel Protein sim. GBank gll130327[sp]P28647[P_LSC_ECOLI - 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (1-AGP ACYLTRANSFERASE) (L-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE) (LPAAT)]	Contains protein domain (PF01553) - Acyltransferase	transferase	264592
656	80416738 (1311, 1312)			UNCLASSIFIED	264602, 264605, 264768, 264691
657	20611010 (1313, 1314)			UNCLASSIFIED	264587, 264558

658	87761815 (1315, 1316)	Novel Protein sim. GBank gl 5689493 dbj BAA83030.1  - (AB029001) KIAA1078 protein [Homo sapiens]	UNCLASSIFIED	22278996, 60432049, 29331822, 29331824, 29331828, 265007, 265009, 33657402, 33657084, 265017, 264448, 21906765, 21906768, 263987, 20281149, 18108370, 18108374, 264482
659	87718663 (1317, 1318)	Novel Protein sim. GBank gl 2137872 pir j 48724 - zinc finger protein PZF - mouse	transcriptfactor	22278999, 60432049, 66714117, 29331827, 265007, 264766, 56181562, 18108359, 18108365, 18108370, 18108381
660	81897922 (1319, 1320)	Novel Protein sim. GBank	UNCLASSIFIED	264757
661	80028023 (1321, 1322)	gl 134180 sp p15401 SACY_BACSU - LEVANSUCRASE AND SUCRASE SYNTHESIS OPERON ANTITERMINATOR	UNCLASSIFIED	264510, 265009, 284600, 264602, 264603, 264604, 264605, 32833988, 18108376, 264636, 18108387, 22279000
662	20463731 (1323, 1324)	Novel Protein sim. GBank gl 4545229 gb AA022450.1 AF11618 - (AF11618) SecA homolog [Actinobacillus actinomycetemcomitans]	UNCLASSIFIED	264605
663	20628080 (1325, 1326)	Novel Protein sim. GBank gl 5689250 dbj BAA82881.1  - (AB024335) similar to orf5 [Comamonas testosteroni]	dehydrogenase	264605
664	80508512 (1327, 1328)	Novel Protein sim. GBank gl 1652848 dbj BAA17766  - (D90909) DNA photolyase [Synecocystis sp.]	UNCLASSIFIED	264769
665	80079053 (1329, 1330)	Novel Protein sim. GBank gl 116841 sp p21640 COBJ_PSEDE - PRECORRIN-3B C17 METHYLTRANSFERASE (PRECORRIN-3 METHYLTRANSFERASE)	isomerase	264600
666	78603142 (1331, 1332)	Novel Protein sim. GBank gl 3261829 emb CAB10927  - (298260) hypothetical protein Rv1230c [Mycobacterium tuberculosis]	glycoprotein	264807, 265007
667	94531802 (1333, 1334)	Novel Protein sim. GBank gl 5688851 dbj BAA82702.1  - (AB017438) Orf5 [Streptomyces coelicolor]	UNCLASSIFIED	264689, 264602, 264593
668	82051891 (1335, 1336)	Novel Protein sim. GBank gl 3581853 emb CAA20809  - (AL031541) 50S ribosomal protein L20 [Streptomyces coelicolor]	ribosomalprot	264805, 264906, 264908, 264600, 264601, 264603, 264605, 264760, 264689, 264636, 264638, 264639
669	12867154 (1337, 1338)	Novel Protein sim. GBank gl 2582531  (AF026444) - 2-isopropylmalate synthase [Streptomyces coelicolor]	UNCLASSIFIED	264637
670	80238548 (1339, 1340)	Novel Protein sim. GBank gl 2582531  (AF026444) - 2-isopropylmalate synthase [Streptomyces coelicolor]	synthase	264905, 264906, 264908, 264601, 264762, 264766, 264689, 264638, 18108385, 264486
671	78601368 (1341, 1342)	Novel Protein sim. GBank gl 2114430  (U92703) - Olf-1/IEBF-like-3 transcription factor [Mus musculus]	UNCLASSIFIED	264690, 264692, 264693, 264636, 18108387
672	79834371 (1343, 1344)	Novel Protein sim. GBank	transcriptfactor	264910, 265017
673	82285798 (1345, 1346)	Novel Protein sim. GBank gl 4569285 gb AA026430.1 AF13515 - (AF135154) ferric acaalgin siderophore receptor [Bordetella pertussis]		264759
674	78189259 (1347, 1348)		UNCLASSIFIED	264629

675	87895870 (1349, 1350)	Novel Protein sim. GBank gi1498075 gb AAD3347.1 AE001708) D- alanine--D-alanine ligase [Thermotoga maritima]	Contains protein domain (PF01820) - D-ala D-ala ligase	UNCLASSIFIED	264488, 22278998, 66714117, 264508, 264511, 265008, 60433438, 264600, 264601, 264602, 264603, 264604, 264605, 264762, 264687, 264769, 60431602, 18108374, 264636, 264638 265010
676	78898607 (1351, 1352)	Novel Protein sim. GBank gi1723566 sp Q10479 YOF7_SCHPO - PUTATIVE GLUCOSYLTRANSFERASE C17C9.07		ATPase-associated	264591, 264632
677	21644312 (1353, 1354)	Novel Protein sim. GBank gi1687208 (U03976) - dynein heavy chain isoform 5C [Tripleneustes grallia]			264758, 264682, 264557
678	84225200 (1355, 1356)	Novel Protein sim. GBank gi1586274 pr 2203365A - laminin alpha5 [Mus musculus]	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)		
679	78868655 (1357, 1358)	Novel Protein sim. GBank gi13928723 emb CAA22219) - (AL034355) putative ABC transporter [Streptomyces coelicolor]		UNCLASSIFIED	22278998, 264693
680	20728424 (1358, 1360)	Novel Protein sim. GBank			264600, 264602
681	94322017 (1361, 1362)	gi15174493 ref NP_006050.1 pLAMC - laminin, gamma 3	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)		264102, 264907, 264908, 265008, 264693, 263972, 83373044, 264566
682	11392478 (1363, 1364)	Novel Protein sim. GBank		UNCLASSIFIED	264595
683	80083680 (1365, 1366)	gi14758208 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain		264634
684	20465367 (1367, 1368)	Novel Protein sim. GBank gi15420387 emb CA846679.1  - (AJ243459) proteophosphoglycan [Leishmania major]			264605
685	80246735 (1369, 1370)	Novel Protein sim. GBank			264809, 263967, 263981
686	78208608 (1371, 1372)	Novel Protein sim. GBank			264631
687	80085829 (1373, 1374)	Novel Protein sim. GBank gi15420387 emb CA846679.1  - (AJ243459) proteophosphoglycan [Leishmania major]			264693, 264635
688	78853412 (1375, 1376)	Novel Protein sim. GBank gi12688962 (AF027768) - LspA [Serratia marcescens]		peptidase	264907, 264638
689	88064256 (1377, 1378)	Novel Protein sim. GBank gi13046931 (AF049330) - PPAR gamma coactivator [Mus musculus]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264906, 264907, 265007, 265009, 60433438, 21908754, 264760, 18108358, 21908766, 21908769, 265021, 18108361, 263974, 18108378, 264557, 18108385, 22279002 264510, 264511, 264764, 264769
690	80369750 (1379, 1380)	Novel Protein sim. GBank gi12498941 sp Q15428 SP62_HUMAN - SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)		UNCLASSIFIED	
691	81854392 (1381, 1382)	Novel Protein sim. GBank gi15420387 emb CA846679.1  - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	264757
692	83608936 (1383, 1384)	Novel Protein sim. GBank		UNCLASSIFIED	55812038, 55811957, 265018, 55811150, 18108351, 264908, 60431528, 264594
693	78586118 (1385, 1386)	Novel Protein sim. GBank gi1854065 emb CAA58337) - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264635
694	82455983 (1387, 1388)	Novel Protein sim. GBank gi1267327 sp Q01033 VC48_HSVSA - HYPOTHETICAL GENE 48 PROTEIN			22278998, 264510, 264602, 264603, 264762, 264687, 264769, 264693

695	94147849 (1389, 1390)	Novel Protein sim. GBank gij4468339[embjCAB38059.1] - (AJ010901) MUC4 [Homo sapiens]	Contains protein domain (PF000094) - von Willebrand factor type D domain	UNCLASSIFIED	56182575, 264509, 264905, 264907, 29331830, 264908, 264909, 264511, 265007, 264910, 264758, 264764, 264288, 65274781, 264905, 264595
696	79830882 (1391, 1392)	Novel Protein sim. GBank gij2649950 (AE001058) - glutamine ABC transporter, ATP-binding protein (ginQ) [Archaeoglobus fulgidus]	Contains protein domain (PF000005) - ABC transporter	transport	
697	11767889 (1393, 1394)	Novel Protein sim. GBank gij1731343[spjQ10694]YY25_MYCTU - HYPOTHETICAL 24.4 KD PROTEIN CY49.25	Contains protein domain (PF01836) - Transposase	UNCLASSIFIED	264682
698	66695862 (1395, 1396)			UNCLASSIFIED	264688, 35695917
699	79582558 (1397, 1398)			UNCLASSIFIED	264682
700	79639038 (1399, 1400)			UNCLASSIFIED	264693
701	80230242 (1401, 1402)	Novel Protein sim. GBank gij1001236[dbjBAA10477] - (D84003) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	264488, 264510, 264511, 264602, 264605, 264689
702	79814789 (1403, 1404)	Novel Protein sim. GBank gij2488935[spjQ46338]SOXG_CORSP - SARCOSINE OXIDASE GAMMA SUBUNIT		UNCLASSIFIED	264604
703	20446820 (1405, 1406)	Novel Protein sim. GBank gij3150513 (AF067219) - contains similarity to the kelch/MIPP family [Caenorhabditis elegans]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	264288, 56181562, 33657109, 264629, 55811576
704	94312224 (1407, 1408)	Novel Protein sim. GBank gij421091[pirjS30730] - hypothetical protein o208 - Escherichia coli		UNCLASSIFIED	265006
705	17932141 (1409, 1410)	Novel Protein sim. GBank gij3024872[spjQ35790]Y074_SYNY3 - HYPOTHETICAL 52.8 KD PROTEIN SLR0074			264600
706	20288082 (1411, 1412)	Novel Protein sim. GBank gij3420608[gbjAAC31907.1] - (AF075709) ABC transporter ATP-binding subunit [Pseudomonas putida]	transport		264603
707	20536065 (1413, 1414)	Novel Protein sim. GBank gij3649741[embjCAA03985] - (AJ000281) mucin [Homo sapiens]	struct		264601, 264692, 18108398, 264637, 264908, 264909
708	20708292 (1415, 1416)	Novel Protein sim. GBank gij3080425[embjCAA18744.1] - (AL022604) putative protein [Arabidopsis thaliana]			264369
709	88001439 (1417, 1418)	Novel Protein sim. GBank gij4758686[refjNP_002323.1]pLRP1 - low density lipoprotein related protein 1 (alpha-2-macroglobulin receptor)	Contains protein domain (PF00058) - Low-density lipoprotein receptor repeat class B	apolipoprotein	265019, 264591
710	11356683 (1419, 1420)	Novel Protein sim. GBank gij1703286[spjQ11056]AM2_MYCTU - PUTATIVE AMIDASE CY50.19C			
711	17931418 (1421, 1422)	Novel Protein sim. GBank gij4502351[refjNP_001692.1]pBAAT - bile acid Coenzyme A: amino acid N-acetyltransferase; glycine N: cholesteryltransferase	hydrolase		264906, 264907
712	80258164 (1423, 1424)				
713	79263126 (1425, 1426)				
714	27847651 (1427, 1428)				264508, 264555

715	78639423 (1429, 1430)	Novel Protein sim. GBank gll1789035 (AE000352) - ori, hypothetical protein [Escherichia coli]		UNCLASSIFIED	264907
716	79559072 (1431, 1432)				264692
717	79491842 (1433, 1434)	Novel Protein sim. GBank gll2494074 (spjP5653) GABD_RHISN - PROBABLE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH)		dehydrogenase	264636
718	94319658 (1435, 1436)	Novel Protein sim. GBank gll3873679 (embjCAA94886) - (Z71178) similar to pro-collagen domains; cDNA EST EMBL:D27978 comes from this gene; cDNA EST EMBL:D27977 comes from this gene; cDNA EST EMBL:D34199 comes from this gene; cDNA EST EMBL:D64392 comes from this gene; cDNA EST EMBL... (Z95387) hypothetical protein Rv2611c [Mycobacterium tuberculosis]	Contains protein domain (PF00093) - von Willebrand factor type C domain	kinase	18108392, 22278994, 22278998, 265008, 265018, 264681, 18108354, 264684, 264685, 264686, 264687, 264689, 21908769, 18108361, 264691, 264692, 55810764, 264635, 18108381, 18108382, 83373044, 18108388
719	17679564 (1437, 1438)	Novel Protein sim. GBank gll2104302 (embjCAB08631) - (Z95387) hypothetical protein Rv2611c [Mycobacterium tuberculosis]		UNCLASSIFIED	265011
720	79841684 (1439, 1440)				264908
721	15020180 (1441, 1442)	Novel Protein sim. GBank gll1235303 (spjP04929) HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	264629
722	9862603 (1443, 1444)	Novel Protein sim. GBank gll498253 (U02372) - integrase [Vibrio cholerae]			264910
723	19755599 (1445, 1446)	Novel Protein sim. GBank gll2253054 (embjCAB10705) - (Z97559) hypothetical protein Rv2114 [Mycobacterium tuberculosis]		UNCLASSIFIED	264691
724	10126494 (1447, 1448)	Novel Protein sim. GBank gll4063015 (AF083061) - protease PrtA [Pseudomonas fluorescens]	Contains protein domain (PF00353) - Hemolysin-type calcium-binding proteins	protease	264909
725	78878679 (1449, 1450)			UNCLASSIFIED	264905, 264907
726	13086282 (1451, 1452)			UNCLASSIFIED	264636
727	13522872 (1453, 1454)				264634
728	20268471 (1455, 1456)	Novel Protein sim. GBank gll2633910 (embjCAB13411) - (Z89112) similar to hypothetical proteins [Bacillus subtilis]			264587
729	11293753 (1457, 1458)			UNCLASSIFIED	264490
730	19500373 (1459, 1460)	Novel Protein sim. GBank gll2494660 (spjQ45291) GALE_BRELA - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		isomerase	264584
731	80058750 (1461, 1462)	Novel Protein sim. GBank gll1146182 (L47838) - putative [Bacillus subtilis]		UNCLASSIFIED	264605
732	80258175 (1463, 1464)	Novel Protein sim. GBank gll1168396 (spjP46681) AIP2_YEAST - ACTIN INTERACTING PROTEIN 2		struct	264591, 264594, 264595
733	20446839 (1465, 1466)				264604
734	20435987 (1467, 1468)	Novel Protein sim. GBank gll3184080 (embjCAA19336) - (AL023781) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	264604
				ubiquitin	

735	11607859 (1469, 1470)	Novel Protein sim. GBank gi 401582 sp P27432 YICE_ECOLI - HYPOTHETICAL 48.9 KD PROTEIN IN GLTS-SELC INTERGENIC REGION				264594
736	10879734 (1471, 1472)	Novel Protein sim. GBank gi 400831 sp P31135 POTH_ECOLI - PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTH	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport		264636
737	78945340 (1473, 1474)		Contains protein domain (PF00615) - Regulator of G protein signaling domain	UNCLASSIFIED		265020
738	17895353 (1475, 1476)	Novel Protein sim. GBank		oxidase		265008
739	79833670 (1477, 1478)	gi 2506867 sp P33225 TORA_ECOLI - TRIMETHYLAMINE- N-OXIDE REDUCTASE PRECURSOR (TMAO REDUCTASE) (TRIMETHYLAMINE OXIDASE)				264910
740	19981557 (1479, 1480)	Novel Protein sim. GBank gi 3261828 emb CA810925  - (Z98260) mrp [Mycobacterium tuberculosis]	Contains protein domain (PF01883) - Domain of unknown function	UNCLASSIFIED		264907, 264764, 264634, 264637
741	79827273 (1481, 1482)	Novel Protein sim. GBank gi 3877494 emb CAA88472.1  - (Z48583) ATP binding protein with similarity to the CDC48/PAS1/SEC18 family; cDNA EST EMBL:D65037 comes from this gene; cDNA EST EMBL:D68340 comes from this gene; cDNA EST EMBL:D65048 comes from this gene; cDNA EST EMBL:D6845...		UNCLASSIFIED		264689, 35696286, 264510, 264908, 18108362
742	82393795 (1483, 1484)	Novel Protein sim. GBank gi 127420 sp P19888 MTBA_BACAR - MODIFICATION METHYLASE BANI (CYTOSINE-SPECIFIC METHYLTRANSFERASE BANI) (M.BANI)	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase			264488, 264259, 264508, 264805, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264596, 264759, 265010, 265011, 18108351, 264763, 264288, 264766, 264768, 264693, 18108370, 264629, 18108372, 264630, 264631, 264634, 264558, 18108385, 264482, 264584, 264587
743	82300051 (1485, 1486)	Novel Protein sim. GBank gi 127420 sp P19888 MTBA_BACAR - MODIFICATION METHYLASE BANI (CYTOSINE-SPECIFIC METHYLTRANSFERASE BANI) (M.BANI)				18108397, 264511, 264690, 264628, 264638, 264692, 264639, 264766
744	80230421 (1487, 1488)			glycoprotein		264906
745	9841963 (1489, 1490)	Novel Protein sim. GBank gi 78921 pir IS04846 - UDP-N- acetylmutamoylalanine-D-glutamate-2, 6-diaminopimelate--D- alanine-D-alanine ligase (EC 6.3.2.15) precursor - Escherichia coli				
746	11073229 (1491, 1492)	Novel Protein sim. GBank gi 3386354 (AF074705) - pyochelin synthetase [Pseudomonas aeruginosa]		synthase		264600
747	94322044 (1493, 1494)	Novel Protein sim. GBank gi 2887411 dbj BAA24848  - (AB007878) KIAA0418 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	oxidase		66714117, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264681, 264288, 264766, 264687, 264768, 264769, 21906768, 35695917, 264691, 264693, 264628, 264634, 264635, 264639, 56182323, 83373044
748	11617923 (1495, 1496)					264690

749	20463118 (1497, 1498)	Novel Protein sim. GBank gll1169727[sp]P44948[FPG_HAEIN - FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY- DNA GLYCOSYLASE)]		UNCLASSIFIED	264604 264600
750	20296427 (1498, 1500)				
751	21635169 (1501, 1502)	Novel Protein sim. GBank gll360088[gb]AAD42851.1[AF15968] - (AF15968) serine/threonine kinase PKN3 [Myxococcus xanthus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264605, 264559
752	82450366 (1503, 1504)	Novel Protein sim. GBank gll116862[sp]P44426[BIOA_HAEIN - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]	Contains protein domain (PF00202) - Aminotransferases class-III pyridoxal phosphate	UNCLASSIFIED	264508, 264907, 264510, 265011, 264762, 264689, 35695855, 264638, 18108387
753	80508718 (1505, 1506)	Novel Protein sim. GBank gll2851530[sp]P32399[YHGE_BACSU - HYPOTHETICAL 84.1 KO PROTEIN IN HEM-GLT INTERGENIC REGION (ORF8)]		UNCLASSIFIED	264909, 264600, 264602, 264604, 264780, 264769, 264634
754	95083741 (1507, 1508)				
755	80185449 (1509, 1510)	Novel Protein sim. GBank gll344927[emb]CAA20420[ - (AL031317) putative dehydrogenase (Streptomyces coelicolor)]		UNCLASSIFIED	264508, 264906, 264907, 264808, 264909, 264759, 264602, 264764, 264769, 264628, 264629, 264630, 264632, 264634, 264635, 264637, 264638, 83373044, 18108385
756	94631688 (1511, 1512)			UNCLASSIFIED	264448, 264690
757	79468533 (1513, 1514)				264769, 264689, 264638, 264639
758	78963176 (1515, 1516)	Novel Protein sim. GBank gll458033[emb]CAB40107.1[ - (AJ001206) putative glycogen debranching enzyme (Streptomyces coelicolor)]		UNCLASSIFIED amylase	264682, 264685 265007, 18108387, 265007, 18108387
759	79475667 (1517, 1518)	Novel Protein sim. GBank gll2911859 (AF047659) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264684, 264686
760	87628688 (1519, 1520)	Novel Protein sim. GBank gll3451312[emb]CAA20449[ - (AL031324) membrane atpase (Schizosaccharomyces pombe)]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	28331822, 264908, 52644045, 56182435, 60170831, 21906754, 265017, 265019, 264681, 264687, 264688, 21906766, 21908768, 265020, 265021, 265022, 264635, 22278000
761	78877968 (1521, 1522)			UNCLASSIFIED	264766
762	80023563 (1523, 1524)	Novel Protein sim. GBank gll3327158[db]BAA31647[ - (AB014572) KIAA0872 protein (Homo sapiens)]		UNCLASSIFIED	264907, 264593, 265020
763	20284813 (1525, 1526)	Novel Protein sim. GBank gll498128[gb]AAD35822.1[AE001744 - (AE001744) lipopolysaccharide core biosynthesis protein KdtB (Thermotoga maritima)]			264600
764	39515024 (1527, 1528)				264603



785	80025347 (1529, 1530)	Novel Protein sim. GBank gi 3845093 (AE001371) - erythrocyte membrane protein PEMP3 [Plasmodium falciparum]		struct	264905, 264906, 264594, 264686, 33657023
766	82417404 (1531, 1532)				264605, 264762, 18108374
767	10296742 (1533, 1534)	Novel Protein sim. GBank gi 541121 pir S40827 - hypothetical protein o300 - Escherichia coli		UNCLASSIFIED	264907
768	79416080 (1535, 1536)			UNCLASSIFIED	264502, 264595
769	80086554 (1537, 1538)	Novel Protein sim. GBank gi 2982501 emb CAA06164 - (AJ004832) neuropathy target esterase [Homo sapiens]		esterase	55810764, 264559
770	80417847 (1539, 1540)	Novel Protein sim. GBank gi 263437 pir S27850 - hypothetical protein - Trypanosoma cruzi (fragment)		UNCLASSIFIED	264905, 264907, 264828, 264909, 265010, 264766, 264628, 264629, 264634, 264636, 264555
771	95329509 (1541, 1542)	Novel Protein sim. GBank gi 4789004 gb AAD29715.1 AF14059 - (AF14059) ring-box protein 1 [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	56182575, 35696286, 264259, 66714117, 264107, 66712502, 56182435, 284112, 55812038, 87168559, 264288, 21908766, 33657023, 65274620, 65274791, 18108381
772	78971362 (1543, 1544)			UNCLASSIFIED	264910
773	78945363 (1545, 1546)			UNCLASSIFIED	265020
774	79856129 (1547, 1548)	Novel Protein sim. GBank gi 5531324 emb CAB51045.1 - (AJ009579) putative alkane 1-monoxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	264909
775	20620141 (1549, 1550)			UNCLASSIFIED	264555
776	78942693 (1551, 1552)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a		265019
777	79960378 (1553, 1554)	Novel Protein sim. GBank gi 4505461 ref NP_003624.1 pNRPB - nuclear restricted protein, BTB domain-like (brain)	Contains protein domain (PF01344) - Kelch motif	protease	21906754, 265020, 60170615, 264691
778	20891310 (1555, 1556)			UNCLASSIFIED	264511
779	80054024 (1557, 1558)				264603
780	95288987 (1559, 1560)	Novel Protein sim. GBank gi 1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]		synthase	264907, 264600, 264601, 264602, 264603, 264604, 264605, 264486
781	80250049 (1561, 1562)				264905, 264907, 265010, 264600, 264601, 18108362, 18108374, 264556
782	8758529 (1563, 1564)	Novel Protein sim. GBank gi 4155447 (AE001517) - proline/betaine transporter [Helicobacter pylori J99]		UNCLASSIFIED	264605
783	16410791 (1565, 1566)				265020
784	80051197 (1567, 1568)			UNCLASSIFIED	264635, 33657023, 29331828, 265017, 264565, 284566
785	56073541 (1569, 1570)	Novel Protein sim. GBank gi 3451335 (AC005525) - F22162_1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	35696032, 264604
786	20438642 (1571, 1572)	Novel Protein sim. GBank gi 138748 sp P10905 UGPA_ECOLI - SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN UGPA		transport	264603
787	80258364 (1573, 1574)			UNCLASSIFIED	264593

788	80507844 (1575, 1576)	Novel Protein sim. GBank gij2746079 (AF015310) - BTH1 [Brassica napus]		synthase	264809, 264602, 264603, 264769, 264638
789	17294715 (1577, 1578)	Novel Protein sim. GBank gij2351849 (U933357) - 40 kDa heat shock chaperone protein [Halobacterium salinarum]		UNCLASSIFIED	265007
790	86284406 (1579, 1580)	Novel Protein sim. GBank gij5706378 [dbj]BAA83099.1 - (AB026118) MAL T1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	22278999, 29331824, 264828, 87188559, 265018, 21906765, 21906767, 21906768, 21906769, 265020, 264692, 22279000, 264563
791	94651827 (1581, 1582)	Novel Protein sim. GBank gij568994 [emb]CAB51985.1 - (AL109863) putative isoleucyl-tRNA synthetase [Streptomyces coelicolor A3(2)]			264601, 264605, 264638
792	80058788 (1583, 1584)	Novel Protein sim. GBank gij393194 (L02375) - S-antigen [Plasmodium falciparum]		struct	265021, 264631, 264635, 264556
793	79638730 (1585, 1586)	Novel Protein sim. GBank gij1345408 [dbj]BAA05046 - (D26046) AT molli-binding factor [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	264693
794	81839284 (1587, 1588)	Novel Protein sim. GBank gij105884 [pir]S24023 - dopamine receptor D4 - human (fragment)		UNCLASSIFIED	264603, 264604, 264910, 264762, 264906, 264639, 264909, 264757
795	80074988 (1589, 1590)	Novel Protein sim. GBank gij187334 [emb]CAB07082 - (Z92771) birA [Mycobacterium tuberculosis]		carboxylase	264488, 35696052, 264905, 264807, 265010, 35698423, 264638
796	86669451 (1591, 1592)				60432229, 55811150, 264630, 264637, 264565
797	87771781 (1593, 1594)	Novel Protein sim. GBank gij2995447 [emb]CAA71519 - (Y10495) CDV-1R protein [Mus musculus]		struct	22278998, 264093, 264094, 68714117, 21906767, 21906769, 265020, 265022
798	79865209 (1595, 1596)	Novel Protein sim. GBank gij4467250 [emb]CAB37575 - (AL035569) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]		transcript factor	264687, 264768, 264693
799	79557818 (1597, 1598)			hydrolase	264808, 264910, 264638, 264638
800	79970189 (1599, 1600)			UNCLASSIFIED	264488
801	80498398 (1601, 1602)	Novel Protein sim. GBank gij2791517 [emb]CAA16054 - (AL021246) hypothetical protein RV2477c [Mycobacterium tuberculosis]		transport	264508, 264511, 265008, 265009, 264769, 264587, 264486
802	79834598 (1603, 1604)	Novel Protein sim. GBank gij4867211 [gb]AAD32237.1 [AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]			264905, 264693
803	20467520 (1605, 1606)	Novel Protein sim. GBank gij1176152 [sp]P44507 [YHAD_HAEIN - HYPOTHETICAL PROTEIN HI0091]		struct	264605
804	10174239 (1607, 1608)			kinase	264510
805	79599993 (1609, 1610)	Novel Protein sim. GBank gij2764612 [emb]CAA04683 - (AJ001330) ornithine transcarbamoylase [Lactobacillus sakei]	Contains protein domain (PF00185) - Aspartate/ornithine carbamoyltransferase	transferase	264508, 264769
806	80484113 (1611, 1612)				
807	80381812 (1613, 1614)	Novel Protein sim. GBank gij283331 [sp]Q21828 [YNFDCAEEL - HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III]			264764

808	35106817 (1615, 1616)	Novel Protein sim. GBank gi3913092 sp Q46170 ARCO_CLOPE - ARGININE/ORNITHINE ANTIporter		transport	264909, 264602, 21906764, 18108374
809	81454254 (1617, 1618)	Novel Protein sim. GBank gi3913016 sp P74309 ALF1_SYNY3 - FRUCTOSE- BISPHOSPHATE ALDOLASE CLASS I (FBP ALDOLASE)	Contains protein domain (PF00274) - Fructose-bisphosphate aldolase class-I	UNCLASSIFIED	264508, 264906, 264909, 265007, 264910, 264758, 264600, 264602, 264603, 264605, 264687, 264769, 264689, 264636, 264486
810	80192761 (1619, 1620)	Novel Protein sim. GBank gi401472 sp P30863 YAFB_ECOLI - HYPOTHETICAL OXIDOREDUCTASE IN ASPU-MLTD INTERGENIC REGION	Contains protein domain (PF00248) - Aldo/keto reductase family	reductase	264369
811	80079280 (1621, 1622)			UNCLASSIFIED	264558
812	10297654 (1623, 1624)			UNCLASSIFIED	264692
813	79612280 (1625, 1626)			UNCLASSIFIED	264906
814	80473427 (1627, 1628)	Novel Protein sim. GBank gi1146168 (J01617) - glutaminyl- RNA synthetase [Escherichia coli]		synthase	264905, 264602, 264605, 264682, 264687, 264769, 264636
815	95419513 (1629, 1630)	Novel Protein sim. GBank gi4589652 dbj BAA76848.1 - (AB023221) KIAA1004 protein [Homo sapiens]		UNCLASSIFIED	264488, 22278998, 22278999, 29331822, 29331824, 29331825, 29331827, 29331828, 29146499, 264905, 264908, 265007, 33657402, 60433356, 60433438, 264758, 265011, 265017, 265018, 265019, 264369, 264288, 264685, 21906765, 21906767, 265020, 285021, 264692, 65274820, 33857109, 264629, 18108376, 264635, 264638, 60170394, 56182323, 264564 264600
816	19881910 (1631, 1632)			UNCLASSIFIED	264595
817	95293316 (1633, 1634)	Novel Protein sim. GBank gi1781144 emb CA062541 - (Z83866) hypothetical protein Rv3069 [Mycobacterium tuberculosis]			
818	80938190 (1635, 1636)	Novel Protein sim. GBank gi11477468 (U35244) - vacuolar protein sorting homolog v-ps33a [Rattus norvegicus]			65274572, 22278999, 60424269, 35696052, 55812038, 21906768, 55811957, 35695917, 33657023, 18108370, 18108374, 55810764, 35696423, 55811576, 264636
819	80254977 (1637, 1638)	Novel Protein sim. GBank gi1001352 dbj BAA10839 - (D64006) ABC transporter [Synecocystis sp.]		transport	264565
820	80059688 (1639, 1640)	Novel Protein sim. GBank gi586814 sp P37484 YYBT_BACSU - HYPOTHETICAL 74.3 KD PROTEIN IN RPLI-COTF INTERGENIC REGION		UNCLASSIFIED	264600, 264602, 264604
821	79762590 (1641, 1642)			UNCLASSIFIED	264910
822	80215310 (1643, 1644)			UNCLASSIFIED	264510, 264594, 264637
823	94992299 (1645, 1646)	Novel Protein sim. GBank gi3878400 emb CAA95828 - (Z71264) predicted using Genefinder. Weak similarity to Mouse T-complex-associated-testes-expressed-1 protein (PIR Acc. No. A45841); cDNA EST EMBL:D32742 comes from this gene; cDNA EST EMBL:D33617 comes from this gene; cDNA EST...		struct	264509, 264687, 264691
824	80411171 (1647, 1648)	Novel Protein sim. GBank gi1370076 emb CAA66887 - (X98235) type I [Drosophila melanogaster]	Contains protein domain (PF01429) - Methyl-CpG binding domain		264910, 264763, 264769, 264693

825	20638600 (1649, 1650)	Novel Protein sim. GBank gi 3025132 sp p77391 YEAG_ECOLI - HYPOTHETICAL 74.5 KD PROTEIN IN GAPA-RND INTERGENIC REGION		UNCLASSIFIED	264592
826	11075047 (1651, 1652)	Novel Protein sim. GBank gi 3242281 emb CAA16689  - (AL021646) hypothetical protein Rv3202c [Mycobacterium tuberculosis]			264605
827	80054207 (1653, 1654)	Novel Protein sim. GBank gi 3417424 emb CAA20312  - (AL031261) putative transport protein [Schizosaccharomyces pombe]			264603
828	95106322 (1655, 1656)	Novel Protein sim. GBank gi 4336692 gb AAD17897  - (AF101361) Abnormal X segregation [Drosophila melanogaster]		UNCLASSIFIED	52645080, 264508, 264905, 264905, 264509, 264908, 264907, 264908, 264908, 264512, 264910, 264591, 264758, 264800, 264768, 264768, 21908768, 35695917, 264691, 264628, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 264639, 83373044, 18108385, 264563, 264568, 264486
829	81742215 (1657, 1658)			UNCLASSIFIED	264758, 264634
830	20396091 (1659, 1660)	Novel Protein sim. GBank gi 3820539 (AF080002) - UDP-N- acetylmutamyl tripeptide synthetase MurC [Helicobacter mobilis]		UNCLASSIFIED	264603
831	87112435 (1661, 1662)			UNCLASSIFIED	66714117, 264910, 264639
832	19536322 (1663, 1664)	Novel Protein sim. GBank gi 1870004 emb CAB08855  - (Z92539) hypothetical protein Rv1024 [Mycobacterium tuberculosis]		UNCLASSIFIED	264908
833	20726654 (1665, 1666)	Novel Protein sim. GBank gi 2500058 sp Q46267 PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME		UNCLASSIFIED	264602
834	21428762 (1667, 1668)	Novel Protein sim. GBank gi 2497531 sp Q46078 KPYK_CORGL - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	kinase	264600, 264602, 264769, 264689, 264636
835	94140482 (1669, 1670)				264768, 263994, 21806767, 264910, 264632, 264635, 264259, 264639, 264693, 83373044, 264758, 35696052, 22279002, 264508, 264905, 264906, 264448, 263972, 264908, 264909
836	66126552 (1671, 1672)	Novel Protein sim. GBank gi 699315 (U15184) - phosphate transport protein PSTC [Mycobacterium leprae]		transport	35695917, 264557
837	79450450 (1673, 1674)			UNCLASSIFIED	264595
838	78184203 (1675, 1676)	Novel Protein sim. GBank gi 728867 sp P40602 APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		UNCLASSIFIED	264687
839	79641125 (1677, 1678)	Novel Protein sim. GBank gi 2498533 sp Q50598 Y0D8_MYCTU - HYPOTHETICAL 69.9 KD PROTEIN CY1A11.08		UNCLASSIFIED	264906
840	80058651 (1679, 1680)	Novel Protein sim. GBank gi 4557753 ref NP_000372.1 pMID1 - midline 1 protein (finger)	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept	264762, 264556

841	80376318 (1681, 1682)	Novel Protein sim. GBank gil139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN Novel Protein sim. GBank gil2114321[dbj]BAA200371 - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264764
842	80078724 (1683, 1684)	Novel Protein sim. GBank gil2114321[dbj]BAA200371 - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00569) - Zinc finger present in cystrophin, CBP/p300	UNCLASSIFIED	264905, 264908, 265008, 265009, 18108374, 56182323, 264558
843	87002847 (1685, 1686)	Novel Protein sim. GBank gil3882325[dbj]BAA34522.11 - (AB018345) KIAA0802 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	struct	264091, 26331825, 264906, 264768, 264563
844	17941439 (1687, 1688)	Novel Protein sim. GBank gil2224721[dbj]BAA208441 - (AB002388) KIAA0390 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	265011
845	18346844 (1689, 1690)	Novel Protein sim. GBank gil2224721[dbj]BAA208441 - (AB002388) KIAA0390 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	kinase	264829 264907
846	79863441 (1691, 1692)	Novel Protein sim. GBank gil825679[pir]JA36929 - virulence regulatory protein VarB - Pseudomonas solanacearum			264909
847	78595348 (1693, 1694)			UNCLASSIFIED	265020
848	78489385 (1695, 1696)			UNCLASSIFIED	264588
849	78756387 (1697, 1698)			UNCLASSIFIED	264909
850	79817849 (1699, 1700)	Novel Protein sim. GBank gil3183245[sp]P78061[JC.K_ECOLI - PUTATIVE GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	
851	95320333 (1701, 1702)	Novel Protein sim. GBank gil5454130[re]NP_006280.1pTLN] - talin	Contains protein domain (PF01608) - I/LVEQ domain		264488, 52644507, 264489, 18108398, 85274572, 56182575, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 20281171, 264490, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29146498, 29146499, 264107, 264905, 264906, 264907, 264908, 52644045, 56182435, 265006, 265007, 265008, 265009, 264910, 60432229, 60431735, 60433358, 33657402, 60433438, 264595, 264758, 264759, 21906754, 33109954, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 264762, 264681, 18108351, 264763, 264448, 264682, 264764, 264683, 18108354, 264288, 264368, 264685, 264766, 264687, 264768, 264769, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 29148629, 55811957, 35695917, 265020, 265021, 265022, 60170815, 52644150, 264691, 264692, 33657023, 264693, 263966, 33657109, 27486261, 27486262, 27486264, 27486265, 35695763, 60431602, 18108370, 20281089, 264629, 18108374, 18108376, 55811576, 35696423, 35695855, 264634, 264635, 264636, 264555, 60431850, 264556, 264691
852	10147366 (1703, 1704)				

853	13032587 (1705, 1706)	Novel Protein sim. GBank gij3402836[embjCAA76082] - (Y16136) 2-enoate reductase [Moorella thermoacetica]		reductase	264638 264568
854	80052438 (1707, 1708)				
855	79641130 (1709, 1710)				264692
856	11594238 (1711, 1712)			UNCLASSIFIED	264591
857	79210165 (1713, 1714)			UNCLASSIFIED	264630, 264634
858	80248910 (1715, 1716)				265008, 265009, 264601, 264602, 264603, 18108351
859	20296634 (1717, 1718)				264558
860	80041748 (1718, 1720)			UNCLASSIFIED	264489
861	85857045 (1721, 1722)			UNCLASSIFIED	33657023, 264630
862	80079467 (1723, 1724)				264600
863	80578931 (1725, 1726)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	264488, 18108398, 35698288, 264259, 18108351, 264288, 265021
864	94939904 (1727, 1728)			UNCLASSIFIED	264259, 264112, 263974
865	80045310 (1729, 1730)	Novel Protein sim. GBank gij5689884[embjCAB52047.1] - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01479) - S4 domain		264635, 264600, 264636, 264591, 264602, 264693
866	80162031 (1731, 1732)	Novel Protein sim. GBank gij4557876[refjNP_000341.1]pABCR - ATP binding cassette transporter	transport		264288, 264557, 264558
867	80062402 (1733, 1734)				264605
868	10075364 (1735, 1736)			UNCLASSIFIED	264909
869	80062408 (1737, 1738)				264605, 264687, 18108374
870	80249651 (1739, 1740)	Novel Protein sim. GBank gij828660[piljS37755 - Adenylyl-transferase - Escherichia coli Novel Protein sim. GBank gij1708180[spjQ10602]HEMK_MYCTU - HEMK PROTEIN HOMOLOG	transferase		264601, 264636
871	20378295 (1741, 1742)			UNCLASSIFIED	264603
872	95197114 (1743, 1744)	Novel Protein sim. GBank gij1545959[embjCAA67763] - (X99384) paladin [Mus musculus]		UNCLASSIFIED	35696286, 22278998, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264509, 284905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 264910, 264591, 60433358, 264596, 52648317, 87188474, 285010, 264602, 264603, 265017, 265018, 264605, 18108351, 264764, 264768, 264768, 52644229, 264769, 21906765, 265021, 264534, 264681, 52645129, 264628, 264629, 35698423, 65274791, 264631, 264632, 264635, 264636, 264558, 264637, 264638, 264639, 60432113, 22278000, 22279002, 264584
873	20189728 (1745, 1746)	Novel Protein sim. GBank gij4156104 (AE001569) - putative Outer membrane protein [Helicobacter pylori J99]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	UNCLASSIFIED	264595

874	80077592 (1747, 1748)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)		UNCLASSIFIED	264600
875	86608446 (1749, 1750)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)			264259, 264448, 264288, 264557, 87168518
876	86465157 (1751, 1752)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)	transport		264907, 264601, 264602, 264605, 265020, 60431602
877	87802548 (1753, 1754)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)	transcript factor		22278998, 264809, 264369
878	80187289 (1755, 1756)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)	ATPase, associated		264369, 264555
879	94328962 (1757, 1758)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)			56182575, 29331824, 264508, 264906, 265018, 18108351, 264448, 264683, 21906768, 21908768, 80170815, 33657023, 65274820, 33657109, 18108374, 35695855, 264563
880	8491135 (1759, 1760)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)	Contains protein domain (PF00051) - Kringle domain		264508
881	11290122 (1761, 1762)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)		UNCLASSIFIED	264508
882	11077011 (1763, 1764)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)		UNCLASSIFIED	264558
883	78582969 (1765, 1766)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)		UNCLASSIFIED	264688
884	13517921 (1767, 1768)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)		UNCLASSIFIED	264636
885	80052457 (1769, 1770)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)		UNCLASSIFIED	264605, 18108362
886	11685138 (1771, 1772)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)			264690
887	94315307 (1773, 1774)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)	dehydrogenase		35696052, 264906, 264600, 264603, 35695917, 35695855, 264636
888	10083399 (1775, 1776)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)	UNCLASSIFIED		264908
889	20385917 (1777, 1778)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)			264603
890	19904337 (1779, 1780)	Novel Protein sim. GBank gi134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)			264629

881	13516879 (1781, 1782)	Novel Protein sim. GBank gi 4959386 gb AAD34331.1 AF11248 - (AF112481) RAD54B protein [Homo sapiens]			UNCLASSIFIED	284636
882	87834157 (1783, 1784)	Novel Protein sim. GBank gi 2828886 sp P80608 CYSK_MAIZE - CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIOL)-LYASE) (CSASE) 1b=transcription factor binding to initiation site of HIV-1 (alternatively spliced) [human, Namata cells, Peptide, 541 aa]			transcript factor	22278896, 22278899, 28331828, 35696052, 264608, 264909, 265009, 265011, 264602, 265019, 264786, 21908765, 21906766, 21906769, 265020, 265021, 56528488, 264689, 263967
883	78168037 (1785, 1786)	Novel Protein sim. GBank gi 2828886 sp P80608 CYSK_MAIZE - CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIOL)-LYASE) (CSASE)			synthase	
884	11102240 (1787, 1788)					263978
885	80239868 (1789, 1790)				UNCLASSIFIED	264508, 284600, 284555, 284559
886	79747803 (1781, 1782)					264632
887	94981923 (1793, 1794)			Contains protein domain (PF00047) - immunoglobulin domain	UNCLASSIFIED	284686, 28331828, 264511
888	87895109 (1795, 1796)					56182575, 60432289, 56182435, 60432229, 55811957, 22279000, 264488
889	11100463 (1787, 1788)					264601
890	80499768 (1799, 1800)	Novel Protein sim. GBank gi 1750127 (U66480) - YncC [Bacillus subtilis]			transport	284789, 284691, 284583
891	80502410 (1801, 1802)	Novel Protein sim. GBank gi 312879 sp O07438 SYA_MYCTU - ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)		Contains protein domain (PF01411) - RNA synthetases class II (A)	synthase	264907, 264602, 264605, 264769, 35695917, 18109376, 264563
892	80503301 (1803, 1804)	Novel Protein sim. GBank gi 3355701 emb CAA20001  - (AL031124) 3-isopropylmalate dehydratase large subunit [Streptomyces coelicolor]		Contains protein domain (PF00330) - aconitase family (aconitate hydratase)	isomerase	264909, 265008, 264602, 264604, 264769, 264689, 264693
893	82060208 (1805, 1806)	Novel Protein sim. GBank gi 2960120 emb CAA18018.1  - (AL022121) glpK [Mycobacterium tuberculosis]		Contains protein domain (PF00370) - FGY family of carbohydrate kinases	kinase	35696052, 284905, 284510, 284511, 284512, 264605, 264760, 18108351, 264762, 264687, 264768, 264769, 264688, 21908764, 35695917, 27486262, 35695855, 264634, 264636, 264488
894	20451078 (1807, 1808)	Novel Protein sim. GBank gi 28887 sp P40906 ARGI_COCIM - ARGINASE		Contains protein domain (PF00491) - Arginase family	hydrolase	264604
895	9398483 (1809, 1810)	Novel Protein sim. GBank gi 4567200 gb AAD23616.1 AC00716 - (AC007168) hypothetical protein [Arabidopsis thaliana]			UNCLASSIFIED	264909
896	80052828 (1811, 1812)	Novel Protein sim. GBank gi 3736200 emb CAA21292  - (AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe]				284595, 284605
897	87913201 (1813, 1814)					
898	11754482 (1815, 1816)				UNCLASSIFIED	60432289, 264601, 264690
899	20727907 (1817, 1818)	Novel Protein sim. GBank gi 3868840 dbj BAA34296  - (AB015054) Alg2 [Rhizomucor pusillus]			UNCLASSIFIED	264638
900	16776206 (1819, 1820)	Novel Protein sim. GBank gi 4589726 dbj BAA76883.1  - (AB003137) DnaJ homolog protein [Salix gligiana]		Contains protein domain (PF00684) - DnaJ central domain (4 repeats)	UNCLASSIFIED	264602
901					eph	265009



911	87454340 (1821, 1822)	Novel Protein sim. GBank gi 548774 sp P35685 RL7A_ORYSA - 60S RIBOSOMAL PROTEIN L7A		ribosomal prot	265010, 264604, 60432113
912	20448663 (1823, 1824)	Novel Protein sim. GBank gi 2314008 gb AA007921.1  - (AE000597) CDP-diglyceride hydrolase (cdh) [Helicobacter pylori 26695]		hydrolase	264559
913	20469357 (1825, 1826)	Novel Protein sim. GBank gi 417657 sp Q03604 RIR1_CAEEL - PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (RIBONUCLEOTIDE REDUCTASE)	Contains protein domain (PF00317) - Ribonucleotide reductase	UNCLASSIFIED - reductase	264604 264636
914	79183351 (1827, 1828)	Novel Protein sim. GBank gi 1655699 emb CA469032  - (Y07752) pherophorin-S [Volvox carter]			
915	87606703 (1829, 1830)	Novel Protein sim. GBank gi 5689571 db BAA83069.1  - (AB029040) KIAA1117 protein [Homo sapiens]			18108398, 22278995, 66714117, 264906, 264591, 21906788, 265020, 55811576, 264638
916	79444091 (1831, 1832)	Novel Protein sim. GBank gi 4186110 emb CAA71790  - (Y10831) putative integrase [Ralstonia eutropha]		UNCLASSIFIED	264595
917	20195985 (1833, 1834)	Novel Protein sim. GBank gi 1655699 emb CA469032  - (Y07752) pherophorin-S [Volvox carter]		UNCLASSIFIED synthase	264605 264259, 28331826, 264808, 265019, 264448, 265020, 264635, 83373044
918	91228795 (1835, 1836)	Novel Protein sim. GBank gi 5689571 db BAA83069.1  - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]			265006, 264512, 264600, 264602, 264604, 264768, 18108370, 264563
919	80436785 (1837, 1838)	Novel Protein sim. GBank gi 168448 sp Q05813 AMP1_STRLI - XAA-PRO AMINOPEPTIDASE I (X-PRO AMINOPEPTIDASE I) (AMINOPEPTIDASE P I) (APP) (PEPP I) (AMINOACYLPROLINE AMINOPEPTIDASE I)		peptidase	264508
920	79506095 (1839, 1840)	Novel Protein sim. GBank gi 2497688 sp Q06093 PAFA_MOUSE - PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2- ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA2)) (2-ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1- ALKYL-2-ACETYLGLYCEROPHO...		UNCLASSIFIED	264600
921	19858634 (1841, 1842)	Novel Protein sim. GBank gi 3850084 emb CAA21911.1  - (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]			265019, 22279002
922	78982805 (1843, 1844)	Novel Protein sim. GBank gi 267079 sp P29514 TB86_ARATH - TUBULIN BETA-6 CHAIN		tubulin	264907, 265008, 265009, 265010, 18108351, 264689, 265021, 18108370, 18108374, 18108385
923	86695830 (1845, 1846)			esterase	264510 264603
924	21431341 (1847, 1848)	Novel Protein sim. GBank gi 2497688 sp Q06093 PAFA_MOUSE - PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2- ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA2)) (2-ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1- ALKYL-2-ACETYLGLYCEROPHO...			
925	20630332 (1849, 1850)	Novel Protein sim. GBank gi 3802325 db BAA34522.1  - (AB018345) KIAA0802 protein [Homo sapiens]			55811957, 283972, 264639
926	79397657 (1851, 1852)			UNCLASSIFIED	264769
927	37036201 (1853, 1854)				

928	80070610 (1855, 1856)	Novel Protein sim. GBank gi 156146 (M30316) - xanthine dehydrogenase (AA at 2538) [Calliphora vicina]		dehydrogenase	264605
929	20630336 (1857, 1858)			UNCLASSIFIED	264603
930	5496348 (1859, 1860)	Novel Protein sim. GBank gi 4115936 gb AAD03446.1  - (AF118223) No definition line found [Arabidopsis thaliana]			264259
931	10245731 (1861, 1862)	Novel Protein sim. GBank gi 4480609 emb CAB38642.1  - (AJ133495) ribonucleotide reductase major subunit [Staphylococcus aureus]	Contains protein domain (PF00317) - ribonucleotide reductase	reductase	264486
932	80420613 (1863, 1864)	Novel Protein sim. GBank gi 5459396 emb CAB50754.1  - (AL096839) putative integral membrane transport protein [Streptomyces coelicolor]		transport	264508, 264905, 264908, 264909, 264600, 264602, 264603, 264605, 264766, 264558, 18108387, 264486
933	94326010 (1865, 1866)	Novel Protein sim. GBank gi 5689523 dbj BAA83045.1  - (AB029016) KIAA1093 protein [Homo sapiens]	Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	264508, 264686, 264693, 27486281, 18108370, 65274791, 264636, 264559, 22279002
934	80038105 (1867, 1868)	Novel Protein sim. GBank gi 119111 sp P12978 EBN2_EBV - EBNA-2 NUCLEAR PROTEIN			264369, 22279002
935	80063162 (1869, 1870)			UNCLASSIFIED	264604, 264605, 264693, 18108370, 18108374
936	80026632 (1871, 1872)	Novel Protein sim. GBank gi 845686 (M32103) - ORF-27 [Staphylococcus aureus]		UNCLASSIFIED	22278995, 22278996, 264602, 264687, 32833986, 18108387
937	80250273 (1873, 1874)	Novel Protein sim. GBank gi 1360669 pir CGHU1V - collagen alpha 1(V) chain precursor - human		synthase	263978
938	80026633 (1875, 1876)	Novel Protein sim. GBank gi 226243 emb CAA74531.1  - (Y14083) hypothetical protein [Bacillus subtilis]		UNCLASSIFIED	264602
939	11071694 (1877, 1878)				264600
940	94144252 (1879, 1880)	Novel Protein sim. GBank gi 3560166 emb CAA20678  - (AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264905, 264906, 264907, 264908, 264909, 264511, 264910, 264592, 33857402, 264598, 264758, 264760, 264683, 264766, 264768, 264769, 33857023, 33857109, 264628, 264629, 264630, 264635, 264636, 264555, 264637, 264556, 264638, 264639, 83373044, 18108385, 264565, 18108391
941	11398414 (1881, 1882)				264593
942	19484122 (1883, 1884)			UNCLASSIFIED	264760
943	80080258 (1885, 1886)	Novel Protein sim. GBank gi 4033728 (AF038595) - apolipoprotein N-acyltransferase [Pseudomonas aeruginosa]		UNCLASSIFIED	264600, 264687, 264689, 264563
944	80216096 (1887, 1888)	Novel Protein sim. GBank gi 2494764 sp Q50729 GUAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)		synthase	264511, 264603
945	80052477 (1889, 1890)	Novel Protein sim. GBank gi 732353 sp P39606 YWCH_BACSU - HYPOTHETICAL 36.6 KD PROTEIN IN QOXD-VPR INTERGENIC REGION	Contains protein domain (PF00818) - ice nucleation protein repeat	UNCLASSIFIED	264906, 264604, 264605, 265020, 18108387
946	76248402 (1891, 1892)				265017

947	81802698 (1893, 1894)	Novel Protein sim. GBank gij2898770[emb CAA17247] - (AL021898) hypothetical protein RV2033c [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	18108394, 22278996, 264907, 264909, 265008, 265009, 264910, 264758, 264600, 264602, 265018, 264605, 264768, 264689, 264693
948	88165538 (1895, 1896)	Novel Protein sim. GBank gij2827284 (AF041037) - novel antagonist of FGF signaling [Homo sapiens]		fgf	18108398, 58182575, 22278997, 22278999, 50432049, 29331822, 29331826, 264907, 56182435, 55811386, 265011, 264600, 265017, 265018, 265019, 18108351, 265020, 265021, 265022, 27486265, 263972, 55811576, 264638, 60170394, 264566
949	88081786 (1897, 1898)	Novel Protein sim. GBank gij4507985[ref NP_003427.1 pZNF1 - zinc finger protein 135 (clone pHZ-17)]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcription factor	29331825, 21906764, 27486261, 21906766, 52644296, 33657349, 87188318, 56994075, 265020, 265021, 87168559, 52644150, 264637
950	78485672 (1899, 1900)	Novel Protein sim. GBank gij1079461[pir S43865 - cytochrome b, type II - poliovirus (fragment)]	Contains protein domain (PF00038) - Intermediate filament proteins	struc	264683, 18108361
951	20451411 (1901, 1902)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264604
952	79566954 (1903, 1904)	Novel Protein sim. GBank gij5305702[gb AA041779.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]		cathepsin	264910, 264691
953	10196003 (1905, 1906)	Novel Protein sim. GBank gij2495842[sp Q47142 YFHS_ECOLI - HYPOTHETICAL 41.6 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION]		transport	264510
954	9893328 (1907, 1908)	Novel Protein sim. GBank gij2360965 (AF016253) - D-amino acid dehydrogenase [Klebsiella aerogenes]		dehydrogenase	264508
955	95313410 (1909, 1910)	Novel Protein sim. GBank gij5454064[ref NP_006319.1 pSIP1 - SYT interacting protein]	Contains protein domain (PF00076) - RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	56994075, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264910, 264758, 264759, 265010, 264601, 264760, 18108351, 264782, 264763, 264764, 264766, 264686, 264767, 264687, 264768, 264769, 264689, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 56182323, 264639, 18108388, 264563, 264564
956	80064224 (1911, 1912)	Novel Protein sim. GBank gij2052129[emb CAB08155] - (Z94752) rimJ [Mycobacterium tuberculosis]			264605
957	80056206 (1913, 1914)			UNCLASSIFIED	264603, 18108362
958	80036446 (1915, 1916)	Novel Protein sim. GBank gij1709787[sp Q00451 PRF1_LYCES - 36.4 KD PROLINE-RICH PROTEIN]		UNCLASSIFIED	264908, 264910, 264762, 263978, 264637
959	80026847 (1917, 1918)	Novel Protein sim. GBank gij2131050[emb CAB09260] - (Z95844) opeA [Mycobacterium tuberculosis]		UNCLASSIFIED	264602, 264692
960	37815406 (1919, 1920)	Novel Protein sim. GBank gij2129478[pir S51939 - chitinase (EC 3.2.1.14) precursor - beet]		UNCLASSIFIED	264259
961	20567383 (1921, 1922)				263978
962	11399318 (1923, 1924)				264593

963	80580374 (1925, 1926)			UNCLASSIFIED	264510, 264288, 264555, 264556, 264559, 264488
964	79832019 (1927, 1928)	Novel Protein sim. GBank gl 4589622 dbj BAA76833.1  - (AB023206) KIAA0989 protein [Homo sapiens]		UNCLASSIFIED	264112, 264910, 264689
965	91229465 (1929, 1930)	Novel Protein sim. GBank gl 5420387 emb CAB46678.1  - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 265017, 264448, 264634, 264558, 83373044
966	95292815 (1931, 1932)			UNCLASSIFIED	264906, 264592, 264596, 264604, 264768, 21906764, 264692, 264693, 264829, 264636, 264638
967	79255708 (1933, 1934)	Novel Protein sim. GBank gl 1731207 sp Q11156 RGX3_MYCTU - SENSORY TRANSDUCTION PROTEIN REGX3	Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase	264760
968	79560269 (1935, 1936)	Novel Protein sim. GBank gl 2661836 emb CAA75187.1 - (Y14864) putative transport protein [Methylophilus methylotrophus]		transport	264693
969	79919470 (1937, 1938)	Novel Protein sim. GBank gl 5419878 emb CAB46422.1  - (AL096747) hypothetical protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	35696286, 264685, 264686, 35895917, 264892, 18108374, 264635
970	95085947 (1939, 1940)			UNCLASSIFIED	18108392, 18108394, 18108398, 22278995, 22278996, 22278998, 29147620, 264828, 265006, 265007, 265008, 285009, 18108348, 33109854, 265010, 265011, 18108351, 264288, 21906767, 21906768, 18108370, 18108374, 18108377, 264630, 264635, 18108380, 83373044, 18108387, 18108388
971	78919770 (1941, 1942)			UNCLASSIFIED	265007, 265020, 22279002
972	20710704 (1943, 1944)				264557
973	20370183 (1945, 1946)	Novel Protein sim. GBank gl 1723119 sp P53990 Y174_HUMAN - HYPOTHETICAL PROTEIN KIAA0174			264804
974	80057103 (1947, 1948)			UNCLASSIFIED	264565
975	10196018 (1949, 1950)			UNCLASSIFIED	264510
976	80205742 (1951, 1952)	Novel Protein sim. GBank gl 3881459 emb CAA92988.1  - (Z68753) predicted using GeneFinder: Similarity to Yeast hypothetical protein YIK9 (SW:YIK9_YEAST); cDNA EST EMBL:D27680 comes from this gene; cDNA EST EMBL:D27679 comes from this gene; cDNA EST EMBL:D64477 comes from this ge...		UNCLASSIFIED	264508, 264906, 264758, 264632, 264639, 264563
977	10355349 (1953, 1954)	Novel Protein sim. GBank gl 549458 sp Q05335 XYS3_PSEPU - XYLDLEGF OPERON TRANSCRIPTIONAL ACTIVATOR 3		UNCLASSIFIED	264906
978	80025927 (1955, 1956)			UNCLASSIFIED	264600, 264602, 264603, 264604
979	80447820 (1957, 1958)	Novel Protein sim. GBank gl 3171904 emb CAA75869j - (Y15908) DIA-12C protein [Homo sapiens]		UNCLASSIFIED	264767, 264768, 265008, 285007, 264908
980	80025928 (1959, 1960)			UNCLASSIFIED	264600, 264602, 264605
981	80098550 (1961, 1962)	Novel Protein sim. GBank gl 3599940 (AF017368) - facio-genital dysplasia protein 2 [Mus musculus]		UNCLASSIFIED	264692, 264555, 264556, 264557, 264559

982	80195670 (1963, 1964)	Novel Protein sim. GBank gii2950220[emb]CAA071575] - (Y10545) fused-codB [Escherichia coli]		UNCLASSIFIED	264404
983	90995041 (1965, 1966)	Novel Protein sim. GBank gii476389[pri]B43402 - myosin heavy chain-B, neuronal - chicken		struct	65274572, 56182575, 264908, 264909, 265007, 265008, 264758, 265010, 55811150, 33657023, 264634, 264557, 264558
984	20466876 (1967, 1968)			UNCLASSIFIED	264605
985	65461368 (1969, 1970)	Novel Protein sim. GBank gii3451504[emb]CAA07660.1] - (AJ007747) hypothetical protein BBLPS1.21 [Bordetella bronchiseptica]	Contains protein domain (PF00534) - Glycosyl transferases group 1	transferase	56182435, 264600
986	87102888 (1971, 1972)			UNCLASSIFIED	264106, 264110, 265020, 60170615
987	78667231 (1973, 1974)			UNCLASSIFIED	264909
988	19858681 (1975, 1976)			UNCLASSIFIED	264600
989	88095329 (1977, 1978)			UNCLASSIFIED	264508, 265017, 264534, 264564
990	88057746 (1979, 1980)	Novel Protein sim. GBank gii5725506[gb]AAD48080.1[AF06015] - (AF060152) METH1 protein [Homo sapiens]	Contains protein domain (PF01421) - Reprolysin (M12B) family zinc metalloprotease	oxidase	264259, 264908, 265008, 264910, 264596, 264369, 264288, 264766, 264628, 264635, 264568
991	10106140 (1981, 1982)	Novel Protein sim. GBank gii2105049[emb]CAB08835] - (Z95436) hypothetical protein Rv3645 [Mycobacterium tuberculosis]	Contains protein domain (PF00211) - Adenylate and Guanylate cyclase catalytic domain	UNCLASSIFIED	264909
992	79845694 (1983, 1984)			UNCLASSIFIED	264508, 264593
993	10814053 (1985, 1986)	Novel Protein sim. GBank gii3329297 (AE001355) - Ribonucleoside Reductase, Large Chain [Chlamydia trachomatis]		reductase	264907
994	11090590 (1987, 1988)				264602
995	94321911 (1989, 1990)	Novel Protein sim. GBank gii5106572[gb]AAD39760.1[AF14394] - transcriptional activator SRCAP [Homo sapiens]	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	18108398, 55274572, 22278996, 264490, 60432049, 29331827, 29146498, 264508, 264905, 264907, 264908, 56182435, 265008, 264591, 264592, 60432229, 60431735, 33657402, 264595, 264758, 21906754, 265010, 265017, 265018, 264605, 264760, 264448, 264763, 264768, 21906765, 21906768, 21906789, 55811957, 264692, 264693, 264629, 35896423, 55811576, 35695855, 264636, 264555, 264556, 264558, 83373044, 22279002, 264563
996	91013745 (1991, 1992)	Novel Protein sim. GBank gii2911719 (AC004227) - KIA001LB [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	phosphatase	83373044, 29331824, 263978, 55811957, 56526486, 87168518, 264910, 264908, 264585, 264566, 264693, 264766
997	80503347 (1993, 1994)	Novel Protein sim. GBank gii2649101 (AE001001) - ABC transporter, ATP-binding protein [Archaeoglobus fulgidus]	Contains protein domain (PF000005) - ABC transporter	transport	35698286, 22278997, 22278999, 264508, 264905, 264908, 265010, 264600, 264602, 264605, 264688, 264769, 265021, 264585, 18108391
998	11397390 (1995, 1996)	Novel Protein sim. GBank gii123530[sp]PQ4929[HRFX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR			264595

999	11768047 (1997, 1998)	Novel Protein sim. GBank gi 2506697 sp P46490 YFCA_HAEIN - HYPOTHETICAL PROTEIN H10198		UNCLASSIFIED	264682	
1000	20727944 (1999, 2000)			UNCLASSIFIED	264602	
1001	66673131 (2001, 2002)	Novel Protein sim. GBank gi 2224699 dbj BAA20833  - (AB002377) KIAA0379 [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	60432049, 264907, 264908, 264511, 264603, 264683, 264684, 264687, 264689, 29148827, 21908769, 264692, 18108385, 22279000 265009, 264369, 265020	
1002	80189603 (2003, 2004)	Novel Protein sim. GBank gi 586121 sp P37709 TRHY_RABIT - TRICHOHYALIN		sinucl		
1003	17933481 (2005, 2006)				265019	
1004	16314987 (2007, 2008)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 8]			264635	
1005	79617144 (2008, 2010)	Novel Protein sim. GBank gi 114073 sp P07672 APT_ECOLI - ADENINE PHOSPHORIBOSYL TRANSFERASE (APRT)		UNCLASSIFIED	264508	
1006	37815429 (2011, 2012)			UNCLASSIFIED	264259	
1007	79620871 (2013, 2014)	Novel Protein sim. GBank gi 4062979 dbj BAA36210.1  - (AB017138) epsilon subunit of malonate decarboxylase [Pseudomonas putida]		synthase	264905	
1008	88094444 (2015, 2016)	Novel Protein sim. GBank gi 2808807 emb CAA04607.1  - (AJ001206) putative trehalose synthase [Streptomyces coelicolor]		synthase	265007, 264602, 264605, 264760, 264638	
1009	57451289 (2017, 2018)	Novel Protein sim. GBank gi 3639077 (AF090113) - AMPA receptor binding protein [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	264102, 264288	
1010	94672537 (2019, 2020)	Novel Protein sim. GBank gi 3746332 (AF016307) - possible NADH-dependent oxidase, may function as a demethylase [Sinorhizobium meliloti]		dehydrogenase	264592	
1011	85546916 (2021, 2022)	Novel Protein sim. GBank gi 2342647 gb AAB86591.1  - (U90653) DHC-domain-containing cysteine-rich protein [Homo sapiens]		UNCLASSIFIED	35696052, 264905, 264764, 264788, 35695917, 264629	
1012	85294456 (2023, 2024)	Novel Protein sim. GBank gi 3413411 emb CAA20272  - (AL031231) guanosine pentaphosphate synthetase/ polyribonucleotide nucleotidyltransferase [Streptomyces coelicolor]	Contains protein domain (PF00013) KH domain	phosphorylase	35696052, 264905, 264600, 264601, 264602, 264605, 264762, 264786, 264788, 264689	
1013	86095772 (2025, 2026)			UNCLASSIFIED	264591, 21806788	
1014	86608828 (2027, 2028)				29331824, 265019, 265020	

1015	95418879 (2029, 2030)	Novel Protein sim. GBank gij4159995 (AF063095) - SELIL [Mus musculus]	Contains protein domain (PF00040) - struct Fibronectin type II domain	22278994, 22278995, 56994075, 22278996, 22278999, 264259, 29331825, 29331828, 264907, 56182435, 264510, 264591, 264593, 60433356, 264594, 55812038, 264758, 21906754, 33657084, 265010, 264600, 265017, 265018, 265019, 18108351, 21906765, 21906768, 21906767, 21906768, 55811957, 265022, 33657023, 65274620, 33657182, 32833986, 18108370, 18108377, 55811576, 35898423, 264630, 22279000, 264565
1016	78559694 (2031, 2032)	Novel Protein sim. GBank gij25069694p41407/ACPD_ECOLI - ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)	esterase	264686, 264693
1017	11069213 (2033, 2034)	Novel Protein sim. GBank gij5103943dbjBAA79259.1 - (AP000059) 802aa long hypothetical oligopeptide-binding protein oppA [Aeropyrum pernix]	Contains protein domain (PF00496) - transport Bacterial extracellular solute-binding proteins, family 5	264600
1018	80072430 (2035, 2036)	Novel Protein sim. GBank gij4493973jembjCAB39032.1 - (AL034559) predicted using hexExon; MAL3P7.14 (PFC0925w), Hypothetical protein, len: 489 aa [Plasmodium falciparum]		22278996, 29148627, 264563
1019	11703807 (2037, 2038)		UNCLASSIFIED	264686
1020	80234432 (2039, 2040)			264508, 264509, 264512, 264600, 264762, 264769, 264688, 18108370, 264636, 264638, 264486
1021	37036243 (2041, 2042)	Novel Protein sim. GBank gij4633807jgbjAAD26859.1jAF12779 - (AF127795) trehalose biosynthetic enzyme TreY [Rhizobium leguminosarum bv. viciae]	synthase	264769
1022	80502627 (2043, 2044)	Novel Protein sim. GBank gij1781230jembjCAB06271 - (Z83867) hypothetical protein Rv3137 [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - phosphatase Inositol monophosphatase family	35696052, 264508, 265008, 265009, 264769, 18108387, 264563
1023	11399341 (2045, 2046)	Novel Protein sim. GBank gij3777495 (U92083) - calcium transporting ATPase [Pichia angusta]	Contains protein domain (PF00122) - ATPase-associated E1-E2 ATPase	264593
1024	80057129 (2047, 2048)		UNCLASSIFIED	52646842, 33657402, 33657023, 18108379, 55811576, 264631, 264556, 264557, 264559, 18108388, 264566
1025	79644200 (2049, 2050)	Novel Protein sim. GBank gij3483045jembjCAA205561 - (AL031371) putative transport system permease protein [Streptomyces coelicolor]	transport	264693
1026	80025946 (2051, 2052)	Novel Protein sim. GBank gij1174922jspQ02322jUVRD_HAEIN - DNA HELICASE II	helicase	264602
1027	17659234 (2053, 2054)	Novel Protein sim. GBank gij4757728jrefjNP_004886.1jPAGTA - angiotensin/vasopressin receptor AII/AVP-like	UNCLASSIFIED	265017

1028	20287828 (2055, 2056)	Novel Protein sim. GBank gij2791409[emb]CAA16003] - (AL021184) acn [Mycobacterium tuberculosis]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	UNCLASSIFIED	264600
1029	94665090 (2057, 2058)			UNCLASSIFIED	264595
1030	80095343 (2059, 2060)			UNCLASSIFIED	264907, 264908, 264510, 264512, 265009, 265010, 265011, 264600, 264602, 264603, 264605, 264769, 18108372, 18108374
1031	95289117 (2061, 2062)			UNCLASSIFIED	264805, 264908, 264909, 264595, 264692, 264630, 264634, 264638
1032	94673275 (2063, 2064)	Novel Protein sim. GBank gij4503895[ref]NP_000145.1[pGALK - galactokinase 1]		UNCLASSIFIED	264689
1033	86464818 (2065, 2066)	Novel Protein sim. GBank gij2982990 (AE000682) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	35896052, 264908, 264510, 18108354, 264687, 264769, 264689, 60431602, 18108385, 264486
1034	79245937 (2067, 2068)	Novel Protein sim. GBank gij405895 (U00007) - methionyl-tRNA synthetase [Escherichia coli]		UNCLASSIFIED	264906
1035	79956355 (2069, 2070)			UNCLASSIFIED	264692
1036	85804998 (2071, 2072)			UNCLASSIFIED	264905, 66712502, 264908, 264768
1037	87896058 (2073, 2074)			UNCLASSIFIED	29331824, 264909, 60433438, 265019
1038	20481015 (2075, 2076)	Novel Protein sim. GBank gij790819 (L39851) - polycystic kidney disease-associated protein [Homo sapiens]	Contains protein domain (PF01477) - PLAT/LH2 domain		264604, 264634
1039	87260021 (2077, 2078)	Novel Protein sim. GBank gij2605967 (AF030027) - 24 [Equine herpesvirus 1]		UNCLASSIFIED	264092, 264093, 264094, 264683, 264689, 263967
1040	80026840 (2079, 2080)	Novel Protein sim. GBank gij2352095 (U97022) - DNA topoisomerase I [Fervidobacterium islandicum]	Contains protein domain (PF01131) - Prokaryotic DNA topoisomerase	isomerase	264595
1041	10156682 (2081, 2082)	Novel Protein sim. GBank gij3256535[dbj]BAA29218.1] - (AP000001) 301aa long hypothetical 2-phosphoglycerate kinase [Pyrococcus horikoshii]		kinase	264907
1042	11084375 (2083, 2084)	Novel Protein sim. GBank gij2058299[emb]CAA66953] - (X98309) ARI protein [Drosophila melanogaster]			264605
1043	80057136 (2085, 2086)	Novel Protein sim. GBank gij1870167[emb]CAA70125] - (Y09821) msK [Streptomyces reticuli]	Contains protein domain (PF00005) - ABC transporter	transport	264565, 264567
1044	80025952 (2087, 2088)			UNCLASSIFIED	265008, 264602, 265017
1045	52415482 (2089, 2090)	Novel Protein sim. GBank gij5689890[emb]CAB52053.1] - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]			28331825, 284637
1046	11754862 (2091, 2092)	Novel Protein sim. GBank gij854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]		helicase	264686
1047	37036258 (2093, 2094)	Novel Protein sim. GBank gij4210471[dbj]BAA74535.1] - (AB018033) orfSA [Pseudomonas sp.]		UNCLASSIFIED	264769
1048	79186400 (2095, 2096)	Novel Protein sim. GBank gij3413419[emb]CAA20279] - (AL031232) hypothetical protein SC10H5.07 [Streptomyces coelicolor]	Contains protein domain (PF00220) - Neurohypophysial hormones, N-terminal Domain	UNCLASSIFIED	264687
1049	81755108 (2097, 2098)	Novel Protein sim. GBank gij5051636[gb]AAD38326.1[AF07372] - (AF073727) EH domain-binding mitotic phosphoprotein [Homo sapiens]		UNCLASSIFIED	264905, 264634
1050	79471521 (2099, 2100)			UNCLASSIFIED	264686



1051	80475471 (2101, 2102)				UNCLASSIFIED	18108374, 264769, 265010, 265011, 264601, 265009, 264604, 264605, 264636, 18108351, 264692
1052	82442962 (2103, 2104)	Novel Protein sim. GBank gij123275 sp P35136 SERA_BACSU - D-3-PHOSPHOGLYCERATE DEHYDROGENASE (PGDH)	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases		dehydrogenase	264508, 264762, 264687, 264486
1053	94851640 (2105, 2106)	Novel Protein sim. GBank gij5441319 emb CAB46717.1  - (AL034396) dJ1158B12.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]				264686, 18108374, 29331824, 83373044, 21906754, 52645158, 56182435, 264689, 29331827, 27486281, 35696052, 21908765, 35696423, 21906768, 56182575, 21908769, 55811957, 87168518, 35696286, 22278997, 265020, 265011, 265021, 265022, 265007, 265018, 22278000, 22279002, 264482, 264906, 52644150, 264909, 264288, 29331822, 52645080, 264766
1054	79580225 (2107, 2108)				UNCLASSIFIED	264686
1055	80594138 (2109, 2110)	Novel Protein sim. GBank gij5052508 gb AAD38584.1 AF14560 - (AF145609) BcDNA.GH02833 [Drosophila melanogaster]	Contains protein domain (PF00270) - DEAD/DEAH box helicase		helicase	264907, 264602, 264681, 264288, 21906768, 33657109, 55810764, 35695855, 264631
1056	17882319 (2111, 2112)	Novel Protein sim. GBank gij3021676 dbj BAA25358 - (D86033) RNA polymerase sigma-70 factor [Pseudomonas fluorescens]			mapolymerase	264906
1057	85667216 (2113, 2114)	Novel Protein sim. GBank gij1226281 (U50308) - No definition line found [Caenorhabditis elegans]			UNCLASSIFIED	264682
1058	80376576 (2115, 2116)					264784
1059	84662754 (2117, 2118)	Novel Protein sim. GBank gij1170016 sp P46808 GREY_MYCLE - TRANSCRIPTION ELONGATION FACTOR GREY (TRANSCRIPT CLEAVAGE FACTOR GREY)			transcription factor	35696052, 35695855, 265009, 264636
1060	79481169 (2119, 2120)	Novel Protein sim. GBank gij2499087 sp Q09332 UGGG_DROME - UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)			glycoprotein	29146499, 264681, 264683, 264687
1061	11034025 (2121, 2122)	Novel Protein sim. GBank gij90254 pir jA28334 - protein-tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse			phosphatase	264634
1062	39567937 (2123, 2124)	Novel Protein sim. GBank gij3334200 sp O49954 GCSP_SOLTU - GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)			dehydrogenase	264593
1063	8490481 (2125, 2126)	Novel Protein sim. GBank gij2499966 sp Q41228 PSE1_NICSY - PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A)				264508
1064	78891783 (2127, 2128)	Novel Protein sim. GBank gij82654 pir jJA0086 - 10K zein precursor - maize				265007, 265008, 18108351, 18108385

1065	80021208 (2129, 2130)	Novel Protein sim. GBank gij2120998[ipr][S70682 - glycosyltransferase homolog - Bordetella pertussis]		transferase	284600, 284602, 284689
1066	17896879 (2131, 2132)	Novel Protein sim. GBank gij2506362[ip]P15042[DNLJ_ECOLI - DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (NAD+))]		synthase	265009
1067	10132178 (2133, 2134)	Novel Protein sim. GBank gij4007669[emb]CAA22355[ - (AL034443) putative oxidoreductase [Streptomyces coelicolor]	Contains protein domain (PF00248) - Aldoketo reductase family	reductase	264908 284688, 18108362, 264558, 284600, 284780
1068	82062057 (2135, 2136)	Novel Protein sim. GBank gij4589484[idb]BAA76770.1[ - (AB023143) KIAA0926 protein [Homo sapiens]		UNCLASSIFIED	284604
1069	83002954 (2137, 2138)	Novel Protein sim. GBank gij120304[ip]P15932[FLGK_SALTY - FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1)]		UNCLASSIFIED	284604, 284780
1070	82101992 (2139, 2140)	Novel Protein sim. GBank gij1750397 [U81261] - glutamate synthase large subunit [Pseudomonas aeruginosa]		synthase	264602
1071	20710589 (2141, 2142)	Novel Protein sim. GBank gij477532[ipr][A49175 - Motch B protein - mouse (fragment)]	Contains protein domain (PF00008) - EGF-like domain	synthase	264909 284906
1072	82366540 (2143, 2144)	Novel Protein sim. GBank gij3893109[emb]CAA76940[ - (Y17820) CALO protein [Drosophila melanogaster]		UNCLASSIFIED	284687, 284688, 21908784, 35696052, 35895917, 35895855, 284600, 284601, 284602, 265009, 284605, 284508, 284905, 284690, 284906, 284762, 284628, 284768
1073	79814400 (2145, 2146)	Novel Protein sim. GBank gij4033487[ip]Q44472[TUD4 - AGRI - PUTATIVE HYDROXYPYRUVATE REDUCTASE]		kinase	264905
1074	80105982 (2147, 2148)	Novel Protein sim. GBank gij3413828[emb]CAA20296[ - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	284600
1075	81850293 (2149, 2150)	Novel Protein sim. GBank gij1178203[ip]P46442[YHCM_ECOLI - HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (F375)]		UNCLASSIFIED	18108394, 284769, 284634, 284636
1076	80477264 (2151, 2152)	Novel Protein sim. GBank gij1178203[ip]P46442[YHCM_ECOLI - HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (F375)]		ATPase-associated	284769
1077	79831334 (2153, 2154)	Novel Protein sim. GBank gij4033487[ip]Q44472[TUD4 - AGRI - PUTATIVE HYDROXYPYRUVATE REDUCTASE]		kinase	264905
1078	20288874 (2155, 2156)	Novel Protein sim. GBank gij3413828[emb]CAA20296[ - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	284600
1079	80494518 (2157, 2158)	Novel Protein sim. GBank gij3413828[emb]CAA20296[ - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	18108394, 284769, 284634, 284636
1080	11787188 (2159, 2160)	Novel Protein sim. GBank gij3413828[emb]CAA20296[ - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	284684
1081	94747080 (2161, 2162)	Novel Protein sim. GBank gij3413828[emb]CAA20296[ - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	83373044, 285019, 22278002, 284482, 18108351, 284682, 284908, 284693, 284487
1082	81490656 (2163, 2164)	Novel Protein sim. GBank gij3413828[emb]CAA20296[ - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	284758, 284768, 284769, 21908787, 284511, 284910, 284634, 284635, 284905, 284636, 284906, 284637, 284907, 284908, 284764, 284638, 20281089, 284768, 284595

1083	87446717 (2165, 2166)	Novel Protein sim. GBank gi 1722945 sp Q10523 Y01N_MYCTU - HYPOTHETICAL 44.6 KD PROTEIN CY427.23		UNCLASSIFIED	60424178, 264905, 264906, 264510, 60432229, 264759, 87168474, 264605, 264769, 264689, 18108364, 18108376, 35695855, 264636
1084	37799308 (2167, 2168)	Novel Protein sim. GBank gi 18384 sp P32057 WCAL_ECOLI - PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAL		UNCLASSIFIED	264769
1085	86475368 (2169, 2170)	Novel Protein sim. GBank gi 1899190 (U90204) - heat shock protein 60 [Tukamurella tyrosinosa]	Contains protein domain (PF00118) - eph TCP-1/cpn60 chaperonin family		60432229, 264687
1086	79608269 (2171, 2172)	Novel Protein sim. GBank gi 1172956 sp P46176 RL14_ACYKS - 50S RIBOSOMAL PROTEIN L14	Contains protein domain (PF00238) - ribosomalprot Ribosomal protein L14		264486
1087	79603979 (2173, 2174)	Novel Protein sim. GBank gi 4160198 emb CAA15431  - (AL008583) dJ327J16.3 (novel CHROMObox family protein) [Homo sapiens]	Contains protein domain (PF00385) - helicase 'chromo' (CHROMatin Organization Modifier) domain		29331827, 264693
1088	79854963 (2175, 2176)	Novel Protein sim. GBank gi 2983155 (AE000693) - phosphoglucosyltransferase/phosphomannomutase [Aquifex aerophilus]		UNCLASSIFIED	264905, 264601, 18108387
1089	80216800 (2177, 2178)	Novel Protein sim. GBank gi 4981768 gb AAD36290.1 AE00177 - (AE001778) NADH dehydrogenase, 30 kDa subunit, putative [Thermotoga maritima]	Contains protein domain (PF00329) - Respiratory-chain NADH dehydrogenase, 30 Kd subunit	UNCLASSIFIED	264488, 264511, 265011, 264682, 264768, 264689, 21906764, 35695917, 265020, 32833986, 18108370, 35695855
1090	11083825 (2179, 2180)	Novel Protein sim. GBank gi 4007680 emb CAA22366  - (AL034443) putative oxidoreductase [Streptomyces coelicolor]			264604
1091	12817471 (2181, 2182)	Novel Protein sim. GBank gi 2495562 sp P77239 YLCD_ECOLI - HYPOTHETICAL 44.3 KD PROTEIN IN NFRB-PHEP INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264637
1092	80252286 (2183, 2184)	Novel Protein sim. GBank gi 2960098 emb CAA17996.1  - (AL022121) nth [Mycobacterium tuberculosis]	Contains protein domain (PF00730) - nuclease Endonuclease III		264566 264769, 35695917, 35695855, 264600, 264602, 264603, 264605, 18108351
1093	80496304 (2185, 2186)	Novel Protein sim. GBank gi 1001642 db BAA10373  - (D84002) dGTP triphosphohydrolase [Synecocystis sp.]	UNCLASSIFIED		264686
1094	10880972 (2187, 2188)	Novel Protein sim. GBank gi 4585587 emb CAB40855.1  - (AL049828) putative adenine glycosylase [Streptomyces coelicolor]	Contains protein domain (PF00455) - nuclease Bacterial regulatory proteins, deoR family		264906, 265007, 264595, 264600, 264602, 264603, 264604, 264605, 264762, 264766, 264769, 264636, 264558, 18108387,
1095	87457250 (2189, 2190)				60432113, 264482, 264486
1096	80025977 (2191, 2192)	Novel Protein sim. GBank gi 15001 sp P19206 BIOB_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)	synthase		264600, 264602, 264603, 264604, 264605, 35695917, 264692, 264631
1097	79239560 (2193, 2194)			UNCLASSIFIED	265019
1098	79166424 (2195, 2196)	Novel Protein sim. GBank gi 114135 sp P08205 ARGA_ECOLI - AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)	synthase		264687

1089	39523838 (2197, 2198)	Novel Protein sim. GBank gi 3915144 sp O33017 TRMD_MYCLE - TRNA (GUANINE- N1)-METHYLTRANSFERASE (MTG- METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)		UNCLASSIFIED	264603
1100	85736571 (2189, 2200)	Novel Protein sim. GBank gi 3023255 sp Q64420 ACOD_MESAU - ACYL-COA DESATURASE (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)-DESATURASE)		desaturase	264259, 264636
1101	80491857 (2201, 2202)	Novel Protein sim. GBank gi 1174735 sp P43012 TOP1_HAEN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)	Contains protein domain (PF01396) - Topoisomerase DNA binding C4 zinc finger	isomerase	264769
1102	78777814 (2203, 2204)			UNCLASSIFIED	264910, 264908
1103	81897259 (2205, 2206)	Novel Protein sim. GBank gi 1906596 U81788  - kinesin-73 [Drosophila melanogaster]		struct	264757
1104	95003115 (2207, 2208)	Novel Protein sim. GBank gi 2935448 AF048976  - synaptic ras GTPase-activating protein p135 SynGAP [Rattus norvegicus]		UNCLASSIFIED	29331822, 21906754, 264555, 264556, 264558, 22278002
1105	80255121 (2209, 2210)				264556
1106	79314110 (2211, 2212)			UNCLASSIFIED	264555, 264369
1107	80470019 (2213, 2214)				264908, 264769
1108	80440616 (2215, 2216)	Novel Protein sim. GBank gi 1173421 sp P43416 SECY_STRSC - PREPROTEIN TRANSLUCASE SECY SUBUNIT		transport	264907, 264510, 264511, 264600, 264602, 264605, 264768, 264769
1109	80064615 (2217, 2218)	Novel Protein sim. GBank gi 2995310 emb CAA18338  - (AL022268) putative ATP-dependent helicase [Streptomyces coelicolor]		helicase	264602, 264605, 264636
1110	80503554 (2219, 2220)				
1111	80071744 (2221, 2222)	Novel Protein sim. GBank gi 2622039 AE000868  - type I restriction modification system, subunit S [Methanobacterium thermoautotrophicum]			264908, 264593, 265010, 264601, 264603, 264604, 264605, 264682, 264769, 264693, 264636
1112	95010088 (2223, 2224)				18108370, 264557
1113	82456352 (2225, 2226)	Novel Protein sim. GBank gi 3218376 emb CAA19628  - (AL023862) putative oxidoreductase [Streptomyces coelicolor]		UNCLASSIFIED	264908 264600, 264602, 264604, 264605, 264762, 264769, 264565
1114	14998014 (2227, 2228)	Novel Protein sim. GBank gi 1083428 pir J54876 - NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor - mouse		dehydrogenase	264636
1115	11765583 (2229, 2230)				
1116	79841152 (2231, 2232)			UNCLASSIFIED	264686
1117					264908

1117	95305465 (2233, 2234)	Novel Protein sim. GBank gij3255965[emb]CAA94089] - (Z70200) U5 snRNP-specific 200KD protein [Homo sapiens]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	18108392, 264488, 263994, 264489, 18108398, 56182575, 22278995, 22278996, 35696286, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 66714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 29146498, 264508, 264805, 264509, 264908, 264907, 264908, 66712502, 264909, 52844045, 56182435, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 60170831, 264591, 264592, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264596, 264758, 264759, 21808754, 33109954, 33657084, 265011, 87168559, 264600, 264601, 264602, 264603, 265017, 264604, 265018, 264605, 265019, 264760, 55811150, 264681, 264762, 18108351, 264448, 264682, 264764, 264683, 264288, 264389, 264684, 264685, 264766, 264767, 264686, 264687, 264768, 264769, 264688, 18108359, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148784, 35695917, 265020, 265021, 265022, 60170615, 264690, 264691, 33657023, 264692, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 264691
1118	79563326 (2235, 2236)			UNCLASSIFIED	264691
1119	79642463 (2237, 2238)			UNCLASSIFIED	264907
1120	79480463 (2239, 2240)	Novel Protein sim. GBank gij5420387[emb]CAB46678.1] - (A243459) proteophosphoglycan [Leishmania major]		collagen	29331827, 265018, 265019, 264681, 265021, 60170615, 18108387
1121	79471716 (2241, 2242)	Novel Protein sim. GBank gij1644450 (U67864) - MEX-3 [Caenorhabditis elegans]	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	264683, 264632, 18108388
1122	79456246 (2243, 2244)			UNCLASSIFIED	264639, 264563
1123	79637119 (2245, 2246)	Novel Protein sim. GBank gij98800[pri]S17768 - 3 - dehydroquinase synthase (EC 4.6.1.3) - Mycobacterium tuberculosis		synthase	264693, 27486265
1124	79811596 (2247, 2248)			UNCLASSIFIED	264909
1125	79757861 (2249, 2250)			UNCLASSIFIED	264910
1126	79758914 (2251, 2252)	Novel Protein sim. GBank gij138154[sp]P03643[VG]_BPPIX - MAJOR SPIKE PROTEIN (G PROTEIN) (GPG)		eph	264905, 264909, 264910
1127	11800930 (2253, 2254)			UNCLASSIFIED	264682
1128	8364885 (2255, 2256)	Novel Protein sim. GBank gij5002704[emb]CAB44358.1] - (A242630) DNA polymerase I [Methylobacterium sp. DM4]	Contains protein domain (PF00476) - DNA polymerase family A	UNCLASSIFIED - polymerase	264511

1129	80422480 (2257, 2258)	Novel Protein sim. GBank gij5689485[dbj]BAA03026.1] - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	265011, 264766
1130	79420151 (2259, 2260)	Novel Protein sim. GBank gij4981328[gb]AAD35881.1(AE00174) bioY protein [Thermotoga maritima]		UNCLASSIFIED	264595
1131	80055391 (2261, 2262)	Novel Protein sim. GBank gij4981328[gb]AAD35881.1(AE00174) bioY protein [Thermotoga maritima]		UNCLASSIFIED	35696286, 22278998, 28331828, 264603, 264605, 264559
1132	82062248 (2263, 2264)	Novel Protein sim. GBank gij1841552 (U89336) - unknown [Homo sapiens]		UNCLASSIFIED	22278996, 264806, 265009, 264600, 264602, 264604, 264605, 264760, 32833986, 18108374
1133	17280437 (2265, 2266)			UNCLASSIFIED	265018
1134	80235376 (2267, 2268)			UNCLASSIFIED	264512, 264534
1135	80029393 (2269, 2270)	Novel Protein sim. GBank gij453917[emb]CAB39700.1] - (AL049485) conserved hypothetical protein [Streptomyces coelicolor]			264508, 264600, 264602, 264603, 18108376
1136	79842052 (2271, 2272)	Novel Protein sim. GBank gij4982454[gb]AAD36931.1(AE00182) ATP-dependent protease LA, putative [Thermotoga maritima]		UNCLASSIFIED	264906, 264908
1137	80931557 (2273, 2274)	Novel Protein sim. GBank gij497274[gb]AAD34768.1] - (AF132180) unknown [Drosophila melanogaster]	Contains protein domain (PF00515) - TPR Domain		22278898, 22278999, 35696052, 264907, 265009, 60433356, 264596, 265010, 264448, 264682, 264767, 264689, 265020, 284692, 55811576, 35695855, 264631, 264632, 22279002
1138	79841163 (2275, 2276)	Novel Protein sim. GBank gij731807[sp]P38739[HYCH8_YEAST - HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR	struct		264908
1139	79633561 (2277, 2278)	Novel Protein sim. GBank gij3650031 (AC005396) - putative proline-rich cell wall protein [Arabidopsis thaliana]		UNCLASSIFIED	264693
1140	39480358 (2279, 2280)			UNCLASSIFIED	264593
1141	79638019 (2281, 2282)			UNCLASSIFIED	265019, 264693
1142	19635948 (2283, 2284)			UNCLASSIFIED	264631
1143	87762158 (2285, 2286)	Novel Protein sim. GBank gij392800[emb]CAA05880] - (AJ003125) procollagen I N-proteinase [Homo sapiens]	Contains protein domain (PF00090) - Thrombospondin type 1 domain		56182575, 264908, 264600, 264632, 87188518
1144	80068888 (2287, 2288)			UNCLASSIFIED	264635, 264636, 264907, 264593, 264908, 264566, 264909
1145	14610262 (2289, 2290)			UNCLASSIFIED	264112
1146	82062092 (2291, 2292)			UNCLASSIFIED	264769, 264689, 35696286, 264760, 264905, 264488, 284559
1147	80071761 (2293, 2294)				284557
1148	80048433 (2295, 2296)	Novel Protein sim. GBank gij2499003[sp]P76422[THID_ECOLI - PHOSPHOMETHYL PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)]	kinase		264591
1149	11607438 (2297, 2298)	Novel Protein sim. GBank gij2896734[emb]CAA17213.1] - (AL021897) hypothetical protein Rv1087c [Mycobacterium tuberculosis]			264591

1150	81325074 (2299, 2300)	Novel Protein sim. GBank gij2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]		ATPase-associated	264488, 35696286, 264907, 264908, 264909, 264910, 264593, 264598, 264768, 264764, 264766, 264768, 264693, 264628, 60431850, 264564, 264566, 264567, 264595
1151	80070874 (2301, 2302)	Novel Protein sim. GBank gij4324655jgb AAD16978  - (AF108191) DNA polymerase III alpha subunit [Streptomyces coelicolor]		polymerase	
1152	80235547 (2303, 2304)	Novel Protein sim. GBank gij3874275jemb CAB07311.1  - (292825) predicted using GeneFinder. Similarity to Yeast low affinity glucose transporter HXT4 (PS:32467): cDNA EST EMBL: C12553 comes from this gene; cDNA EST yk404c10.3 comes from this gene; cDNA EST yk404c10.5 comes from thi...		glycoprotein	264488, 22278988, 264905, 284629, 264486
1153	80027783 (2305, 2306)	Novel Protein sim. GBank gij4240315jdbj BAA74936.1  - (AB020720) KIAA0913 protein [Homo sapiens]		UNCLASSIFIED	264910, 264555, 264557, 265008
1154	83002995 (2307, 2308)			UNCLASSIFIED	264690, 264636, 264603
1155	79411098 (2309, 2310)	Novel Protein sim. GBank gij586655jlp P37617 ATZN_ECOLI - ZINC-TRANSPORTING ATPASE (ZNF11)-TRANSLATING P. TYPE ATPASE)	Contains protein domain (PF00122) - E1-E2 ATPase		
1156	57147843 (2311, 2312)	Novel Protein sim. GBank gij418480jlp P32139 YIHR_ECOLI - HYPOTHETICAL 34.0 KD PROTEIN IN GLNA-RBN INTERGENIC REGION		UNCLASSIFIED	264906, 264907, 264758, 264766, 264769, 264689, 264638, 264566
1157	95287711 (2313, 2314)	Novel Protein sim. GBank gij2496481jlp Q50724 Y09S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C		UNCLASSIFIED	264906, 264762, 264687, 264769, 264689, 18108374, 35695855
1158	82454917 (2315, 2316)	Novel Protein sim. GBank gij2496481jlp Q50724 Y09S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C		UNCLASSIFIED	264687, 264689, 264762, 264687, 264769, 264689, 18108374, 35695855
1159	79188451 (2317, 2318)	Novel Protein sim. GBank gij1138406jdbj BAA11490  - (D79995) similar to pig tubulin-tyrosine ligase. [Homo sapiens]		UNCLASSIFIED	264687, 264689, 264762, 264687, 264769, 264689, 18108374, 35695855
1160	91229893 (2319, 2320)	Novel Protein sim. GBank gij1138406jdbj BAA11490  - (D79995) similar to pig tubulin-tyrosine ligase. [Homo sapiens]		UNCLASSIFIED	264687, 264689, 264762, 264687, 264769, 264689, 18108374, 35695855
1161	7417143 (2321, 2322)	Novel Protein sim. GBank gij2443342jdbj BAA22380  - (D88764) alpha 2 type I collagen [Rana catesbeiana]		UNCLASSIFIED	264687, 264689, 264762, 264687, 264769, 264689, 18108374, 35695855
1162	79635357 (2323, 2324)	Novel Protein sim. GBank gij4503375jre NP_001376.1 pDPYS - dihydropyrimidinase		UNCLASSIFIED	264687, 264689, 264762, 264687, 264769, 264689, 18108374, 35695855
1163	79563186 (2325, 2326)	Novel Protein sim. GBank gij5032554jgb AAD38607.1 AF145632 - (AF145632) BcDNA.GH06032 [Drosophila melanogaster]		UNCLASSIFIED	264687, 264689, 264762, 264687, 264769, 264689, 18108374, 35695855
1164	79650829 (2327, 2328)	Novel Protein sim. GBank gij5032554jgb AAD38607.1 AF145632 - (AF145632) BcDNA.GH06032 [Drosophila melanogaster]		UNCLASSIFIED	264687, 264689, 264762, 264687, 264769, 264689, 18108374, 35695855
1165	80481888 (2329, 2330)			UNCLASSIFIED	264687, 264689, 264762, 264687, 264769, 264689, 18108374, 35695855
1166	88096456 (2331, 2332)	Novel Protein sim. GBank gij4589476jdbj BAA76766.1  - (AB023139) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	264687, 264689, 264762, 264687, 264769, 264689, 18108374, 35695855
1167	88096456 (2331, 2332)	Novel Protein sim. GBank gij4589476jdbj BAA76766.1  - (AB023139) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	264687, 264689, 264762, 264687, 264769, 264689, 18108374, 35695855

1167	79963862 (2333, 2334)	Novel Protein sim. GBank gij2580433[dbj BAA23138] - (D78414) ppGpp hydrolase [Staphylococcus aureus]		kinase	264488
1168	80094678 (2335, 2336)			UNCLASSIFIED	264259, 28331827, 56182435, 60433438, 265019, 33857023, 35695855, 284586
1169	11805403 (2337, 2338)			UNCLASSIFIED	284681
1170	21632244 (2339, 2340)			UNCLASSIFIED	264602
1171	20434582 (2341, 2342)	Novel Protein sim. GBank gij2772914 (AF029249) - procollagen D [Mytilus edulis]		UNCLASSIFIED	284556
1172	79610113 (2343, 2344)	Novel Protein sim. GBank gij4757846[ref NP_004317.1 pBCL9 - B-cell CLL/lymphoma 9		UNCLASSIFIED	55810764, 35896052, 264634, 264488
1173	80235713 (2345, 2346)	Novel Protein sim. GBank gij2564053[dbj BAA22846] - (AB007832) Bm trachealless [Bombyx mori]			264508, 264906, 264907, 264909, 264591, 284632, 284638, 264639
1174	20293077 (2347, 2348)	Novel Protein sim. GBank gij291102[emb CAA17520] - (AL021958) rrmSA [Mycobacterium tuberculosis]		dehydrogenase	264600
1175	20711847 (2349, 2350)	Novel Protein sim. GBank gij118333[sp P23234 DCIP_ENTCL - INDOLE-3-PYRUVATE DECARBOXYLASE (INDOLEPYRUVATE DECARBOXYLASE)]	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	carboxylase	264601
1176	80252845 (2351, 2352)	Novel Protein sim. GBank gij1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]	Contains protein domain (PF00368) - AIR synthase related protein	synthase	264509, 264805, 284593, 284602, 264605
1177	80064647 (2353, 2354)	Novel Protein sim. GBank gij118791[sp P28643 FABG_CUPLA - 3-OXOACYL-ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)	Contains protein domain (PF00106) - short chain dehydrogenase	reductase	264605
1178	94128841 (2355, 2356)	Novel Protein sim. GBank gij5031697[ref NP_005594.1 pFIC1 - familial intrahepatic cholestasis 1, (progressive, Byler disease and benign recurrent)]	Contains protein domain (PF00122) - ATPase associated E1-E2 ATPase		65274572, 18108398, 22278998, 22278999, 28331828, 264508, 264808, 284828, 33657402, 33109954, 264769, 21806765, 21808788, 21808788, 55811957, 33857023, 284629, 55811576, 35696423, 264636, 264556, 56182323, 60432113, 22278000, 22278002
1179	80055575 (2357, 2358)	Novel Protein sim. GBank gij2980090[emb CAA17988.1] - (AL022121) dppA [Mycobacterium tuberculosis]	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5	transport	264603
1180	11794446 (2359, 2360)	Novel Protein sim. GBank gij2558614[emb CAA04787] - (AJ001493) dehydroquininate dehydratase [Streptomyces coelicolor]	Contains protein domain (PF01220) - Dehydroquinase class II	synthase	284638
1181	17946362 (2361, 2362)			UNCLASSIFIED	265017
1182	81404284 (2363, 2364)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	265007, 265009, 264564, 264908, 264693
1183	79574044 (2365, 2366)				
1184	52559933 (2367, 2368)	Novel Protein sim. GBank gij4091877 (AF061331) - alpha galactosidase precursor [Saccharopolyspora erythraea]		UNCLASSIFIED	264689, 35696423, 284638, 18108395
1185	79491185 (2369, 2370)	Novel Protein sim. GBank gij2129478[ref S51939] - chitinase [EC 3.2.1.14] precursor - beet		glycoprotein	263967



1186	20224012 (2371, 2372)				UNCLASSIFIED	264559	
1187	79248834 (2373, 2374)				UNCLASSIFIED	29331825, 265017, 18108351	
1188	79831387 (2375, 2376)	Novel Protein sim. GBank gij2996039 (AF054525) - hypothetical protein [Synecococcus PCC7002]			UNCLASSIFIED	264905, 264906	
1189	79609367 (2377, 2378)					264692	
1190	78930589 (2379, 2380)					265018	
1191	80310105 (2381, 2382)				UNCLASSIFIED	264600, 264605, 264764, 35695855, 264638, 264486	
1192	13521641 (2383, 2384)			Contains protein domain (PF01581) - FMRFamide related peptide family		264636	
1193	11103584 (2385, 2386)				UNCLASSIFIED	263978	
1194	78893947 (2387, 2388)	Novel Protein sim. GBank gij854065[emb CAA58337] - (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	265007, 265008	
1195	20445442 (2389, 2390)	Novel Protein sim. GBank gij1790277 (AE000459) - putative oxidoreductase [Escherichia coli]			UNCLASSIFIED	264605	
1196	13000688 (2391, 2392)					264689	
1197	11392317 (2393, 2394)	Novel Protein sim. GBank gij2497360[sp Q50715 MDH_MYCTU - INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD)]		Contains protein domain (PF00571) - CBS domain	dehydrogenase	264594	
1198	95280101 (2395, 2396)					264603	
1199	81882011 (2397, 2398)	Novel Protein sim. GBank gij1709525[sp P54673 P3K1_DICD1 - PHOSPHATIDYLINOSITOL 3-KINASE 1 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)]				264259, 264757, 33109954, 21906768	
1200	9848880 (2399, 2400)					264910	
1201	80503751 (2401, 2402)	Novel Protein sim. GBank gij2499877[sp P70645 BLMH_RAT - BLEOMYCIN HYDROLASE (BLM HYDROLASE) (BMH)]			UNCLASSIFIED	264766, 264769	
1202	80082633 (2403, 2404)	Novel Protein sim. GBank gij606342 (U18997) - ORF_o622; reading frame open far upstream of start; possible frameshift, linking to previous ORF [Escherichia coli]			ribosomalprot	264600, 264558	
1203	82125373 (2405, 2406)				UNCLASSIFIED	264768, 264769, 35695917, 284910, 264760, 264908, 264907, 264629, 264908, 264909, 264768	
1204	60503916 (2407, 2408)	Novel Protein sim. GBank gij2500728[sp Q59912 SECY_STRGB - PREPROTEIN TRANSLOCASE SECY SUBUNIT				264905, 264769, 264636	
1205	80053961 (2409, 2410)				UNCLASSIFIED	264566	
1206	80241963 (2411, 2412)				UNCLASSIFIED	264556, 264557, 264558	
1207	79841192 (2413, 2414)					29331824, 264909, 265021, 18108370	
1208	87755217 (2415, 2416)	Novel Protein sim. GBank gij2645580 (AF027954) - Bcl-2-related ovarian killer protein [Rattus norvegicus]		Contains protein domain (PF00452) - Apoptosis regulator proteins, Bcl-2 family	apoptosis	29331824, 29331825, 29331827, 265007, 264764, 264683, 264769, 264688, 264689	

1209	79185742 (2417, 2418)	Novel Protein sim. GBank gi1175033 sp P44398 XYLA_HAEIN - XYLOSE ISOMERASE	Contains protein domain (PF00259) - Xylose isomerase	isomerase	264687, 264688
1210	58426884 (2419, 2420)				
1211	84865655 (2421, 2422)	Novel Protein sim. GBank gij421095 pir J30688 - hypothetical protein o246 - Escherichia coli		UNCLASSIFIED transferase	264807, 264693 264591, 264592, 264595
1212	79167928 (2423, 2424)	Novel Protein sim. GBank gij3880625 emb CAB07859  - (Z93785) predicted using Genefinder; similar to RNA recognition motif (aka RRM, RBD, or RNP domain); cDNA EST EMBL:U01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL:D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf		264689, 263967
1213	79859633 (2425, 2426)	Novel Protein sim. GBank gij226292 pir J1505375A - vir gene [Bordetella pertussis]		kinase	264909
1214	10144308 (2427, 2428)	Novel Protein sim. GBank gi15726285 gb AAD48396.1 AF12616 - (AF126162) HERV-H LTR associated protein 2 [Homo sapiens]		UNCLASSIFIED	264808
1215	80050106 (2429, 2430)	Novel Protein sim. GBank gij2326739 emb CAB10953  - (Z98268) recN [Mycobacterium tuberculosis]		UNCLASSIFIED	265009, 264601, 264602, 264603, 33657109
1216	20438324 (2431, 2432)	Novel Protein sim. GBank gi1417329 sp P33038 MURA_ENTCL - UDP-N- ACETYLGLUCOSAMINE 1- CARBOXYVINYL TRANSFERASE (ENOYLPIRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE ENOYLPIRUVYL TRANSFERASE) (EPT)		transferase	264604
1217	95011344 (2433, 2434)				
1218	11093680 (2435, 2436)	Novel Protein sim. GBank gi11805460 dbj BA009022  - (D50453) homologue of succinate semialdehyde dehydrogenase GabD of E. coli [Bacillus subtilis]		UNCLASSIFIED	264905, 264907, 264908, 264591, 264766, 264691, 264693, 264629, 264630, 264636, 264564 264801
1219	81216252 (2437, 2438)			dehydrogenase	
1220	91241524 (2439, 2440)	Novel Protein sim. GBank gi14240315 dbj BA074936.1  - (AB020720) KIAA0913 protein [Homo sapiens]		oncogene	56181686, 28331822, 60432289, 264601, 264692, 264629 52844507, 264905, 264908, 265008, 265018, 265020, 52844150, 33657023, 264693, 33657182, 35695763, 264634, 22279000, 22279002, 264482
1221	83045055 (2441, 2442)	Novel Protein sim. GBank gi12143886 pir J152523 - nucleoporin p62 homolog - rat (fragment)		UNCLASSIFIED	264768, 265020, 264906
1222	20711865 (2443, 2444)	Novel Protein sim. GBank gi1730805 sp P39663 SPHR_SYNP7 - ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY PROTEIN SPHR	Contains protein domain (PF00486) - Transcriptional regulatory protein, C terminal	phosphatase	264601
1223	11615647 (2445, 2446)				264593
1224	80432645 (2447, 2448)	Novel Protein sim. GBank gi1172827 sp P46546 PROB_CORGL - GLUTAMATE 5- KINASE (GAMMA-GLUTAMYL KINASE) (GK)	Contains protein domain (PF01472) - PUA domain	kinase	264593, 264600, 264601, 264603, 264605, 264768, 18108376, 264635, 18108387

1225	80434427 (2449, 2450)	Novel Protein sim. GBank gij2105050[emb]CAB08836] - (Z95438) hypothetical protein RV3644c [Mycobacterium tuberculosis]			polymerase	264768 264905, 264512, 264689
1226	80237518 (2451, 2452)					
1227	79422138 (2453, 2454)	Novel Protein sim. GBank gij1706768[sp]P98133[FBN1_BOVIN - FIBRILLIN 1 PRECURSOR (MP340)]			UNCLASSIFIED	264908, 264637, 264639
1228	79209027 (2455, 2456)	Novel Protein sim. GBank gij1663801[dbj]BAA18811] - (D90917) acriflavine resistance protein [Synecocystis sp.]	Contains protein domain (PF00873) - ActB/AcrD/AcrF family		UNCLASSIFIED	264605, 264634
1229	94329135 (2457, 2458)					
1230	80049357 (2459, 2460)	Novel Protein sim. GBank gij116230[sp]P28598[CH60_BACSU - 60 KD CHAPERONIN (PROTEIN CPN60)] (GROEL PROTEIN)	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family			87168474, 265011, 87168559, 264681, 264689, 264693, 65274620, 18108374
1231	79843141 (2461, 2462)	Novel Protein sim. GBank gij1215733 [U48718] - OphC [Agrobacterium tumefaciens]			UNCLASSIFIED	264908 264909
1232	79853104 (2463, 2464)	Novel Protein sim. GBank gij116298[sp]P20730[CHHC_BOMMO - CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR (HC-B.13)]			UNCLASSIFIED	265017, 264564
1233	80255179 (2465, 2466)	Novel Protein sim. GBank gij129671[sp]P40280[H2A_MAIZE - HISTONE H2A]	Contains protein domain (PF00125) - Core histone H2A/H2B/H3/H4	histone		265008, 265010, 18108381
1234	79242158 (2467, 2468)					
1235	79914423 (2469, 2470)	Novel Protein sim. GBank gij3875133[emb]CAA94750] - (Z70750) similar to actin binding domain; cDNA EST			UNCLASSIFIED	264634, 264762
1236	81927147 (2471, 2472)	EMBL:D34443 comes from this gene; cDNA EST				265018, 55811150, 264585, 264757
1237	83371782 (2473, 2474)	EMBL:D37508 comes from this gene; cDNA EST				264758, 264601, 264786, 264687, 18108372, 264555, 264559
1238	87411577 (2475, 2476)	EMBL:D64247 comes from this gene; cDNA EST EMBL... Novel Protein sim. GBank gij3885470 (AF061443) - G protein-coupled receptor LGR4 [Rattus norvegicus]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein		264259, 26331822, 29331824, 35696052, 264508, 264906, 52644045, 52646317, 264288, 264769, 264693, 264632, 264634, 264558, 87168518, 264563
1239	82197449 (2477, 2478)	Novel Protein sim. GBank gij4007990[gb]AAC95339] - (AF084363) DOK protein [Mus musculus]		oncogene		264509, 264511, 264759, 264760, 264764, 264557
1240	80497259 (2479, 2480)	Novel Protein sim. GBank gij1176192[sp]P45420[YHCD_ECOLI - HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN IN GLTF-NANT INTERGENIC REGION PRECURSOR]				264769
1241	80020711 (2481, 2482)	Novel Protein sim. GBank gij121383[sp]P19904[GLNA_VIBAL - GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)]	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED		264601, 264604, 264638
1242	79775690 (2483, 2484)					264908, 264907, 264908, 264634

1243	79779458 (2485, 2486)	Novel Protein sim. GBank gij335567[embjCAA19971] - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor]		UNCLASSIFIED	18108374, 35695817, 35695855, 265009, 264508, 264809
1244	10284821 (2487, 2488)	Novel Protein sim. GBank gij2870846 (AF051945) - Xin [Mus musculus]		UNCLASSIFIED	264691
1245	80437103 (2489, 2490)	Novel Protein sim. GBank gij4586338[idbjBAA76357.1] - (AB016787) cytochrome o ubiquinol oxidase B [Pseudomonas putida]	Contains protein domain (PF00115) - Cytochrome C and Quinol oxidase polypeptide 1	oxidase	264768
1246	80059321 (2491, 2492)	Novel Protein sim. GBank gij3581849[embjCAA20805] - (AL031541) putative phenylalanine-tRNA synthetase beta chain [Streptomyces coelicolor]		UNCLASSIFIED	264604, 264636, 264557, 264564
1247	80064831 (2493, 2494)	Novel Protein sim. GBank gij2621684 (AE000842) - adhesion protein [Methanobacterium thermoautotrophicum]			264758, 264605, 264639
1248	88070353 (2495, 2496)	Novel Protein sim. GBank gij1352403[idjP09467]F16P_HUMAN - FRUCTOSE-1,6-BISPHOSPHATASE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)	Contains protein domain (PF00316) - Fructose-1,6-bisphosphatase	UNCLASSIFIED	18108392, 264259, 29331826, 264106, 264508, 264907, 264828, 265009, 80433356, 264757, 264758, 21808754, 285010, 285011, 285018, 265019, 264760, 18108351, 18108354, 265021, 18108376, 18108377, 264630, 18108385
1249	80056657 (2497, 2498)	Novel Protein sim. GBank gij2791407[embjCAA16001] - (AL021184) hypothetical protein Rv1473 [Mycobacterium tuberculosis]		transport	264908, 265010, 264600, 264603, 264691, 18108376
1250	12694385 (2498, 2500)	Novel Protein sim. GBank gij112785[idjP05100]3MG1_ECOLI - DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I)		UNCLASSIFIED	264689
1251	79850448 (2501, 2502)				264909
1252	79458087 (2503, 2504)			UNCLASSIFIED	264683, 263976
1253	80050121 (2505, 2506)	Novel Protein sim. GBank gij567017[idjAAD46616.1]AF16131 - (AF161317) NRAMP manganese transport protein MnaA [Salmonella typhimurium]		glycoprotein	264600, 264603, 18108378
1254	87716767 (2507, 2508)	Novel Protein sim. GBank gij103160[idjJ22126] - finger protein unkempt - fruit fly [Drosophila melanogaster]		UNCLASSIFIED	35696286, 264910, 264764, 264688, 21908767, 55811957, 264892, 284556, 264639
1255	79168728 (2509, 2510)				264636
1256	87889508 (2511, 2512)	Novel Protein sim. GBank gij2985353[embjCAA04608.1] - (AJ001206) pep2 [Streptomyces coelicolor]		UNCLASSIFIED	60432289, 264600, 264605, 264784, 264687, 264769, 264689, 27486265, 18108374, 18108376
1257	80201435 (2513, 2514)	Novel Protein sim. GBank gij3193306 (AF069300) - contains similarity to Arabidopsis membrane-associated salt inducible-like protein (GB:AL021637) [Arabidopsis thaliana]		UNCLASSIFIED	264094, 285019
1258	20708150 (2515, 2516)			UNCLASSIFIED	264602, 263978
1259	80186012 (2517, 2518)			UNCLASSIFIED	264906, 264448, 264908
1260	80084608 (2519, 2520)			UNCLASSIFIED	264634, 264639

1261	87412802 (2521, 2522)	Novel Protein sim. GBank glij5689511dbj BAA33039.1  - (AB029010) KIAA1087 protein [Homo sapiens]	Contains protein domain (PF01699) - Sodium/calcium exchanger protein	cadherin	29331824, 264906, 264809, 264768, 264769, 264689, 264693, 264639, 18108384, 264563, 264634
1262	13504589 (2523, 2524)	Novel Protein sim. GBank glij95100 pir S21334 - hypothetical protein 4 - Agrobacterium tumefaciens		UNCLASSIFIED	
1263	20710997 (2525, 2526)	Novel Protein sim. GBank glij3550958 (AF004840) - CDO [Rattus norvegicus]		struct	264602, 264634
1264	80083396 (2527, 2528)			UNCLASSIFIED	264563
1265	80253578 (2529, 2530)			UNCLASSIFIED	264768, 264636, 264638, 264567
1266	79914604 (2531, 2532)	Novel Protein sim. GBank glij1085002 pir S55056 - mitochondrial carrier protein DJF-1 homolog - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264259, 21908754, 264369
1267	80558918 (2533, 2534)				
1268	88178473 (2535, 2536)	Novel Protein sim. GBank glij4886445 emb CAB43370.1  - (AL050269) hypothetical protein [Homo sapiens]	Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	18108398, 22278995, 56994075, 60424269, 29331827, 264109, 264512, 265007, 265008, 265009, 264595, 33109954, 33657084, 87168559, 264600, 265018, 265019, 264369, 264688, 21908767, 265020, 52844150, 264691, 33657023, 33657349, 18108374, 264556, 18108385, 60432113, 22279002, 264486
1269	79821946 (2537, 2538)	Novel Protein sim. GBank glij3334791 emb CAA1939  - (AL031107) hypothetical protein SC5A7.10c [Streptomyces coelicolor]		UNCLASSIFIED	264508, 264905, 264906, 264687, 264693
1270	80031420 (2539, 2540)	Novel Protein sim. GBank glij2851634 sp Q50591 Y0D1_MYCTU - HYPOTHETICAL 50.0 KD PROTEIN CY1A11.01	Contains protein domain (PF01574) - IMP dehydrogenase / GMP reductase N terminus	dehydrogenase	265010, 264601
1271	79840499 (2541, 2542)			ATPase associated	35696032, 264908
1272	79462878 (2543, 2544)				264686, 264689
1273	80220315 (2545, 2546)	Novel Protein sim. GBank glij1655865 emb CAB03731  - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis]		UNCLASSIFIED	264509, 264639
1274	95010802 (2547, 2548)	Novel Protein sim. GBank glij123726 sp P10413 HTPG_ECOLI - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C82.5)		UNCLASSIFIED	
1275	20730763 (2549, 2550)	Novel Protein sim. GBank glij2129478 pir S51939 - chitinase (EC 3.2.1.14) precursor - beet	Contains protein domain (PF00183) - Hsp90 protein	eph	264905, 264908, 264909, 264769, 264602
1276	21148644 (2551, 2552)			UNCLASSIFIED	264369
1277	20438195 (2553, 2554)	Novel Protein sim. GBank glij1175473 sp P44555 YAAJ_HAEIN - HYPOTHETICAL PROTEIN HI0183		UNCLASSIFIED	264558, 264603
1278	11088365 (2555, 2556)			UNCLASSIFIED	
1279	21658756 (2557, 2558)	Novel Protein sim. GBank glij1929513 (U64318) - ATP synthase subunit beta [Moodella thermoacetica]		synthase	264605
1280	79310959 (2559, 2560)	Novel Protein sim. GBank glij4938504 emb CAB43862.1  - (AL074665) putative protein [Arabidopsis thaliana]		struct	263976

1281	94323988 (2561, 2562)	Novel Protein sim. GBank gj1136501 (U39546) - surface protein MCA-32 [Rattus norvegicus]	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	28331825, 28331828, 264766, 83373044
1282	87537685 (2563, 2564)	Novel Protein sim. GBank gj3328190 (AF074266) - proto-oncogene AF4 [Mus musculus]		UNCLASSIFIED	265008
1283	20466305 (2565, 2566)	Novel Protein sim. GBank gj3261721[emb]CAB070571 - (Z92770) hypothetical protein Rv0153c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
1284	20638325 (2567, 2568)	Novel Protein sim. GBank gj3929022 (AF057696) - LspB [Haemophilus ducreyi]			264604
1285	80427330 (2569, 2570)	Novel Protein sim. GBank gj1417154[sp]P33128[HS82_ORYSA - HEAT SHOCK PROTEIN 82]	Contains protein domain (PF00183) - eph Hsp90 protein		264766, 264689, 263967
1286	20466254 (2571, 2572)	Novel Protein sim. GBank gj2078004[emb]CAB084511 - (Z95207) gorA [Mycobacterium tuberculosis]		reductase	264605, 264639
1287	80417530 (2573, 2574)			UNCLASSIFIED	265011, 264602, 284766, 264687, 264769, 264689, 18108370, 264636, 18108385, 264563
1288	95338101 (2575, 2576)	Novel Protein sim. GBank gj5353510[gb]AAD42181.1[AF08891 - (AF088916) emilin precursor [Homo sapiens]	Contains protein domain (PF00386) - collagen C1q domain		35868052, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 33657402, 264595, 264758, 265011, 265019, 264760, 18108351, 264681, 264784, 264288, 264685, 264766, 264687, 264768, 264769, 265020, 265021, 264534, 264692, 18108370, 264628, 18108374, 35696423, 264555, 264556, 264557, 264558, 18108385, 264564, 264566, 264567, 264486, 18108391
1289	11813647 (2577, 2578)	Novel Protein sim. GBank gj1169995[sp]P46023[GPCR_LYMST - G-PROTEIN COUPLED RECEPTOR GRL101 PRECURSOR]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	UNCLASSIFIED	264637
1290	19526027 (2578, 2580)	Novel Protein sim. GBank gj2072674[emb]CAB083051 - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	Im7	284563
1291	80470286 (2581, 2582)	Novel Protein sim. GBank gj1835755 (U86338) - zinc finger protein Png-1 [Mus musculus]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	285007, 265008, 264769
1292	94723316 (2583, 2584)	Novel Protein sim. GBank gj1835755 (U86338) - zinc finger protein Png-1 [Mus musculus]	Contains protein domain (PF01530) - Zinc finger, C2HC type		
1293	80067536 (2585, 2586)	Novel Protein sim. GBank gj12129173[sp]JF64453 - oxaloacetate decarboxylase (EC 4.1.1.3) alpha subunit - Methanococcus jannaschii		transcript factor	264092, 264259, 28331822, 28331824, 264508, 264908, 264909, 264512, 265008, 265009, 264591, 265019, 264369, 264288, 264688, 264768, 264693, 18108374, 264632, 56182323, 264639, 83373044, 22279002, 264482, 264563
1294	82125908 (2587, 2588)	Novel Protein sim. GBank gj15441779[emb]CAB46803.11 - (AL096611) putative alcohol dehydrogenase (zinc-binding) [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	265008, 55812038, 264369, 264556
1295	11688651 (2589, 2590)	Novel Protein sim. GBank gj15441779[emb]CAB46803.11 - (AL096611) putative alcohol dehydrogenase (zinc-binding) [Streptomyces coelicolor A3(2)]		bioindop	264602, 264605, 264760, 18108351, 264689, 33657023, 264559
				dehydrogenase	264689

1296	11687804 (2591, 2592)	Novel Protein sim. GBank				264591, 264639	
1297	79639300 (2593, 2594)	gi14982191 gb AAD36886.1 AE001805 DNA-directed DNA polymerase I [Thermotoga maritima]	Contains protein domain (PF01367) - 5'-3' exonuclease	UNCLASSIFIED	polymerase	264693	
1298	94239506 (2595, 2596)	Novel Protein sim. GBank gi11943770 (U97191) - F53F10.1 gene product [Caenorhabditis elegans]			struct	18108348, 265017	
1299	80255378 (2597, 2598)	Novel Protein sim. GBank gi13445181 (AC005498) - R31665.2 [Homo sapiens]	Contains protein domain (PF01352) - KRAB box		transcriptfactor	264488, 264906, 264909, 22278002, 264566	
1300	80064867 (2599, 2600)	Novel Protein sim. GBank gi14062973 gb BAA36204.1  (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida]		UNCLASSIFIED		264906	
1301	17939614 (2601, 2602)						
1302	95416188 (2603, 2604)					85658542, 265020	
1303	9684121 (2605, 2606)					264908	
1304	79377186 (2607, 2608)			UNCLASSIFIED		264508	
1305	19905899 (2609, 2610)					264566	
1306	13069230 (2611, 2612)	Novel Protein sim. GBank gi13242273 emb CAB07017  (Z92669) hypothetical protein Rv0236c [Mycobacterium tuberculosis]		UNCLASSIFIED		264636	
1307	82201029 (2613, 2614)	Novel Protein sim. GBank gi11502421 (U59433) - 3-ketoacyl	Contains protein domain (PF00516) - reductase	UNCLASSIFIED		264907, 264592, 264764	
1308	21426814 (2615, 2616)	acyl carrier protein reductase [Bacillus subtilis]	Envelope glycoprotein GP120			264555	
1309	79263011 (2617, 2618)	Novel Protein sim. GBank gi195819 pir J516298 - ferric enterobactin transport protein fepC - Escherichia coli			transport	264906, 18108354	
1310	20466319 (2619, 2620)	Novel Protein sim. GBank gi15459220 emb CAB48893.1  (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED		264605	
1311	87613142 (2621, 2622)					35698286, 29331827, 264908, 265008, 264784, 264766, 264686, 21906767, 21905769, 35695917, 264691, 264693	
1312	88061720 (2623, 2624)	Novel Protein sim. GBank gi14455118 gb AAD21084  (AF125158) zinc finger DNA binding protein 99 [Homo sapiens]	Contains protein domain (PF00096) - dna_rna_bind Zinc finger, C2H2 type			22278995, 22278998, 22278999, 264905, 264908, 265011, 265017, 265019, 264687, 21906768, 265020, 265021, 33657023, 22279002, 264564	
1313	91225458 (2625, 2626)	Novel Protein sim. GBank gi14929733 gb AAD34127.1 AF15189 - (AF151890) CGI-132 protein [Homo sapiens]	Contains protein domain (PF00886) - ribosomalprot Ribosomal protein S16			22278996, 22278999, 264259, 20281099, 29146498, 264508, 264908, 66712502, 60433356, 60433438, 265011, 265017, 264683, 264288, 21906765, 21906767, 29148627, 21906768, 35695917, 265021, 33657023, 33657109, 18108370, 18108377, 35695855, 60432113, 22279000, 264563, 18108390	
1314	56926053 (2627, 2628)					264693	
1315	84357192 (2629, 2630)	Novel Protein sim. GBank gi12589223 (AF026565) - ring finger protein [Mus musculus]	Contains protein domain (PF00097) - ring Zinc finger, C3HC4 type (RING finger)		interleukinrecept	264691	

1316	85381609 (2631, 2632)	Novel Protein sim. GBank glij5689407[dbj]BAA02987.1] - (AB028958) KIAA1035 protein [Homo sapiens]		kinase	56182575, 56181886, 20281171, 29331822, 29331824, 60424269, 29331825, 35986052, 52844045, 264391, 60432229, 265018, 265019, 55811150, 56181562, 21908765, 21908767, 21908768, 35695917, 60170615, 33857023, 65274620, 33857108, 35695783, 35695855, 18108387, 87168518, 60432113, 22279002, 264584
1317	88055187 (2633, 2634)	Novel Protein sim. GBank glij4836757[gbj]AAD30541.1[AF13491] - (AF134918) semaphorin subclass 4 member G [Mus musculus]		UNCLASSIFIED	264083, 284806, 264809, 264369, 264684
1318	95322893 (2635, 2636)	Novel Protein sim. GBank glij4680204[gbj]AAD27567.1[AF11417] - (AF114171) hypothetical protein [Sorghum bicolor]		UNCLASSIFIED	18108392, 18108348, 265011, 265017, 18108359, 18108362, 58182323, 18108385, 22279000
1319	94238546 (2637, 2638)				264908, 264909, 265006, 265008, 264592, 265019, 264786, 56181562, 18108388, 284628, 284629, 18108377, 264638
1320	86603567 (2638, 2640)	Novel Protein sim. GBank glij4240183[dbj]BAA74870.1] - (AB020854) KIAA0847 protein [Homo sapiens]		UNCLASSIFIED	35696286, 55812038, 265018, 21908768, 265020, 263978, 22279002
1321	86676351 (2641, 2642)	Novel Protein sim. GBank glij4886505[embj]CAB43377.1] - (AL050276) hypothetical protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	transcription factor	60432049, 29331828, 264907, 264908, 264909, 264910, 55812038, 264601, 264762, 264764, 264766, 264768, 264769, 264628, 18108374, 264634, 264635, 18108385
1322	87755272 (2643, 2644)	Novel Protein sim. GBank glij5282591[embj]CAB45736.1] - (AL080143) hypothetical protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_bind	29331828, 264808, 265020, 33657023, 264693, 264404
1323	94845931 (2645, 2646)	Novel Protein sim. GBank glij5459516[dbj]BAA82407.1] - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 56994076, 264259, 29331822, 29331827, 264104, 56182435, 87168474, 18108351, 264288, 21908766, 21908787, 35695917, 265020, 264693, 65274781, 58182323, 18108387
1324	87737614 (2647, 2648)	Novel Protein sim. GBank glij5031717[re]NP_005704.1pGPBP - goodpasture antigen-binding protein	Contains protein domain (PF01852) - START domain		22278996, 22278998, 29331828, 284905, 284907, 29331830, 264908, 264510, 265008, 264595, 264759, 21908754, 265018, 264288, 264768, 264769, 21908768, 265022, 18108376, 264631, 264632, 264634, 264636, 284638, 264583, 284584, 284585, 264586
1325	94847471 (2649, 2650)	Novel Protein sim. GBank glij3294501 (U64857) - similar to the DPT/Kunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor [Caenorhabditis elegans]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	protease	35696286, 264905, 264906, 264907, 264908, 264909, 264910, 264593, 33857402, 264758, 85658542, 264760, 284788, 264769, 264691, 35696423
1326	87316289 (2651, 2652)	Novel Protein sim. GBank glij1397275 (U61947) - C0603.8 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264259, 66712502, 264682, 264683, 264635



1327	95322897 (2653, 2654)	Novel Protein sim. GBank gi728832 sp P39189 ALU2_HUMAN - III  ALU SUBFAMILY SB WARNING ENTRY III	Contains protein domain (PF00279) - Plant lipid transfer protein family	UNCLASSIFIED	18108398, 22278996, 22278997, 22278999, 264051, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264105, 264905, 56182435, 264112, 265008, 265009, 21908754, 265010, 265011, 265017, 265019, 264681, 264448, 264764, 264684, 264288, 264685, 264768, 264688, 21908767, 21908769, 26148629, 265020, 264690, 264691, 264692, 264693, 263967, 33657109, 33657182, 27486262, 33657349, 18108370, 18108374, 55810764, 35695855, 264634, 56182323, 83373044, 87168518, 60432113, 22279000, 22279002, 264563, 264567
1328	87753493 (2655, 2656)			UNCLASSIFIED	264488, 22278997, 29331826, 264595, 18108351, 264766, 22279002, 264482, 264567
1329	87755276 (2657, 2658)	Novel Protein sim. GBank gi4678224 gb AAD28969.1 AC00713 - (AC007135) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	22278996, 29331827, 264684, 264692, 33657109
1330	87727737 (2659, 2660)	Novel Protein sim. GBank gi437310 (L23504) - nodulin [Medicago truncatula]		UNCLASSIFIED	264259, 29331825, 264512, 265019, 265021, 264555, 264558, 56528486
1331	87376764 (2661, 2662)	Novel Protein sim. GBank gi4589586 dbj BAA76815.1  - (AB023188) KIAA0971 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331826, 29331827, 35696032, 29331828, 60170831, 264448, 264686, 21908765, 55811957, 265020, 33657023, 33657109, 263973, 55811576, 35696423, 35695855, 56182323
1332	94845937 (2663, 2664)	Novel Protein sim. GBank gi5459516 dbj BAA82407.1  - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	63274572, 22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331826, 60432289, 29331827, 35696052, 52644045, 56182435, 264510, 21908754, 87168559, 265018, 265019, 264448, 264288, 264369, 264686, 21908765, 21908766, 21908767, 21908768, 265020, 265021, 52644150, 33657023, 56182323, 18108387, 60432113, 22279002
1333	88098476 (2665, 2666)	Novel Protein sim. GBank gi5689527 dbj BAA83047.1  - (AB029018) KIAA1095 protein [Homo sapiens]		UNCLASSIFIED	60432289, 66712502, 264591, 60433358, 60433438, 55812038, 265010, 264639, 56528486
1334	87592388 (2667, 2668)	Novel Protein sim. GBank gi2662536 (AF036685) - Similar to protein-tyrosine phosphatase [Caenorhabditis elegans]		phosphatase	264905
1335	87644798 (2669, 2670)	Novel Protein sim. GBank gi4240285 dbj BAA74921.1  - (AB020705) KIAA0898 protein [Homo sapiens]	Contains protein domain (PF00843) - B-box zinc finger.	UNCLASSIFIED	22278998, 22278999, 29331827, 264509, 264511, 265007, 265008, 265009, 60433438, 21908754, 87168559, 265017, 264288, 21908765, 21908767, 21908768, 21908769, 265020, 33657109, 27486284, 18108374, 264556, 264638, 264557, 60170394, 264559, 18108385, 264563

1336	87787890 (2871, 2872)	Novel Protein sim. GBank gi465445ip33485jvnuA - PROBABLE NUCLEAR ANTIGEN			UNCLASSIFIED	264509, 264905, 264512, 264764, 264693, 264635, 264637
1337	84312042 (2673, 2674)	Novel Protein sim. GBank gi45689471dbjBAA83019.1 - (AB028990) KIAA1067 protein [Homo sapiens]			UNCLASSIFIED	56182375, 56994075, 22278998, 22278999, 264092, 264259, 60432289, 29331826, 264906, 264908, 264909, 264112, 265008, 265009, 60433358, 55812038, 33857084, 265011, 265017, 265018, 265019, 264682, 264448, 264683, 264369, 264688, 264689, 21906766, 21906769, 265020, 264681, 27488261, 20281069, 18108379, 55811578, 35695855, 56182323, 60432113, 22278002, 264587
1338	80366114 (2675, 2676)				UNCLASSIFIED	29331822, 265010, 264288, 264689, 18108370, 35695855
1339	80249231 (2877, 2878)	Novel Protein sim. GBank gi1176422 (U43194) - rhophilin [Mus musculus]			UNCLASSIFIED	35686052, 264909, 264688, 264556, 264558
1340	80316311 (2878, 2880)					264905, 264907, 87168559, 264764
1341	86101485 (2681, 2882)					264681, 264685, 264688, 264692
1342	80089017 (2683, 2684)	Novel Protein sim. GBank gi5019564jembCAB44507.1 - (AL035542) dJ984E9.5 (hs6M1-17 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein)) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family) (rhodopsin family)	im7		264629
1343	80082862 (2685, 2686)	Novel Protein sim. GBank gi4557543jrefNP_001384.1pECM2 - extracellular matrix protein 2	Contains protein domain (PF00560) - Leucine Rich Repeat	struct		264910, 264686, 264534
1344	20562559 (2687, 2688)	Novel Protein sim. GBank gi2144101pirj55210 - tricarboxylate carrier - rat (fragment)			glycoprotein	263978 264909, 60170394
1345	91225546 (2689, 2690)					
1346	80255717 (2691, 2692)	Novel Protein sim. GBank gi3881052jembCAG195231 - (AL023843) predicted using Genefinder; similar to serine/threonine kinase; cDNA EST yk246a12.3 comes from this gene; cDNA EST yk358c10.5 comes from this gene; cDNA EST EMBL M89047 comes from this gene; cDNA EST yk246a12.5 comes...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase		22278998, 264907, 264681, 264685, 264689, 265020, 264693, 22278000, 22278002, 264566
1347	80417393 (2693, 2694)	Novel Protein sim. GBank gi4504379jrefNP_003658.1pHG38 - orphan G protein- coupled receptor HG38	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein		264906, 264908, 264809, 265008, 264910, 265011, 265017, 264764, 264766, 264767, 264769, 264631, 264634, 264638, 264567, 264486
1348	87352335 (2695, 2696)	Novel Protein sim. GBank gi3399720dbjBAA321001 - (AB010999) peptidylarginine deiminase type IV [Rattus norvegicus]			UNCLASSIFIED	264488, 264489, 264508, 264509, 264510, 264511, 264512, 264591, 264592, 264601, 264684, 264685, 264769, 264532, 264534, 264555, 264556, 264557, 264558, 22278002, 264486

1349	91225548 (2697, 2698)	Novel Protein sim. GBank gij2144101 pir  55210 - tricarboxylate carrier - rat (fragment)		UNCLASSIFIED	52646842, 35696286, 22278996, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 264910, 60170831, 264591, 60433438, 264757, 21908754, 265017, 265018, 264605, 264760, 264762, 264288, 264766, 264689, 21908765, 21908768, 21908767, 21908768, 55811957, 35695917, 265020, 264534, 264691, 264692, 33657023, 264693, 33657349, 18108374, 18108376, 35696423, 60170394, 22279000, 22279002, 264563, 264564
1350	87093136 (2699, 2700)			UNCLASSIFIED	52646842, 264259, 29331825, 264908, 264511, 264604, 264286, 21908769, 265020, 33657182, 33657349, 18108374, 35695855, 264555, 264556, 18108385, 22279002, 264486
1351	87361327 (2701, 2702)	Novel Protein sim. GBank gij4887239 gb AAD32246.1  - (AF064584) BAW protein [Fugu rubripes]		UNCLASSIFIED	264906, 264907, 264638
1352	80076386 (2703, 2704)			UNCLASSIFIED	264603, 263981
1353	95345417 (2705, 2706)	Novel Protein sim. GBank gij2144101 pir  55210 - tricarboxylate carrier - rat (fragment)			35696286, 60424269, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264758, 264596, 55811386, 265011, 264605, 55811150, 264762, 264764, 264766, 52644229, 56181562, 35695917, 265022, 33657023, 264693, 35695763, 60431528, 264629, 263978, 35696423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264566
1354	95350845 (2707, 2708)	Novel Protein sim. GBank gij4889108 gb AAD27763.1 AF07703 - (AF077030) hypothetical 43.2 kDa protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 29331826, 264906, 265008, 33657402, 21908754, 265011, 87168559, 264684, 264369, 264769, 264689, 21908765, 21908768, 52644150, 33657023, 264692, 264693, 18108374, 83373044, 87168518, 22279000
1355	88260186 (2709, 2710)	Novel Protein sim. GBank gij1469199 gb BAA09487  - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	22278996, 22278997, 264259, 66714117, 264511, 21908754, 265010, 264769, 264689, 21908765, 21908768, 21908769, 264532, 27486282, 264629, 264636, 264556, 264638, 264639, 264482, 264484

1356	85313991 (2711, 2712)	Novel Protein sim. GBank gij1113865 (U40342) - ninein [Mus musculus]		sinud	18108397, 22278995, 22278996, 22278998, 284094, 29331828, 284905, 285006, 285007, 285008, 285010, 285017, 285018, 285019, 284764, 18108354, 284688, 21908785, 285022, 18108364, 35696423, 83373044, 18108387
1357	88260268 (2713, 2714)	Novel Protein sim. GBank gij897603[emb]CAA90330] - (Z50026) phosphatidylcholine transfer protein [Bos taurus]	Contains protein domain (PF01852) - START domain		284259, 29331822, 29331825, 264510, 87168559, 285018, 264448, 264288, 21908785, 21908786, 21908788, 285021, 284693, 18108376
1358	38719455 (2715, 2716)	Novel Protein sim. GBank gij556219 (L36831) - transcription regulator [Mus musculus]			284757
1359	8771843 (2717, 2718)			UNCLASSIFIED	284907, 284909, 284510, 284511, 284512, 18108351, 284764, 284534, 33637023, 18108374, 284634, 284635, 284638, 284639, 18108385, 284486, 284567
1360	87738272 (2719, 2720)	Novel Protein sim. GBank gij2598282[emb]CAA75612] - (Y15417) acetate-CoA ligase [Coprinus cinereus]		synthase	60432289, 284605
1361	87593527 (2721, 2722)	Novel Protein sim. GBank gij5689443[db]BAA83005.1] - (AB028976) KIAA1053 protein [Homo sapiens]	Contains protein domain (PF00536) - SAM domain (Sterile alpha motif)	UNCLASSIFIED	35696286, 22278997, 22278999, 284259, 29331826, 284508, 284509, 284905, 284907, 284908, 285007, 285009, 33109954, 21908754, 87168474, 285011, 284761, 284683, 284288, 284766, 284769, 284689, 21908788, 285020, 285021, 33637023, 55811578, 35696423, 284634, 60432113, 22279002, 264482, 284488
1362	95287961 (2723, 2724)	Novel Protein sim. GBank gij5689411[db]BAA82988.1] - (AB028960) KIAA1037 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	eph	56182575, 56181866, 60432049, 264259, 28331822, 56182181, 29331827, 35696052, 29331828, 284905, 284906, 284908, 284595, 55812036, 85858542, 55811150, 284681, 284288, 284369, 56181562, 60431528, 55810784, 35696423, 60431850, 284558
1363	85758476 (2725, 2726)	Novel Protein sim. GBank gij1130494 (U35776) - ADP-ribosylation factor 1-directed GTPase activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	284488, 29331826, 284907, 284687, 284689, 264693
1364	88179488 (2727, 2728)				60432289, 60433356, 60433438, 87168559, 284603, 18108351, 21908788, 35696423, 60432113
1365	83003108 (2729, 2730)	Novel Protein sim. GBank gij4589562[db]BAA76803.1] - (AB023176) KIAA0959 protein [Homo sapiens]		oncogene	284766
1366	87003262 (2731, 2732)	Novel Protein sim. GBank gij1084944[pir]IS4495 - hypothetical protein YPR021c - yeast [Saccharomyces cerevisiae]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	265007

1367	87721210 (2733, 2734)	Novel Protein sim. GBank gi 488408 emb CAB43240.1  - (AL050019) hypothetical protein [Homo sapiens]	Contains protein domain (PF01342) - SAND domain	UNCLASSIFIED	264488, 52648842, 52646385, 22278995, 58994075, 35898286, 22278996, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35896052, 264905, 264907, 264908, 264909, 264510, 265006, 265007, 264512, 264910, 265009, 60170831, 33657402, 55812038, 21908754, 265011, 87168559, 265017, 265019, 18108351, 264448, 264682, 264683, 264288, 264369, 264686, 264767, 264688, 21908765, 21908766, 21908768, 21908769, 55811957, 265020, 265021, 265022, 264534, 80170615, 264690, 264691, 18108362, 33657023, 33657109, 33657349, 264628, 18108370, 18108374, 18108376, 55811576, 35896423, 35895855, 264635, 264555, 264637, 264556, 52844332, 60170394, 264558, 18108381, 18108385, 56526486, 22279000, 264583, 264587
1368	84320078 (2735, 2736)	Novel Protein sim. GBank gi 464561 sp P35289 RB15_RAT RAS-RELATED PROTEIN RAB-15	Contains protein domain (PF00071) - Ras family	oncogene	264259, 29331822, 29331826, 60432289, 29331827, 35896052, 264508, 264905, 264906, 264908, 264909, 264510, 265007, 264910, 60433438, 264758, 85658542, 87168558, 264600, 264601, 264780, 264764, 264765, 264768, 52644229, 264689, 35895917, 265020, 265021, 264631, 264632, 264634, 264637, 52644332, 264558, 264639, 83373044, 264563, 264588, 264486, 264587, 265008, 60432228, 60433356, 33657084, 21906764, 21906768, 264555, 264638, 264559, 264587
1369	86634033 (2737, 2738)	Novel Protein sim. GBank gi 2062702 (U90550) - butyrophilin [Homo sapiens]		UNCLASSIFIED	
1370	95316910 (2739, 2740)	Novel Protein sim. GBank gi 5031823 ref NP_005823.1 pKCNM - potassium large conductance calcium-activated channel, subfamily M, beta member 2		potassium_channel	22278996, 264259, 29331822, 29331824, 29331826, 29331827, 35896052, 264508, 264509, 264905, 264908, 264907, 264808, 264909, 264510, 264511, 264512, 264758, 265011, 265019, 264764, 264768, 264769, 21908767, 35895917, 18108362, 35896423, 264832, 264635, 264636, 264555, 264638, 264558, 264639, 18108385, 65274727, 264404, 264583, 264586, 264488
1371	95336512 (2741, 2742)	Novel Protein sim. GBank gi 5032203 ref NP_005714.1 PTSPA - tetraspan 5	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	glycoprotein	22278996, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264905, 264508, 29331830, 66712502, 265008, 265009, 264758, 33657084, 85658542, 265010, 265018, 265019, 264762, 264448, 35895917, 33657109, 33657182, 33657349, 35895855, 264558, 22279002, 264563

1372	80248517 (2743, 2744)	Novel Protein sim. GBank gijb40708jdbj[BAA09334] - (D50685) trans-sialidase [Trypanosoma cruzi]		collagen	263978	264769, 21906765, 21906767, 22278989, 264691, 264910, 55812038, 265010, 264681, 264684
1373	80499421 (2745, 2746)			UNCLASSIFIED		264907, 264510, 265007, 264512, 265008, 60432229, 264689, 65274781, 264555, 264556, 264557, 83373044, 60432113
1374	95087036 (2747, 2748)	Novel Protein sim. GBank gij111876jprj[JC1241 - beta-interferon-induced protein - rat		interferon		52644507, 52645156, 52646842, 52646365, 56182575, 56181686, 22278989, 56994075, 35896288, 22278987, 22278988, 22278989, 264259, 29331822, 52645080, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 35696970, 264905, 264509, 264908, 264907, 264908, 29331830, 264909, 265008, 264511, 265007, 265008, 265009, 33657402, 60433356, 52646317, 33108954, 33657084, 52644296, 87188474, 87168559, 264600, 265017, 265018, 265019, 55811150, 18108351, 264448, 264764, 264288, 264369, 264766, 52644228
1375	94236942 (2748, 2750)	Novel Protein sim. GBank gij5648176jbj[AAD03500.2] - (AF051155) G beta-like protein GBL [Rattus norvegicus]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase		21906765, 21906768, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264693, 65274620, 52645129, 33657109, 27486261, 33657349, 27486265, 35695763, 18108376, 55810764, 35696423, 35695855, 264630, 264631, 264634, 264636, 264555, 264638, 18108385, 87168518, 60432113, 22278000, 22278002, 264583, 264564, 264566, 264567
1376	87399050 (2751, 2752)	Novel Protein sim. GBank gij138350jplp28968jVGLX_HSVB - GLYCOPROTEIN X PRECURSOR		UNCLASSIFIED		264788, 264769, 35695917, 22278997, 264691, 264259, 29331822, 264693, 35696052, 264508, 264509, 264905, 264906, 264628, 264908, 264629, 18108372, 264809, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 264592, 264637, 264638, 264558, 264639, 33657402, 264595, 18108385, 56528488, 265010, 265011
1377	86964242 (2753, 2754)	Novel Protein sim. GBank gij1663648 (U75321) - chromaffin granule ATPase II homolog [Mus musculus]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase-associated		264600, 264563, 264762, 264564, 264565, 29331824, 264591, 265019, 264686, 264768, 55811957, 264693, 22278002

1378	87595071 (2755, 2756)	Novel Protein sim. GBank gij4107015[dbj BAA36293] - (AB001772) PEM-5 [Ciona savignyi]			22278994, 22278998, 264093, 264094, 264259, 29331824, 29331827, 265009, 265018, 265019, 18108351, 264369, 264288, 29148627, 55811957, 264691, 18108366, 33657109, 18108368, 264035, 263981, 18108385
1379	85679344 (2757, 2758)	Novel Protein sim. GBank gij3252872 (AF035620) - BRCA1-associated protein 2 [Homo sapiens]			265020
1380	87627962 (2759, 2760)	Novel Protein sim. GBank gij4837737[gb AAD30662.1] - (AF098834) germ cell specific Y-box binding protein [Homo sapiens]	nuc_recpt		264510, 264512, 265009, 264288, 264564
1381	86179656 (2761, 2762)	Novel Protein sim. GBank gij4731580[gb AAD28508.1] (AF12538 - (AF125384) L82A [Drosophila melanogaster]	UNCLASSIFIED		87168559, 265017, 264628, 22279002
1382	94847576 (2763, 2764)		Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	22278994, 22278997, 22278999, 29331822, 29331824, 29331826, 265007, 60432229, 60433366, 85858542, 265017, 265018, 264685, 264768, 21906766, 35695917, 33657023, 27486261, 27486262, 35695763, 35695855, 87168518, 22279002
1383	87860598 (2765, 2766)			UNCLASSIFIED	18108396, 264692
1384	86915895 (2767, 2768)			UNCLASSIFIED	264488, 264508, 264509, 264905, 264906, 264908, 264909, 264511, 264512, 264910, 264760, 18108351, 264766, 264769, 35695855, 264630, 264636, 264555, 264638, 264483, 264564, 264486
1385	86376788 (2769, 2770)	Novel Protein sim. GBank gij2384732 (AF015911) - NAC-1 protein [Rattus norvegicus]	UNCLASSIFIED		35696052, 55811386, 264688, 21906765, 265020, 33657023, 18108385
1386	91013049 (2771, 2772)	Novel Protein sim. GBank gij2384910 (AF022982) - contains similarity to the A-type potassium current class of channel proteins [Caenorhabditis elegans]	Inf		60432289, 29331828, 264906, 264907, 56182435, 265011, 264681, 60170815, 33657023, 83373044, 264568
1387	87797958 (2773, 2774)	Novel Protein sim. GBank gij4160304[emb CAA10600] - (AJ132192) HS1 binding protein 3 [Mus musculus]	UNCLASSIFIED		264591
1388	95101652 (2775, 2776)	Novel Protein sim. GBank gij4895164[gb AAD32753.1] (AC00723 - (AC007231) putative disease resistance protein [Arabidopsis thaliana])	glycoprotein		55274572, 22278999, 264259, 29331826, 29331827, 35696052, 264509, 264907, 264908, 264909, 265006, 265008, 60170831, 33657402, 60433438, 264596, 21906754, 87168559, 264600, 265017, 264683, 18108354, 52844229, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 264692, 33657023, 33657109, 35695855, 264558, 60170394, 83373044, 22279000

1389	91256016 (2777, 2778)	Novel Protein sim. GBank gl 5689387 dbj BAA82977.1  - (AB028948) KIAA1025 protein [Homo sapiens]	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	UNCLASSIFIED	65274572, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29146499, 264908, 66712502, 55812038, 265017, 265018, 265019, 18108351, 264369, 21908765, 21908766, 21908767, 21908768, 265020, 265021, 264692, 33657023, 33657349, 18108370, 18108374, 55811576, 264555, 264556, 264557, 60170394, 83373044, 22278000, 264583, 264584
1390	94111916 (2779, 2780)	Novel Protein sim. GBank gl 3702295 (AC005783) - R33083_1 [Homo sapiens]		peptidase	52645156, 52646365, 264259, 52645080, 29331825, 29331826, 264908, 52644045, 265009, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 264760, 264682, 264288, 264686, 264687, 56181582, 52644229, 21908765, 21908769, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 27486281, 27486284, 65274781, 264631, 264555, 52644332, 87168518, 22279000, 264587
1391	91227345 (2781, 2782)	Novel Protein sim. GBank gl 1346910 sp P28650 PUA1_MOUSE - ADENYLOSUCCINATE SYNTHETASE, MUSCLE (ISOZYME (IMP--ASPARTATE LIGASE))	Contains protein domain (PF00709) - Adenylosuccinate synthetase		29331826, 29331828, 29331830, 264448, 264288, 33657023, 18108365, 264555, 264556, 83373044
1392	94311097 (2783, 2784)	Novel Protein sim. GBank gl 726286 (U22394) - mSin3A [Mus musculus]			52646842, 65274572, 22278994, 22278995, 35695286, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35696052, 29331828, 33656970, 264907, 52644045, 265006, 265007, 265008, 60431735, 60433356, 52646317, 55811386, 52644296, 265010, 87168559, 265017, 264604, 265018, 265019, 264448, 264288, 264369, 264766, 21906764, 21906767, 35695917, 265020, 265021, 33657109, 52645129, 27486281, 27486282, 27486265, 33657349, 35695763, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264636, 52644332, 18108382, 18108385, 87168518, 60432113, 22279000, 264484, 264588, 18108391
1393	80409472 (2785, 2786)		Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264763, 264631
1394	15028819 (2787, 2788)			UNCLASSIFIED	264629
1395	95361471 (2789, 2790)	Novel Protein sim. GBank gl 2274845 dbj BAA21534  - (D88461) N-WASP [Rattus rattus]		UNCLASSIFIED	265009, 18108381



1396	95363253 (2781, 2792)	Novel Protein sim. GBank gi 2135904 pri j54810 - pH-L EIF1 - human			22278997, 22278999, 264259, 28331825, 60432289, 29331828, 29148498, 29148499, 264907, 264908, 29331830, 264909, 265006, 265007, 265008, 265009, 60433356, 265010, 264602, 265017, 265018, 265019, 18108354, 52644229, 18108358, 21908767, 29148827, 21908768, 21908769, 29148629, 29148784, 265021, 265022, 18108368, 18108374, 56182323, 18108385, 264563, 264567, 35696286, 264907, 66712502, 264510, 35695917, 264692, 264693, 35696423, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 33658970, 87168474, 265018, 265019, 264682, 264768, 21908767, 265020, 33657023, 27486261, 55811576, 264632, 264639, 83373044, 87168518, 22279002
1397	87631317 (2793, 2794)			UNCLASSIFIED	
1398	91233667 (2795, 2796)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]			
1399	87631076 (2797, 2798)	Novel Protein sim. GBank gi 2496887 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	
1400	95419064 (2799, 2800)	Novel Protein sim. GBank gi 283920 pri j527939 - tensin - chicken	Contains protein domain (PF00017) - Src homology domain 2	UNCLASSIFIED	56182575, 22278994, 22278997, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264908, 56182435, 264112, 265009, 265011, 265017, 265018, 265019, 264760, 264762, 264765, 264288, 264685, 264687, 56181562, 264769, 21906766, 21906767, 55811957, 264691, 264692, 264628, 264629, 55811576, 264634, 264555, 264637, 264557, 264638, 18108381, 264558, 18108384, 60432113, 22279000
1401	91226379 (2801, 2802)	Novel Protein sim. GBank gi 3256185 emb CAA15485 - (AL008635) dJ510H16.1 [Homo sapiens]	Contains protein domain (PF00790) - VHS domain	UNCLASSIFIED	65274572, 60432289, 264909, 264758, 264768, 21908769, 22279002
1402	95361475 (2803, 2804)	Novel Protein sim. GBank gi 1515427 (U57523) - nei homolog [Homo sapiens]	Contains protein domain (PF00008) - Igf EGF-like domain		264905, 264907, 264908, 264909, 264112, 264693, 33657109, 264634
1403	94147933 (2805, 2806)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1 - (AL080156) hypothetical protein [Homo sapiens]			65274572, 66712502, 265017, 264448, 264288, 21908765, 21908769, 264693, 55811576, 65274791, 60432113
1404	90935393 (2807, 2808)			UNCLASSIFIED	65274572, 22278998, 29331822, 29331828, 66712502, 265008, 60433438, 265017, 264693, 18108385

1405	95095068 (2809, 2810)	Novel Protein sim. GBank gij854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]			264488, 56994075, 35696286, 29331822, 29331824, 29331826, 29331828, 35696052, 264508, 264906, 264907, 264908, 264510, 264511, 264910, 33657402, 264594, 264758, 264600, 264604, 264762, 18108351, 264764, 33657023, 33657109, 264628, 264634, 83373044, 22279002, 264563, 264482, 264486, 264587, 264907, 264605
1406	87612369 (2811, 2812)	Novel Protein sim. GBank gij624076[gol]AAC96425.1] - (U42580) contains Pro-rich Px motifs: SPKPP (20X), PEPPA (9X); similar to soybean pro-rich cell wall protein, corresponds to Swiss-Prot Accession Number P13993 [Paramedum bursaria Chlorella virus 1]	collagen		
1407	94129872 (2813, 2814)	Novel Protein sim. GBank gij2827886 (AF015037) - endo oligopeptidase A related protein; EOPA related protein [Oryzologus cuniculus]	UNCLASSIFIED		35696286, 22278999, 264094, 264259, 66714117, 29331826, 29331827, 29331828, 29148498, 264107, 264908, 265006, 265008, 264910, 60433438, 265011, 265017, 18108351, 264448, 264288, 264886, 21808765, 21808769, 264892, 33657109, 18108370, 264828, 263972, 18108374, 35696423, 55811576, 264631, 264557, 264558, 83373044, 18108385, 87168518, 60432113, 22279002
1408	95361477 (2815, 2816)	Novel Protein sim. GBank gij2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00009) - oncogene EGF-like domain		264488, 264489, 35696286, 264109, 264508, 264805, 264509, 264906, 264807, 264908, 264909, 265008, 265009, 264910, 33657402, 264757, 264758, 265011, 264601, 265017, 264760, 264762, 264683, 264885, 264766, 264887, 264689, 21808767, 265021, 264690, 264891, 33657023, 264692, 264693, 33657109, 264628, 264829, 35698423, 35695855, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 56182323, 264639, 264563, 264564, 264565, 264566, 264567, 264693
1409	86644365 (2817, 2818)	Novel Protein sim. GBank gij2662165[db]BAA23714] - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]			
1410	86612587 (2819, 2820)	Novel Protein sim. GBank gij2493790[sp]Q60994[ACR3_MOUSE - 30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ)]	Contains protein domain (PF00386) - complement C1q domain		29331826, 264112, 264512, 265009, 265010, 264601, 264686, 264769, 21906787, 263974, 264631, 264566

1411	87818641 (2821, 2822)	Novel Protein sim. GBank gi 3123155 sp P91343 YM3M_CAEEL - HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME 1	Contains protein domain (PF00400) - WD domain, G-beta repeat	Kinasereceptor	22278995, 22278997, 22278999, 29331822, 60432289, 29331828, 264907, 265017, 265018, 264682, 21906767, 21906768, 21906769, 265020, 264690, 264691, 33657023, 33657109, 27486264, 264628, 263972, 264634, 264558, 18108385
1412	84390919 (2823, 2824)			UNCLASSIFIED	264757
1413	95416559 (2825, 2826)	Novel Protein sim. GBank gi 3879121 emb CAA94370  - (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:U01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	homeobox	56994075, 29331822, 35696052, 29331828, 29331830, 264909, 52644045, 264510, 52644298, 85658542, 87168474, 265017, 265018, 264681, 264687, 21906768, 35695917, 265020, 52644150, 264692, 263967, 27486264, 35695763, 264639, 18108387, 264566
1414	94675860 (2827, 2828)	Novel Protein sim. GBank gi 3252981 (AF068921) - Ras- binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - Leudine Rich Repeat	UNCLASSIFIED	264682, 264683, 265022, 264636
1415	94326948 (2829, 2830)	Novel Protein sim. GBank gi 1871187 (U90439) - unknown protein [Arabidopsis thaliana]			52646365, 56182575, 22278994, 22278995, 56994075, 22278998, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 66712502, 29331830, 52644045, 264113, 264511, 33657402, 264757, 21908754, 55811386, 265017, 265018, 265019, 264761, 264683, 264369, 264288, 264686, 264689, 21906766, 21906767, 29148627, 21906769, 55811957, 265020, 265021, 264690, 33657023, 65274620, 52645129, 27486262, 27486264, 60431528, 264629, 35695855, 56182323, 264559, 60432113, 264404, 22279002, 264482

1416	84325977 (2831, 2832)	Novel Protein sim. GBank gi 5106557 gb AAD39749.1 AF123052 - (AF123052) MLL septilin-like fusion protein [Homo sapiens]	Contains protein domain (PF00735) - struct Cell division protein	18108392, 18108394, 18108397, 18108398, 22278995, 22278998, 35696286, 22278997, 22278998, 22278999, 29331822, 35696052, 29331828, 29148498, 264905, 264907, 264908, 264828, 264909, 264113, 265006, 265007, 265008, 265009, 60170831, 264595, 18108348, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264762, 18108351, 264681, 264763, 264682, 264683, 264766, 52644229, 264688, 264689, 21906785, 21906786, 21906787, 29148627, 21908788, 55811957, 29148629, 265020, 52644150, 18108361, 33657023, 18108382, 18108368, 264628, 18108370, 264629, 18108374, 18108379, 55811578, 65274791, 264634, 264638, 58182323, 18108381, 60170394, 18108385, 58528486, 87188518, 22279000
1417	87826663 (2833, 2834)	Novel Protein sim. GBank gi 4958935 dbj BAA78095.1  - (AB027570) suppressor of potassium transport defect 3 [Rattus norvegicus]	ATPase_associated	264107, 264448
1418	87594276 (2835, 2836)		UNCLASSIFIED	264259, 264908, 265010, 52644229, 21906784, 21906788, 264690, 264639, 18108388
1419	87757168 (2837, 2838)	Novel Protein sim. GBank gi 2072294 (U95097) - mitotic phosphoprotein 43 [Xenopus laevis]	struct	264259, 60432289, 265006, 87168474, 264288
1420	87296628 (2839, 2840)	Novel Protein sim. GBank gi 5174421 ref NP_006023.1 pCPNE - copine VI (neuronal)	ATPase_associated	29331824, 265007, 264563
1421	94746986 (2841, 2842)	Novel Protein sim. GBank gi 3876090 emb CAA93459.1  - (Z89635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this gene....	kinase	18108358, 18108396, 18108397, 21906766, 18108398, 21906767, 56182575, 21908768, 21906769, 56181886, 55811957, 35695917, 35696286, 22278996, 22278997, 22278998, 22278999, 265021, 265022, 60170615, 264259, 33657023, 28331822, 56182181, 29331824, 66714117, 29331825, 33657109, 29331828, 27486261, 29331828, 35696052, 33657349, 264905, 264509, 20281149, 18108370, 264907, 60431528, 66712502, 263972, 55811576, 35696423, 35695855, 264512, 285007, 60431850, 60432229, 60431735, 56182323, 264558, 60170394, 83373044, 55812038, 264758, 18108385, 21906754, 55811386, 87168518, 87168559, 60432113, 265017, 265018, 265019, 22279002, 55811150, 264563, 264682, 264763, 264448, 264566, 264486, 18108391

1422	88178777 (2843, 2844)	Novel Protein sim. GBank gi 4505939 ref NP_000928.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide A (220kd)		mapolymerase	56994075, 35696286, 87168559, 55811857, 55811576, 264555, 264557, 87168518
1423	86997762 (2845, 2846)			UNCLASSIFIED	264686, 264489, 264692, 264594, 264603, 265018, 264908
1424	95201610 (2847, 2848)	Novel Protein sim. GBank gi 437181 (U02289) - GTPase- activating protein [Caenorhabditis elegans]	Contains protein domain (PF00620) - struct RhoGAP domain		29331822, 29331825, 29331827, 29146498, 264905, 264906, 264908, 264909, 265007, 264910, 265009, 33109954, 265010, 87168559, 265019, 264766, 264687, 21906765, 21906766, 21906767, 21906768, 29148627, 55811857, 29148629, 265021, 264691, 264692, 56526486, 22279002, 264563
1425	21662314 (2849, 2850)	Novel Protein sim. GBank gi 100788 pt S14959 - proline- rich protein - wheat		UNCLASSIFIED	265007, 264558
1426	94322115 (2851, 2852)	Novel Protein sim. GBank gi 2078441 (U56954) - weak similarity to S. cerevisiae intracellular protein transport protein US1 (SP-P25386) [Caenorhabditis elegans]		UNCLASSIFIED	264488, 60424179, 35696286, 22278997, 22278998, 22278999, 264259, 60432048, 29331822, 29331825, 29331827, 56182435, 264910, 60433356, 60433438, 21906754, 265018, 264288, 21906765, 21906766, 21906767, 21906769, 265020, 265022, 33657109, 18108370, 18108376, 264558, 83373044, 18108385, 56526486, 22279002, 264482
1427	91227510 (2853, 2854)	Novel Protein sim. GBank gi 5816074 gb AAD45616.1 AF06194 - (AF061943) prolate- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain		22278994, 56994075, 22278997, 29331828, 29331830, 264628, 265006, 265007, 265008, 265009, 264683, 264288, 18108354, 21906765, 21906768, 29148629, 33657023, 18108374, 35695855, 83373044, 22279002, 264564
1428	94323008 (2855, 2856)	Novel Protein sim. GBank gi 138350 sp P28968 VGLX_HSVB - GLYCOPROTEIN X PRECURSOR		glycoprotein	56181686, 264259, 284907, 265007, 265009, 264595, 265010, 284688, 65274620, 264629, 65274791, 22279002, 264566
1429	87886689 (2857, 2858)			UNCLASSIFIED	264112, 264595, 265017, 265019, 21906765, 263977, 264555
1430	94735021 (2859, 2860)	Novel Protein sim. GBank gi 118161 g db BAA11565  - (D82364) a variant of TSC-22 [Gallus gallus]			264094, 29331824, 264591, 264593, 265018, 264681, 21906765, 21906767, 65274620, 55811576, 264639, 87168518, 22279002
1431	80429081 (2861, 2862)	Novel Protein sim. GBank gi 5420389 emb CAB46880.1  - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264768, 265020, 264691, 264693, 264638
1432	87463004 (2863, 2864)	Novel Protein sim. GBank gi 414787 (L18966) - pyruvate dehydrogenase phosphatase [Bos taurus]		phosphatase	18108394, 29146498, 265007, 60433438, 264763, 29148629, 263969
1433	87605403 (2865, 2866)	Novel Protein sim. GBank gi 2460316 (AF022147) - uterus - ovary specific putative transmembrane protein [Rattus norvegicus]	Contains protein domain (PF00100) - Zona pellucida-like domain	UNCLASSIFIED	264259, 264510, 264591, 264603, 264565
1434	85713730 (2867, 2868)			UNCLASSIFIED	264682, 264691

1435	94708213 (2659, 2870)	Novel Protein sim. GBank gij3970850dbj[BAA34789.1] - (AB015330) HRIHFB2007 [Homo sapiens]		transcript factor	22278997, 22278998, 22278999, 60432048, 264259, 29331822, 29331824, 69714117, 29331828, 33656970, 264508, 264905, 69712502, 29331830, 264909, 265007, 265008, 264910, 265009, 60433358, 60433438, 264596, 21906754, 265010, 265017, 265018, 265019, 18108351, 264762, 264448, 264288, 264769, 21906767, 21906768, 21906769, 285020, 285021, 285022, 264690, 264691, 33657109, 264628, 18108374, 18108376, 55811576, 264636, 60170394, 56182323, 264559, 83373044, 87168518, 60432113, 22279000, 22279002, 264563, 264482, 264565, 263978, 264557, 264559
1436	86635024 (2871, 2872)	Novel Protein sim. GBank gij3183977jemb[CAA39515] - (X55044) protein Hf9C [Mus musculus]		UNCLASSIFIED	
1437	87631082 (2873, 2874)	Novel Protein sim. GBank gij2496887[sp]Q09232YQ22, CAEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	22278997, 66714117, 29331826, 264907, 56182435, 265009, 18108351, 264692, 264693
1438	85544280 (2875, 2876)	Novel Protein sim. GBank gij1905906 (AD000092) - hypothetical human serine-threonine protein kinase R31240_1 [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	264488, 264508, 264906, 264909, 264757, 264600, 264601, 264605, 264788, 264789, 264690, 35898423, 264559, 264563, 264568
1439	91231894 (2877, 2878)	Novel Protein sim. GBank gij3876299jemb[CAA94892] - (Z71180) similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabditis...]	Contains protein domain (PF00450) - Serine carboxypeptidase	cathepsin	264489, 18108394, 65274572, 56182575, 22278994, 22278996, 35896286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331824, 60432289, 29331828, 29331827, 29331828, 35896052, 33858970, 264107, 264508, 264509, 264907, 66712502, 29331830, 56182435, 264511, 265006, 265007, 265009, 60432229, 60433438, 264595, 55812038, 55811386, 265011, 285017, 265018, 265019, 18108351, 264448, 18108354, 264288, 18108355, 264767, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35895917, 265020, 265021, 265022, 33657109, 18108370, 18108374, 55810764, 35895855, 264634, 264636, 56182323, 83373044, 18108387, 87168518, 60432113, 22279000, 264488
1440	87423643 (2879, 2880)	Novel Protein sim. GBank gij2662165dbj[BAA23714] - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]		UNCLASSIFIED	264887, 264259, 264906, 264907, 264908, 264909, 265008, 265010, 265017, 265018, 265019, 18108351, 264369, 265020, 33657023, 33657109, 60431528, 55811576, 264635

1441	95317662 (2881, 2882)	Novel Protein sim. GBank gij493956[embjCAB11123.2] - (Z98551) predicted using hexExon; MAL3P6.28 (PF00845c). Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe), C.elegans protein ZK287.5 (TR:....	Contains protein domain (PF00646) - F-box domain.	18108392, 264488, 263994, 264489, 56182575, 22278994, 22278995, 56994075, 35696286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 56182181, 66714117, 29331826, 29331827, 29331828, 35696052, 29146498, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264910, 264592, 264593, 33657402, 60433438, 264595, 264758, 21906754, 85658542, 87168474, 265010, 87168559, 264600, 264602, 265017, 264604, 265018, 264605, 265019, 264760, 264761, 264762, 264681, 264448, 264764, 264683, 264288, 264766, 264768, 264769, 52644229, 264689, 21906765, 21906766, 21906787, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 264691, 264692, 33657023, 65274620, 33657109, 35695763, 264628, 18108370, 264629, 18108374, 55811576, 35696423, 65274791, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 56182323, 264558, 80170394, 264639, 264559, 83373044, 18108385, 18108388, 56526486, 22279000, 22279002, 264563, 264483, 264564, 264566, 264567, 264486
1442	83367491 (2883, 2884)	Novel Protein sim. GBank gij5103027[dbjBAA78765.1] - (AB023419) mSox7 [Mus musculus]	transcription factor	264587, 264486
1443	87109935 (2885, 2886)	Novel Protein sim. GBank gij4887229[gbjAAD32244.1]AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - Spectrin repeat	52645080, 264691, 264628, 264555
1444	87620478 (2887, 2888)	Novel Protein sim. GBank gij3874447[embjCAB02772] - (Z81039) predicted using GeneFinder; cDNA EST EMBL: T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com....	UNCLASSIFIED	264259, 29331822, 29331824, 66714117, 29331828, 264288, 35695917, 33657023, 264635, 60170394
1445	94990470 (2889, 2890)	Novel Protein sim. GBank gij2959886[embjCAA11022] - (AJ222966) L-perixin [Mus musculus]	UNCLASSIFIED	264369
1446	85079268 (2891, 2892)	Novel Protein sim. GBank gij5081810[gbjAAD39464.1]AF13544 - (AF135440) huntington yeast partner C [Mus musculus]	Contains protein domain (PF01846) - FF domain	264369
1447	86945392 (2893, 2894)	Novel Protein sim. GBank gij3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]	Contains protein domain (PF00439) - Bromodomain	18108396, 35696286, 22278997, 66714117, 29331828, 265009, 264758, 265018, 264288, 21906766, 21906767, 264692, 264634, 264566
1448	94990477 (2895, 2896)	Novel Protein sim. GBank gij3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]	Contains protein domain (PF00439) - Bromodomain	29331827, 264509, 264909, 265008, 264595, 18108357, 18108385, 264566, 264496

1449	87860859 (2897, 2898)				UNCLASSIFIED	68714117, 284906, 284908, 284591, 284601, 284764, 284632
1450	87456696 (2899, 2900)	Novel Protein sim. GBank gij1707074 (U80450) - MO1E11.2 [Caenorhabditis elegans]			UNCLASSIFIED	35686286, 35696052, 265008, 265009, 60170831, 33109954, 264683, 264689, 35696423, 35695855, 56528486
1451	87797970 (2901, 2902)	Novel Protein sim. GBank gij160304[emb]CAA106001 - (AJ132192) HS1 binding protein 3 [Mus musculus]			UNCLASSIFIED	29331826, 284683, 284693, 263978, 264630
1452	85692899 (2903, 2904)	Novel Protein sim. GBank gij2832808[db]BAA24608.1 - (D89340) dipeptidyl peptidase III [Rattus norvegicus]			peptidase	264681, 33657023, 264629
1453	86130434 (2905, 2906)	Novel Protein sim. GBank gij728831[sp]P39188/ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III			kinase	264510, 264768
1454	11204696 (2907, 2908)					
1455	87797896 (2909, 2910)				UNCLASSIFIED	264556 29331822, 66714117, 29331825, 264905, 29331830, 265008, 265008, 265009, 265011, 265019, 18108351, 21908768, 33657109, 18108376, 264632, 56182323, 87168518
1456	86320218 (2911, 2912)	Novel Protein sim. GBank gij729230[sp]P41004[CUT3_SCHPO - CHROMOSOME SEGREGATION PROTEIN CUT3]			transport	22278995, 22278996, 22278997, 22278998, 22278999, 29331827, 284107, 265017, 21906765, 21908768, 21908767, 21908769, 29148629, 18108370, 22278000
1457	80076900 (2913, 2914)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]			UNCLASSIFIED	264107, 264566
1458	87800460 (2915, 2916)				transport	56182575, 22278999, 60432049, 264259, 29331826, 29331827, 29331828, 265017, 265018, 264107, 264110, 265009, 60432229, 265019, 265020, 263972, 263976, 264635, 22279002, 264566
1459	95360920 (2917, 2918)	Novel Protein sim. GBank gij5524667[sp]A044333.1[AF15935] Munc13-4 protein [Rattus norvegicus]	Contains protein domain (PF00168) - C2 domain		kinase	22278997, 264259, 29331824, 29331826, 29331827, 29331828, 265017, 265018, 264760, 264682, 264448, 264288, 264766, 265021, 284692, 33657023, 33657109, 35695855, 284566
1460	95354602 (2919, 2920)				UNCLASSIFIED	29331822, 264591, 55811957, 264691, 264693, 65274820
1461	94741513 (2921, 2922)	Novel Protein sim. GBank gij1707274 (U80931) - strong similarity to class-III of pyridoxal-phosphate-dependent aminotransferases [Caenorhabditis elegans]	Contains protein domain (PF00202) - gaba Aminotransferases class-III pyridoxal phosphate			22278997, 29331822, 35696052, 265009, 264758, 265017, 265018, 265019, 264780, 264369, 264687, 21908765, 21908768, 265022, 33657109, 27486261, 264555, 83373044
1462	87732018 (2923, 2924)				UNCLASSIFIED	264555, 264556
1463	88090605 (2925, 2926)	Novel Protein sim. GBank gij1770466[emb]CAA66912 - (X98259) M-phase phosphoprotein 8 [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHR)romatin Organization MOdifier domain	struct		60432049, 264259, 29146499, 284908, 264907, 284512, 265017, 264783, 264768, 18108370, 18108374, 264636, 18108385, 18108388



1464	87620482 (2927, 2928)	Novel Protein sim. GBank gij3874447[emb CAB02772] - (Z81039) predicted using Genefinder; cDNA EST EMBL:701209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com....		UNCLASSIFIED	264569, 22278995, 22278996, 22278997, 22278998, 29331822, 29331824, 29331825, 35696052, 20281100, 264905, 29331830, 264909, 265007, 33657402, 21906754, 265017, 265018, 264882, 264884, 264369, 264288, 264766, 21906765, 21906766, 21906767, 21906769, 35695917, 264691, 33657023, 264692, 35696423, 35695855, 264630, 264631, 264639, 264565
1465	87425182 (2928, 2930)	Novel Protein sim. GBank gij4589599[db BAA76821.1] - (AB023194) KIAA0977 protein [Homo sapiens]	glucoamylase		264486, 22278994, 56994075, 60432049, 264259, 56182181, 60432289, 29331827, 52644045, 264511, 265007, 265008, 264596, 55812038, 55811386, 264600, 264602, 265017, 265018, 264604, 265019, 18108351, 18108354, 56181562, 21906769, 285021, 33657023, 33657182, 55811576, 264557, 18108382, 60432113
1466	87606227 (2931, 2932)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	UNCLASSIFIED	struct	264512, 265017, 264689, 264558
1467	87614328 (2933, 2934)	Novel Protein sim. GBank gij4507241[ref NP_003137.1 pSSRP - structure specific recognition protein 1			264683, 264636
1468	95342862 (2935, 2936)	Novel Protein sim. GBank gij4507241[ref NP_003137.1 pSSRP - structure specific recognition protein 1			22278998, 264758, 265018, 265019, 21906769, 265020, 33657109, 22279002
1469	79236174 (2937, 2938)	Novel Protein sim. GBank gij1906596 (U81788) - kinesin-73 [Drosophila melanogaster]	struct		18108394, 18108397, 18108398, 35696052, 29146499, 265007, 265008, 265009, 265010, 265011, 18108354, 18108365, 18108366, 18108374, 18108381, 18108382, 18108384, 18108388
1470	94990482 (2939, 2940)	Novel Protein sim. GBank gij5649170[gb AAD43131.2 AF15909 - (AF159092) syld709613 protein [Homo sapiens]	UNCLASSIFIED		18108394, 18108398, 56182575, 264259, 29331822, 29331824, 29331825, 60432289, 264907, 264909, 265007, 264910, 265009, 264591, 60432229, 60433356, 264595, 60433438, 264758, 33109954, 265010, 265011, 265018, 264760, 264448, 264764, 264288, 264369, 18108357, 264769, 18108358, 21906767, 21906769, 55811957, 265021, 18108361, 264691, 18108362, 18108365, 18108368, 264628, 18108379, 264637, 264557, 18108381, 56182323, 18108382, 83373044, 18108384, 18108388, 87168518, 60432113, 264404, 22279002, 264482, 264567, 264487
1471	87826842 (2941, 2942)	Novel Protein sim. GBank gij3876148[emb CAB01750] - (Z78542) similar to Mitochondrial carrier proteins; cDNA EST EMBL:701651 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	-transport	29331822, 29331824, 29331825, 264828, 264603, 264689, 264693, 18108374, 55811576

1472	87756616 (2943, 2944)	Novel Protein sim. GBank gi 4680707 gb AAD27743.1 AF13286 - (AF13286) CGI-34 protein [Homo sapiens]		UNCLASSIFIED	264805, 18108351, 21906765, 264486
1473	87791608 (2945, 2946)	Novel Protein sim. GBank gi 3688780 (AF042180) - lesis- specific Y-encoded-like protein [Mus musculus]	Contains protein domain (PF00956) - Nucleosome assembly protein (NAP)	MHC	18108394, 22278995, 56994075, 22278999, 29331822, 29331824, 68714117, 29331825, 29331826, 35696052, 264908, 264907, 56182435, 265007, 264758, 265018, 265019, 264760, 264764, 264288, 264685, 264686, 264768, 21908769, 55811957, 285021, 264691, 264693, 264629, 55811578, 264634, 264638, 56182323, 22279002, 264586, 264486
1474	85800989 (2947, 2948)	Novel Protein sim. GBank gi 2494890 sp Q92176 CORO_BOVIN - CORONIN-LIKE PROTEIN P57	Contains protein domain (PF00400) - WD domain, G-beta repeat	struct	264488, 35695917, 35696286, 264692, 33657023, 264693, 33637109, 35696052, 264508, 264905, 264906, 264907, 264629, 264908, 264909, 35696423, 35695855, 264511, 264910, 264632, 264634, 264635, 264636, 264637, 264556, 264557, 264639, 264758, 60432113, 264604, 264605, 264565, 264586, 264784, 264486, 264685, 264786, 264681, 264682, 264288, 264566
1475	86871835 (2949, 2950)		Contains protein domain (PF00041) - Fibronectin type III domain	UNCLASSIFIED	
1476	87548855 (2951, 2952)	Novel Protein sim. GBank gi 475752 ref NP_004684.1 PANGP - angiopoietin 3	Contains protein domain (PF00147) - Fibrinogen beta and gamma chains, C-terminal globular domain	glycoprotein	60424179, 56181886, 29331824, 60424269, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264512, 265007, 265008, 265009, 264910, 33637402, 264595, 264596, 55812038, 265011, 264801, 264762, 18108351, 264288, 264369, 264685, 264766, 264689, 55811957, 264691, 264692, 264693, 18108370, 60431528, 18108374, 35696423, 264634, 264635, 264636, 60431850, 264555, 264638, 264557, 264639, 18108382, 18108388, 60432113, 22279002, 264259, 264107, 264905, 265008, 265010, 265011, 264682, 264288, 265020, 265021, 263974
1477	87774279 (2953, 2954)	Novel Protein sim. GBank gi 2498308 sp Q60870 DP1_MOUSE - POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106)		UNCLASSIFIED	
1478	11754412 (2955, 2956)				264686

1479	91640140 (2957, 2958)	Novel Protein sim. GBank gi 5499741 gb AAD43978.1 AF15296 - (AF15296) chromatin-specific transcription elongation factor FACT 140 kDa subunit [Homo sapiens]		peptidase	56162575, 22278995, 22278996, 22278998, 22278999, 29331822, 29331824, 66714117, 264906, 264907, 56182435, 265006, 60170831, 33657402, 264758, 33108954, 21906754, 265017, 265019, 264448, 264288, 264767, 264687, 52644229, 21906764, 264689, 21906765, 21906768, 21906769, 265020, 265021, 60170815, 264691, 33657023, 33657109, 33657182, 27486261, 27486282, 33657349, 18108370, 60431528, 263976, 55811576, 264556, 264557, 60170394, 87168518, 264404, 22279000, 22279002, 264563, 264482
1480	94312412 (2959, 2960)	Novel Protein sim. GBank gi 3550456 emb CAA06329.1  - (AJ005073) Alix [Mus musculus]		UNCLASSIFIED	18108394, 55274572, 56182575, 22278995, 35696286, 56994075, 22278996, 22278997, 22278998, 22278999, 264091, 264259, 35696032, 29146499, 264103, 264105, 264108, 264907, 52644045, 264112, 265007, 265008, 265009, 60433356, 60433438, 264596, 33109954, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264448, 264682, 264683, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657109, 33657182, 263972, 35695855, 264557, 263981, 83373044, 18108385, 87168518, 264566, 264089, 264486
1481	87021442 (2961, 2962)	Novel Protein sim. GBank gi 436607 gb AAD30586.1 AF14679 - (AF146793) PFT27 [Mus musculus]		MHC	265006, 265007, 265010, 18108374
1482	85320442 (2963, 2964)	Novel Protein sim. GBank gi 4585372 gb AAD25403.1 AF12292 - (AF122923) Vnt inhibitory factor-1 [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264908, 264910, 264758
1483	94115503 (2965, 2966)	Novel Protein sim. GBank gi 535428 (U13736) - calmodulin- like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	- struct	264259, 29331822, 52645080, 29331825, 29331826, 33656970, 29331830, 265007, 55812038, 33109954, 265017, 264288, 21906768, 21906769, 264636, 18108380, 87168518, 22279000
1484	94131544 (2967, 2968)	Novel Protein sim. GBank gi 1911774 bbs 180090 - (S83384) putative Rab5-interacting protein (clone L1-57) [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]		UNCLASSIFIED	264489, 35696286, 264259, 264107, 264909, 265008, 60433356, 33657402, 60433438, 264288, 21906765, 21906766, 29148627, 33657023, 27486262, 18108374, 35696423, 83373044, 60432113
1485	80194441 (2969, 2970)	Novel Protein sim. GBank gi 5360129 gb AAD42883.1 AF15511 - (AF155117) NY-REN 62 antigen [Homo sapiens]	Contains protein domain (PF00225) - Kinesin motor domain	- struct	264369, 265020, 18108374

1486	94125066 (2971, 2972)	Novel Protein sim. GBank gi 4589518 gb BAA76780.1  - (AB023153) KIAA0936 protein [Homo sapiens]	Contains protein domain (PF00089) - kinase Eukaryotic protein kinase domain	kinase	56182575, 22278999, 264906, 264907, 21906754, 87168474, 265017, 265019, 18108351, 264288, 265020, 264566, 21906754, 264486
1487	86452711 (2973, 2974)	Novel Protein sim. GBank gi 5018275 emb CAB44431.1  - (AJ132751) xenobiotic/medium-chain fatty acid:CoA ligase form XL-III [Bos taurus]		synthase	
1488	87732028 (2975, 2976)	Novel Protein sim. GBank gi 5712131 gb AAO47379.1  (AF120499) DEM1 protein [Homo sapiens]	Contains protein domain (PF01443) - Igt Viral (Superfamily 1) RNA helicase	Igt	264686, 264769, 264689, 264692, 264693, 264508, 264906, 264907, 18108370, 264908, 264628, 264909, 264510, 265008, 264512, 265007, 265008, 265009, 264555, 264556, 264557, 264558, 264782, 264564, 264682
1489	95104277 (2977, 2978)	Novel Protein sim. GBank gi 2497303 sp Q62788 FPRP_RAT - PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN)	Contains protein domain (PF00047) - prostaglandin Immunoglobulin domain	prostaglandin	21906767, 22278999, 265022, 264259, 264693, 29331824, 29331825, 29331826, 29331827, 29331828, 264103, 263972, 68712502, 35896423, 35895855, 265007, 265008, 265009, 83373044, 21906754, 56528486, 265017, 264563, 18108351, 264564, 264566, 264389, 264288
1490	87390127 (2979, 2980)			UNCLASSIFIED	56182575, 264259, 29331822, 29331824, 66714117, 29331827, 29331828, 264508, 264906, 66712502, 265007, 265008, 264594, 33657402, 55812038, 87168474, 265018, 18108351, 264389, 264288, 264789, 264689, 21906767, 21906768, 55811957, 60170615, 33657109, 35895855, 264635, 60170394, 56528486, 22278902, 264563
1491	83594305 (2981, 2982)	Novel Protein sim. GBank gi 295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]		UNCLASSIFIED	265007, 264448, 18108372, 264558, 56182323
1492	85805363 (2983, 2984)	Novel Protein sim. GBank gi 1656005 (U71205) - rli [Mus musculus]	Contains protein domain (PF00071) - oncogene Ras family	oncogene	22278997, 22278998, 29331822, 264907, 66712502

1493	91677215 (2985, 2986)	Novel Protein sim. GBank gij5689515[dbj BAA83041.1] - (AB029012) KIAA1089 protein [Homo sapiens]		UNCLASSIFIED	264488, 52646365, 65274572, 56182575, 22278994, 35696286, 56994075, 22278999, 50432049, 29331824, 29331828, 35696052, 264508, 264905, 264906, 52644045, 264909, 56182435, 265006, 265008, 265009, 60170831, 33657402, 55812038, 265010, 265011, 265017, 265018, 265019, 55811150, 264448, 264682, 264685, 264686, 52644229, 21908765, 21908768, 21908769, 265020, 265021, 60170615, 52644150, 33657023, 18108384, 18108385, 33657109, 33657182, 27488261, 27488262, 27488264, 33657349, 27488265, 35895763, 18108370, 264629, 18108374, 52644332, 56182323, 87168518, 22279002, 264564, 264566, 264567
1494	87605265 (2987, 2988)	Novel Protein sim. GBank gij728832[sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF01352) - KRAB box	kinase	264907, 265009, 264769, 18108370, 55811576, 264639, 264565, 264488
1495	87605267 (2989, 2990)	Novel Protein sim. GBank gij4589588[dbj BAA76816.1] - (AB023189) KIAA0972 protein [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcript factor	22278997, 264259, 264906, 264907, 265009, 264594, 33657084, 265017, 264760, 264448, 33657109, 264630, 264634, 56526486, 264563, 264565, 264566, 264488, 264567
1496	87784322 (2991, 2992)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	35696286, 264906, 265019, 264693
1497	81695428 (2993, 2994)	Novel Protein sim. GBank gij3874925[emb CAA92591] - (Z68296) Similarity to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW:KRAA_MOUSE); cDNA EST EMBL:D27610 comes from this gene; cDNA EST EMBL:T01018 comes from this gene; cDNA EST EMBL:D33256 comes from this gene;...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264910, 264758, 265011, 264784, 264288, 264690, 264634, 264635, 56526488
1498	80934938 (2995, 2996)	Novel Protein sim. GBank gij728836[sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		oncogene	264488, 65274572, 29331822, 265017, 265018, 21905765, 29148627, 29148629, 18108374, 264637, 264638, 264567
1499	86451589 (2997, 2998)	Novel Protein sim. GBank gij2570198 (U54556) - (microfilament sheath protein SHP3 [Litomosoides sigmodontis])		glucosylase	263978, 264568
1500	80499386 (2999, 3000)	Novel Protein sim. GBank gij2078483 (U43200) - anilfreeze		UNCLASSIFIED	22278999, 264769, 18108379
1501	85795297 (3001, 3002)	glycopeptide AFGP polyprotein precursor [Boreogadus salda]		UNCLASSIFIED	264559
1502	80206141 (3003, 3004)				264508, 264112, 264604, 264684, 52644150, 55811576, 264632, 264558, 264638, 56182323, 264563, 264486
1503	87012701 (3005, 3006)	Novel Protein sim. GBank gij3900855 (AC004874) - similar to N-acetylgalactosaminyltransferase; similar to Q07537 (PID:g1171989) [Homo sapiens]	Contains protein domain (PF00535) - Glycosyl transferases	transferase	29331822, 265007, 264369

1504	79840051 (3007, 3008)		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264693
1505	86102672 (3008, 3010)	Novel Protein sim. GBank gi 4753775 emb CAB41970.1  - (AJ132545) protein kinase [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	29331826, 35696052, 284509, 264906, 264807, 264908, 264909, 264511, 264910, 55812038, 264759, 264763, 264764, 264689, 35695917, 265022, 33657109, 18108374, 264631, 264635, 264638, 264568
1506	94143219 (3011, 3012)	Novel Protein sim. GBank gi 1304201 db BAA06170  - (D29768) alternatively spliced product [Rattus norvegicus]	Contains protein domain (PF00018) - SH3 domain	glycoprotein	65274572, 56182375, 56994075, 22278997, 22278998, 22278999, 264091, 264092, 60432048, 264259, 52845080, 29331822, 29331827, 264106, 29331830, 264908, 56182435, 264110, 264511, 264512, 55812038, 21906754, 87168559, 264600, 265017, 265018, 264681, 18108354, 264369, 264687, 264689, 21906765, 29148627, 21906768, 21906769, 29148629, 52844150, 33657023, 18108376, 65274781, 56182323, 264558, 264559, 18108385, 87168518, 60432113, 22279000, 284565
1507	83738250 (3013, 3014)	Novel Protein sim. GBank gi 5689513 db BAA83040.1  - (AB029011) KIAA1088 protein [Homo sapiens]		helicase	264639
1508	11618758 (3015, 3016)	Novel Protein sim. GBank gi 5031975 ref NP_005875.1 pPAK4 - protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264593
1509	87318451 (3017, 3018)	Novel Protein sim. GBank gi 13161 sp P28614 ACOR_ALCEU - ACETOIN CATABOLISM REGULATORY PROTEIN		UNCLASSIFIED	264259, 29331822, 265007, 18108374, 264556
1510	95362843 (3019, 3020)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	264259, 29331822, 29331824, 29331827, 264509, 264907, 264510, 264511, 265007, 264512, 265008, 87168559, 284288, 265022, 33657023, 35695855, 264637, 264638, 264563
1511	88318073 (3021, 3022)	Novel Protein sim. GBank gi 4559353 gb AAD23014.1 AC00658 - (AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family		52645156, 18108396, 56994075, 60432289, 265006, 60433356, 60433438, 21908754, 87168474, 87168559, 265018, 264782, 264783, 264887, 21906765, 21906769, 27486262, 35695763, 18108374, 35696423, 264555, 18108385, 18108387, 18108388, 87168518, 264482
1512	95345390 (3023, 3024)	Novel Protein sim. GBank gi 4559353 gb AAD23014.1 AC00658 - (AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]			35696052, 264905, 264906, 264907, 264908, 264909, 264910, 264591, 264788, 264689, 264692, 264629, 264636
1513	87436228 (3025, 3026)	Novel Protein sim. GBank gi 1330394 (U58761) - COT1F1.6 gene product [Caenorhabditis elegans]			

1514	95345392 (3027, 3028)	Novel Protein sim. GBank gi14559353[gb AAD23014.1 AC00658 - (AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family	UNCLASSIFIED	52644507, 52645156, 52646365, 52646842, 65274572, 22278994, 35698288, 56994075, 264259, 52645080, 29331822, 29331825, 35696052, 29331830, 52644045, 56182435, 265006, 60433358, 60433438, 55812038, 21906754, 52646317, 52644296, 87169474, 87168559, 264448, 52644229, 21906765, 21906768, 21906767, 21906768, 35695917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486284, 27486265, 35695763, 18108376, 35696423, 35695855, 52644332, 18108385, 18108387, 87168518, 60432113 265020, 264639
1515	79163536 (3028, 3030)	Novel Protein sim. GBank gi13879501[emb CAA87795] - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...	ubiquitin	UNCLASSIFIED	
1516	86073539 (3031, 3032)	Novel Protein sim. GBank gi1498015 (L27479) - X123 [Homo sapiens]		UNCLASSIFIED	265008, 56182323, 22279002
1517	87793325 (3033, 3034)	Novel Protein sim. GBank gi13415134 (AF082024) - Phyb1 [Pimpinella brachycarpa]			264091, 18108370, 264404
1518	87350697 (3035, 3036)	Novel Protein sim. GBank gi1728838[sp P39195 ALU8_HUMAN - IIII ALU SUBFAMILY SX WARNING ENTRY IIII]	lm7		66714117, 264508, 264509, 264905, 264510, 264910, 264591, 264595, 264288, 264766, 264769, 18108374, 264636, 264638, 264486 264569, 264489, 60432049, 265009
1519	94328689 (3037, 3038)	Novel Protein sim. GBank gi15262681[emb CA945771.1] - (AL080198) hypothetical protein [Homo sapiens]			33657402, 264596, 21906754, 265018, 264369, 21906765, 21906768, 21906769, 264691, 65274620, 33657182, 27486261, 18108374, 264557, 264639, 87168518, 22279002
1520	87592855 (3039, 3040)	Novel Protein sim. GBank gi12662161[dbj BAA23712] - (AB007900) HH0452 cDNA clone for KIAA0440 has a 438- bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]	UNCLASSIFIED		18108392, 60432049, 264259, 29331824, 265007, 60433356, 265010, 21906768, 264636
1521	86970696 (3041, 3042)	Novel Protein sim. GBank gi15052351[gb AAD38516.1 AF13542 - (AF135421) GDP- mannose pyrophosphorylase B [Homo sapiens]	Contains protein domain (PF00483) - Nucleosidyl transferase	synthase	18108394, 264259, 66714117, 265011, 264603, 265019, 18108384, 35696423, 264557, 264558, 18108388
1522	78960687 (3043, 3044)	Novel Protein sim. GBank gi13776567 (AC005388) - Strong similarity to F21B7.33 gi12809264 from A. thaliana BAC gb AC002560. EST gb N65119 comes from this gene. [Arabidopsis thaliana]	UNCLASSIFIED	UNCLASSIFIED	29331824, 265018, 265020, 265021
1523	91005151 (3045, 3046)			UNCLASSIFIED	65274572, 21906768, 264693
1524	80203723 (3047, 3048)			UNCLASSIFIED	264112, 21906754, 263974
1525	87799667 (3049, 3050)	Novel Protein sim. GBank gi14759040[ref NP_004283.1 pRIN1 - ras inhibitor		UNCLASSIFIED	264683, 264687, 264689, 264690, 264692, 264693

1526	95105344 (3051, 3052)	Novel Protein sim. GBank gij728850 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		glycoprotein	35896286, 56182181, 60431735, 264595, 55812038, 264605, 264683, 21906785, 55811957, 265020, 65274791, 264555, 264556, 264557, 264558, 264559, 83373044
1527	88262512 (3053, 3054)	Novel Protein sim. GBank gij2792496 (AF041107) - tulip 2 [Rattus norvegicus]			56182575, 264259, 60432049, 29331822, 60432289, 264908, 66712502, 60433438, 87168558, 265017, 264288, 21906768, 21906769, 263977, 55811576, 56182323, 18108381
1528	94130918 (3055, 3056)			UNCLASSIFIED	22278995, 22278997, 264259, 66712502, 264596, 265017, 265019, 264682, 264448, 264683, 264764, 264685, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 264693, 83373044, 18108385
1529	94120793 (3057, 3058)	Novel Protein sim. GBank gij4406663 gb AAD20053  - (AF131826) Unknown [Homo sapiens]		UNCLASSIFIED	264488, 263994, 56182575, 22278995, 35896286, 22278997, 264259, 29331822, 60432289, 29331827, 35896052, 264509, 264906, 264907, 264908, 264909, 52844045, 58182435, 264511, 265009, 264910, 60433356, 60433438, 265017, 265018, 264760, 264448, 264764, 264368, 264288, 264766, 18108357, 264768, 52844229, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 52844150, 33657109, 264629, 35895855, 60432113, 22278002, 264583, 264584, 264486, 264587
1530	95012765 (3059, 3060)	Novel Protein sim. GBank gij2828710 (AF043842) - matrin cyclophilin [Rattus norvegicus]			264488, 264489, 35896286, 29331825, 35896052, 264508, 264905, 264906, 264907, 264909, 264510, 264511, 264512, 264910, 264592, 264595, 18108351, 264764, 264683, 264684, 264766, 264768, 18108357, 264769, 35895917, 264628, 264629, 18108374, 35895855, 264630, 264631, 264634, 264555, 264636, 264637, 264404, 264583, 264586, 264486
1531	85419351 (3061, 3062)	Novel Protein sim. GBank gij1905874 (U90878) - carboxyl terminal LIM domain protein [Homo sapiens]	Contains protein domain (PF00595) - kinase PDZ domain (Also known as DHR or GLGF).		56182575, 35896286, 264097, 264259, 29331822, 29331825, 29331826, 29331827, 35896052, 264509, 58182435, 264510, 264511, 265007, 60433356, 55811386, 264681, 264369, 264288, 264766, 264687, 55811957, 35895917, 33657023, 35895763, 55810764, 35896423, 55811576, 283981, 60170394, 56182323, 83373044, 60432113, 264556



1532	85716224 (3063, 3064)	Novel Protein sim. GBank gi 3874716 emb CAA91265  - (Z86494) cDNA EST EMBL:D85271 comes from this gene; cDNA EST EMBL:D64845 comes from this gene; cDNA EST EMBL:D64449 comes from this gene; cDNA EST EMBL:D67438 comes from this gene; cDNA EST EMBL:D68087 comes from this gene; cDN...		UNCLASSIFIED	264689
1533	94239830 (3065, 3066)	Novel Protein sim. GBank gi 1490324 emb CA801543  - (Z78141) unknown [Mus musculus]	struct		29331824, 29146499, 264907, 264112, 265008, 265011, 265017, 265018, 264762, 18108351, 263967, 20281149, 18108374, 263981, 264566
1534	95343941 (3067, 3068)	Novel Protein sim. GBank gi 81286 pr S22697 - extensin - (Z78141) unknown [Mus musculus]	UNCLASSIFIED		264905, 264907, 264766, 264637
1535	90936732 (3069, 3070)	Volvox carter (fragment)			65274572, 22278997, 264259, 60432049, 29331822, 60432289, 29331827, 29146499, 265006, 265008, 60170831, 60433438, 33109954, 87168559, 265018, 18108357, 21906768, 29148828, 265021, 265022, 18108377, 56182323, 60432113, 22279000, 22279002
1536	87602856 (3071, 3072)	Novel Protein sim. GBank gi 106024 pr B32891 - finger protein 2, placental - human	transcript factor	Contains protein domain (PF00096) - Zinc finger, C2H2 type	264686, 18108357, 18108394, 21906767, 21906768, 29148829, 35698286, 265020, 265021, 52844150, 264693, 66714117, 29331825, 29331828, 264508, 264905, 20281149, 264909, 18108374, 35696423, 35695855, 265009, 264634, 264636, 264638, 18108385, 56526486, 265017, 265018, 264563, 264762, 18108351, 264448, 264369, 264766
1537	95354556 (3073, 3074)	Novel Protein sim. GBank gi 3876332 emb CA802096  - (Z79754) cDNA EST EMBL:T01054 comes from this gene; cDNA EST EMBL:D73600 comes from this gene; cDNA EST yk426f12.5 comes from this gene; cDNA EST yk342f10.5 comes from this gene; cDNA EST yk475c5.5 comes from this gene; cDNA ES...			65274572, 56182575, 60432049, 264259, 29331826, 265006, 265007, 60433356, 60433438, 264601, 18108351, 264448, 264369, 264288, 33657023, 65274820, 33657109, 60432113
1538	85724628 (3075, 3076)	Novel Protein sim. GBank gi 403440 (M81787) - [Gallus domesticus skeletal muscle mRNA, partial cds.], gene product [Gallus gallus]	Kinase	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	18108394, 18108397, 264909, 265008, 265009, 265010, 18108351, 264638, 18108382, 18108385, 18108388

1539	95337628 (3077, 3078)	Novel Protein sim. GBank gi 3218411 emb CAA19575.1  - (AL023859) SPBC19C7.07c, putative RNA splicing endonuclease ge mma subunit, len:284aa, similar eg. to YAR008W, YAH8_YEAST, P39707, YAR008W, RNA splicing endonuclease gamma subunit, (275aa), fasta scores, opt:269, E(0.64e-2...		nuclease	22278994, 22278998, 35888288, 56994075, 22278997, 22278998, 22278999, 60432049, 284258, 29331822, 29331824, 60424269, 29331825, 60432288, 29331826, 29331827, 29331828, 35888032, 33656970, 56182435, 265009, 33657402, 60433336, 60433438, 55812038, 21906754, 87168559, 265017, 265018, 265019, 18108351, 264288, 32644229, 18108359, 21906764, 21906767, 21906768, 35695917, 265020, 265021, 52844150, 33657023, 33857109, 27486281, 18108370, 18108376, 35888423, 55811576, 65274791, 264558, 56182323, 60170394, 83373044, 87168518, 60432113, 22278900, 22278902, 264568
1540	95352858 (3079, 3080)	Novel Protein sim. GBank gi 5052834 gb AAD38647.1 AF14567 - (AF145672) BcDNA.GH12174 [Drosophila melanogaster]		UNCLASSIFIED	264369, 264691, 263978
1541	95317848 (3081, 3082)	Novel Protein sim. GBank gi 5052349 gb AAD38515.1 AF13501 - (AF135016) protein phosphatase 2A 48 kDa regulatory subunit [Homo sapiens]		phosphatase	264488, 264489, 22278999, 264259, 29331822, 35888052, 264508, 264509, 264905, 264907, 264908, 264511, 264512, 264910, 264592, 264761, 264762, 264448, 264764, 264288, 264687, 21808769, 55811957, 35885917, 265020, 264691, 33657023, 264692, 33657109, 264628, 18108374, 264632, 264634, 264635, 264639, 18108385, 264563, 264564, 264565, 264566, 264486
1542	90937549 (3083, 3084)	Novel Protein sim. GBank gi 5305702 gb AAD41779.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]		cathepsin	18108392, 18108394, 65274572, 29331822, 264508, 265007, 265008, 265009, 265011, 264682, 18108354, 18108355, 52644150, 18108368, 264638, 18108381, 18109382
1543	84348768 (3085, 3086)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		nuclease	264106, 33109954, 265019, 264683, 35885917, 264690, 264692, 33657109
1544	87757295 (3087, 3088)	Novel Protein sim. GBank gi 3493162 (AF084259) - bromodomain-containing protein BP75 [Mus musculus]	Contains protein domain (PF00439) - Bromodomain	nuc_ recpt	35888288, 56994075, 22278999, 35888052, 60433356, 60433438, 265011, 264683, 33657109, 35888423, 264631, 87168518, 22278900
1545	85757973 (3089, 3090)	Novel Protein sim. GBank gi 1086591 (U41007) - similar to S. cerevisiae nuclear protein SNF2 (SP:P22082) in a region of gly-arg repeats [Caenorhabditis elegans]		UNCLASSIFIED	264112, 264692, 264693, 55811576
1546	78476589 (3091, 3092)			UNCLASSIFIED	264905, 264686
1547	86999594 (3093, 3094)	Novel Protein sim. GBank gi 2661132 (AF035683) - p21 [Mus musculus]		UNCLASSIFIED	264259, 29331822, 66714117, 265007, 55811386, 265010, 264600, 265017, 265019, 264288, 264768, 265020, 265022, 55811576, 18108390, 264563

1548	94233063 (3095, 3096)	Novel Protein sim. GBank gi 3043692 dbj BAA25510  - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	29331824, 60431528, 264639, 56182323
1549	95330048 (3097, 3098)	Novel Protein sim. GBank gi 5689519 dbj BAA83043.1  - (AB028014) KIAA1091 protein [Homo sapiens]		eph	60424179, 22278995, 35696286, 22278998, 22278999, 264092, 264094, 29331822, 56182181, 29331824, 35696052, 264905, 264906, 264908, 264909, 285006, 264511, 265008, 60431735, 60433356, 21906754, 55811386, 87168559, 265017, 265018, 265019, 55811150, 264682, 264288, 264369, 56181562, 264769, 21908765, 21906788, 21906769, 55811957, 265020, 264691, 33657109, 60431528, 35896423, 35695855, 56528486, 60432113, 22279002, 264563, 264566
1550	95201907 (3099, 3100)	Novel Protein sim. GBank gi 544463 sp P33530 GUSB_BOVIN - POSSIBLE GUSTATORY RECEPTOR TYPE B (PPR1 PROTEIN)	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	65274572, 60432289, 265008, 264910, 265011, 265017, 265019, 264768, 56182323
1551	88077111 (3101, 3102)	Novel Protein sim. GBank gi 4758566 ref NP_004798.1 pHS6S - heparan-sulfate 6-sulfotransferase		UNCLASSIFIED	22278999, 29331822, 264508, 264509, 264906, 264907, 264909, 265007, 264512, 264910, 21908754, 265018, 265019, 264881, 264764, 264766, 264688, 264769, 21906769, 264692, 35695763, 264635, 264555, 264556, 264557, 264638, 264558, 264563
1552	87617114 (3103, 3104)			UNCLASSIFIED	264259, 29331828, 66712502, 264764, 264288, 264686, 33657109, 264558
1553	94725512 (3105, 3106)	Novel Protein sim. GBank gi 4589570 dbj BAA76807.1  - (AB023180) KIAA0963 protein [Homo sapiens]	Contains protein domain (PF00304) - Gamma-thionins family	dehydrogenase	56182575, 35696286, 29146499, 264509, 264907, 264908, 264909, 56182435, 265006, 265008, 265009, 264910, 264757, 264758, 265017, 55811150, 18108351, 264764, 56181562, 35695917, 264693, 33657109, 18108374, 35696423, 65274791, 35695855, 264635, 264555, 56182323, 18108382, 83373044, 22279000
1554	94233069 (3107, 3108)	Novel Protein sim. GBank gi 3043692 dbj BAA25510  - (AB011156) KIAA0584 protein [Homo sapiens]	Contains protein domain (PF00446) - Gonadotropin-releasing hormones	transferase	35696286, 22278997, 264259, 29331822, 29331824, 29331825, 29331828, 265007, 265009, 60432229, 33657402, 55812038, 265011, 265019, 264681, 264369, 264686, 264767, 264768, 21906765, 21906769, 35695917, 264693, 18108370, 60431528, 55811576, 264831, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002

1555	87332870 (3109, 3110)	Novel Protein sim. GBank gij2257495[dbj BAA21392] - (AB004534) p1015 [Schizosaccharomyces pombe]	Contains protein domain (PF000400) - WD domain, G-beta repeat	UNCLASSIFIED	264258, 28331828, 35698052, 264508, 264905, 284908, 284907, 284908, 52644045, 284909, 284910, 60432229, 60433356, 55812038, 264758, 284759, 33657084, 265011, 87168559, 284601, 265018, 265019, 264763, 284764, 284288, 264766, 264768, 21906765, 35695917, 265022, 264691, 33657023, 35698423, 35695855, 264635, 284555, 264636, 284638, 284639, 18108365, 56528486
1556	91229268 (3111, 3112)			UNCLASSIFIED	83373044, 284758, 285022, 264600, 35698052, 284630, 35698423, 265018, 264832, 264682, 29331822, 265020, 265011, 60432289, 284509, 284906, 284907, 284908, 264909, 284910, 264758, 55811386, 264761, 264762, 264766, 284769, 284890, 263978, 264634, 264635, 284639, 264584, 264486, 22278984, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 284448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811578, 83373044, 87168518, 22278900, 22279002, 284259, 29331822, 60432289, 35698052, 264107, 264110, 21906754, 33109954, 87168559, 264760, 284783, 21906764, 21906765, 21906769, 265021, 264690, 35695855
1557	87640609 (3113, 3114)	Novel Protein sim. GBank gij3329611 (AF078783) - contains similarity to C3HC4-type zinc fingers (Pfam; zfc3HC4.hmm, score: 34.08); most similar to drosophila goliath protein (SW: Q06003) [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278984, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 284448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811578, 83373044, 87168518, 22278900, 22279002, 284259, 29331822, 60432289, 35698052, 264107, 264110, 21906754, 33109954, 87168559, 264760, 284783, 21906764, 21906765, 21906769, 265021, 264690, 35695855
1558	94840376 (3115, 3116)	Novel Protein sim. GBank gij5360105[gijAAD42871.1]AF155105 putative zinc finger protein NY-REN-34 antigen [Homo sapiens]			22278984, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 284448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811578, 83373044, 87168518, 22278900, 22279002, 284259, 29331822, 60432289, 35698052, 264107, 264110, 21906754, 33109954, 87168559, 264760, 284783, 21906764, 21906765, 21906769, 265021, 264690, 35695855
1559	86224865 (3117, 3118)	Novel Protein sim. GBank gij112908[sp P02750 A2GL_HUMAN - LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278984, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 284448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811578, 83373044, 87168518, 22278900, 22279002, 284259, 29331822, 60432289, 35698052, 264107, 264110, 21906754, 33109954, 87168559, 264760, 284783, 21906764, 21906765, 21906769, 265021, 264690, 35695855
1560	84580675 (3119, 3120)	Novel Protein sim. GBank gij3880146[emb CAA92704] - (Z68319) Similarity to Human hnRNP F protein (PIR Acc. No. S43484); cDNA EST EMBL:D34218 comes from this gene; cDNA EST EMBL:D37248 comes from this gene; cDNA EST EMBL:D71817 comes from this gene; cDNA EST EMBL:D74531 comes from...		UNCLASSIFIED	22278984, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 284448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811578, 83373044, 87168518, 22278900, 22279002, 284259, 29331822, 60432289, 35698052, 264107, 264110, 21906754, 33109954, 87168559, 264760, 284783, 21906764, 21906765, 21906769, 265021, 264690, 35695855
1561	86809158 (3121, 3122)			UNCLASSIFIED	22278984, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 284448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811578, 83373044, 87168518, 22278900, 22279002, 284259, 29331822, 60432289, 35698052, 264107, 264110, 21906754, 33109954, 87168559, 264760, 284783, 21906764, 21906765, 21906769, 265021, 264690, 35695855
1562	83359682 (3123, 3124)			UNCLASSIFIED	22278984, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 284448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811578, 83373044, 87168518, 22278900, 22279002, 284259, 29331822, 60432289, 35698052, 264107, 264110, 21906754, 33109954, 87168559, 264760, 284783, 21906764, 21906765, 21906769, 265021, 264690, 35695855
1563	85508694 (3125, 3126)			UNCLASSIFIED	22278984, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 284448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811578, 83373044, 87168518, 22278900, 22279002, 284259, 29331822, 60432289, 35698052, 264107, 264110, 21906754, 33109954, 87168559, 264760, 284783, 21906764, 21906765, 21906769, 265021, 264690, 35695855
1564	87766371 (3127, 3128)	Novel Protein sim. GBank gij1168287[sp P45953 ACDV_RAT - ACYL-COA DEHYDROGENASE, VERY LONG-CHAIN SPECIFIC PRECURSOR (VLCAD)]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	dehydrogenase	22278984, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 284448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811578, 83373044, 87168518, 22278900, 22279002, 284259, 29331822, 60432289, 35698052, 264107, 264110, 21906754, 33109954, 87168559, 264760, 284783, 21906764, 21906765, 21906769, 265021, 264690, 35695855

1565	87783381 (3129, 3130)	Novel Protein sim. GBank gij129728[sp]P05307[POI_BOVIN] - PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55)		isomerase	264488, 264689, 18108398, 55811957, 264434, 264259, 264508, 264905, 264508, 264908, 18108372, 264510, 264511, 264512, 265008, 264630, 265009, 264910, 264635, 264636, 264591, 264555, 264592, 264637, 264593, 264594, 264595, 264596, 265011, 264603, 22279002, 18108351, 264762, 264565, 264567
1566	87424749 (3131, 3132)	Novel Protein sim. GBank gij3880445[emb]CAA20329[ - (AL031266) VM108R.1 [Caenorhabditis elegans]		Inf	22278996, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 66712502, 264908, 265008, 18108351, 52644229, 21906765, 21906767, 21906768, 21906769, 33657109, 264555, 264639, 264482
1567	84999006 (3133, 3134)	Novel Protein sim. GBank gij4929699[gb]AAD34110.1[AF15187] CGI-115 protein [Homo sapiens]		UNCLASSIFIED	56182575, 21906769, 264692
1568	87648761 (3135, 3136)	Novel Protein sim. GBank gij4827063[ref]NP_005072.1[pZNF1 - zinc finger protein 142 (clone pHZ-48)]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	transcriptfactor	29331827, 29331830, 264511, 265009, 264758, 21906767, 21906768, 264691, 264893, 22279000, 22279002
1569	90936668 (3137, 3138)	Novel Protein sim. GBank gij5689451[db][BAA83009.1] - (AB028880) KIAA1057 protein [Homo sapiens]	Contains protein domain (PF000443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	65274572, 29331822, 29331824, 29331828, 264905, 56182435, 265007, 265019, 264764, 21906765, 21906768, 55811957, 60170615, 52644150, 264692, 33657023, 33657109, 18108377, 264563, 264567
1570	86943981 (3139, 3140)	Novel Protein sim. GBank gij1255430 (U53155) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264595, 264682, 265021
1571	91210340 (3141, 3142)	Novel Protein sim. GBank gij4507731[ref]NP_001061.1[pTUBG - tubulin, gamma polypeptide]	Contains protein domain (PF000091) - Tubulin/FtsZ family	tubulin	22278996, 35696286, 22278997, 264091, 264259, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 56182435, 264510, 265007, 264758, 265011, 18108351, 264448, 264288, 264369, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 264693, 18108370, 18108377, 35696423, 35695855, 264634, 264555, 264558, 18108384
1572	81201664 (3143, 3144)			UNCLASSIFIED	35696052, 264905, 264906, 264908, 264910, 264758, 264766, 35695917, 264637
1573	80207066 (3145, 3146)			UNCLASSIFIED	263972

1574	94216142 (3147, 3148)	Novel Protein sim. GBank gi 4756334 ref NP_004256.1 pFADS - delta-6 fatty acid desaturase	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	Cytochrome	18108384, 264887, 18108397, 18108398, 22278996, 22278997, 22278998, 264259, 29331825, 29331827, 29146488, 29146489, 264107, 264907, 264908, 2644045, 264511, 265008, 264810, 265009, 264591, 21908754, 265011, 265018, 18108351, 264682, 264763, 264764, 18108354, 264389, 264288, 264685, 264766, 264688, 264768, 264688, 21908765, 21908766, 21908767, 21908768, 21908769, 29148629, 264690, 264691, 264693, 20281069, 18108370, 18108374, 18108379, 35695855, 264634, 18108384, 18108385, 22278002, 264563, 264566
1575	95340019 (3149, 3150)	Novel Protein sim. GBank gi 3881810 emb CA494856  - (Z70783) similar to EF-hand calcium binding protein; cDNA EST EMBL:CO8700 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00036) EF hand	phosphatase	26594075, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 264909, 265008, 265008, 265009, 265010, 87168559, 55811150, 264448, 18108354, 264389, 264288, 18108357, 55811857, 265020, 265021, 60170615, 264691, 33657023, 33657109, 60431528, 65274791, 35695855, 18108385, 60432113, 22279002, 264482 264569, 264092, 264094, 264095, 264259, 264508, 264905, 264509, 264907, 264909, 264510, 264511, 265006, 264910, 21908754, 265010, 265011, 87168559, 264761, 264762, 264288, 264766, 264769, 264691, 264693, 35695855, 264632, 264634, 264635, 264636, 83373044, 264486
1576	95314019 (3151, 3152)	Novel Protein sim. GBank gi 2773195 (AF039711) - contains similarity to Physcomitrella patens glyceraldehyde 3-phosphate dehydrogenase (GB:X72381) [Caenorhabditis elegans]		UNCLASSIFIED	18108385, 60432113, 22279002, 264482 264569, 264092, 264094, 264095, 264259, 264508, 264905, 264509, 264907, 264909, 264510, 264511, 265006, 264910, 21908754, 265010, 265011, 87168559, 264761, 264762, 264288, 264766, 264769, 264691, 264693, 35695855, 264632, 264634, 264635, 264636, 83373044, 264486
1577	87613800 (3153, 3154)	Novel Protein sim. GBank gi 2489130 sp P70315 WASP_MOUSE - WISKOTT- ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)		UNCLASSIFIED	264511, 265011, 264681, 264369, 264686, 264689, 264629, 264555, 264558, 264559
1578	87123138 (3155, 3156)				264259, 29331828, 265017, 264689, 264693, 60432113
1579	88085141 (3157, 3158)	Novel Protein sim. GBank gi 2978255 db BAA25190  - (AB007407) myeloid zinc finger protein-2 [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	35696288, 264908, 264909, 60433438, 55811386, 264369, 264685, 33657023, 264555, 264556, 264557, 87168518
1580	87255702 (3159, 3160)	Novel Protein sim. GBank gi 4324682 gb AAD16986  - (AF109674) late gestation lung protein 1 [Rattus norvegicus]	Contains protein domain (PF00188) - SCP-like extracellular protein	glycoprotein	22278998, 35696052, 29331830, 52644045, 55812038, 87168474, 265018, 264448, 265022, 264638, 56526486, 22279000
1581	95087431 (3161, 3162)	Novel Protein sim. GBank gi 2088038 (AF003386) - F59E12.4 gene product [Caenorhabditis elegans]			22278995, 29331822, 29331824, 29331826, 56182435, 264595, 55812038, 87168559, 265017, 264288, 21908764, 55811957, 35695917, 264692, 55811576, 264637, 56182323, 264559, 83373044, 60432113

1582	95356052 (3163, 3164)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		phosphatase	264259, 60432289, 29331827, 264509, 264905, 264906, 264907, 264909, 264910, 264762, 264288, 264768, 264769, 264632, 264555, 264639, 56526486, 22279000
1583	87622715 (3165, 3166)	Novel Protein sim. GBank gij5578958[emb]CAB51351.1] - (AL050306) dJ475B7.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	60170831, 33657402, 264682, 21906766, 35695855, 264563
1584	95337722 (3167, 3168)	Novel Protein sim. GBank gij5531815[gb]AAD44482.1] - (AF078850) steroid dehydrogenase homolog [Homo sapiens]	Contains protein domain (PF00108) - short chain dehydrogenase	dehydrogenase	60424179, 52646842, 65274572, 56182575, 22278995, 35696286, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 60424269, 60432289, 29331827, 29331828, 35696052, 29146498, 66712502, 29331830, 52644045, 58182435, 264510, 264512, 265008, 60433356, 33657402, 60433438, 55812038, 21906754, 55811386, 52644296, 87168474, 87168559, 265018, 265019, 264448, 264359, 264288, 18108358, 21906765, 21906767, 21906788, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108374, 55810784, 55811578, 35696423, 65274791, 35695855, 56182323, 83373044, 18108387, 87168518, 60432113, 22279002
1585	87626117 (3169, 3170)	Novel Protein sim. GBank gij4240132[db]BAA74846.1] - (AB020630) KIAA0823 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	phosphatase	35696286, 22278998, 264259, 29331822, 29331824, 29331825, 264905, 265006, 265007, 265008, 60433356, 33109954, 87168474, 265011, 265017, 264604, 264369, 264288, 264685, 264769, 18108359, 21906765, 18108364, 18108370, 264629, 263972, 18108383, 18108388, 264482, 264564
1586	88067081 (3171, 3172)	Novel Protein sim. GBank gij3786494 (AF098993) - No definition line found [Caenorhabditis elegans]			265017, 265018, 264689, 33657023, 263978, 264638, 264563
1587	87617126 (3173, 3174)	Novel Protein sim. GBank gij3253159 (AF005555) - [translation initiation factor eIF2C [Oryctolagus cuniculus]		UNCLASSIFIED	264907, 264908, 264511, 284910, 264591, 264594, 264629, 264631, 264563, 264483, 264567
1588	87802536 (3175, 3176)	Novel Protein sim. GBank gij1077573[pir]S52680 - probable ribosomal protein L34, mitochondrial - yeast [Saccharomyces cerevisiae]	Contains protein domain (PF00468) - Ribosomal protein L34	UNCLASSIFIED	264259, 29331828, 264905, 265006, 264758, 21906754, 264761, 264762, 21906765, 21906769, 60170615, 52644150, 33657109, 35695855, 56182323, 18108385
1589	90980653 (3177, 3178)	Novel Protein sim. GBank gij2137756[pir]I48746 - semaphorin C - mouse (fragment)		UNCLASSIFIED	65274572, 264490, 29331822, 66714117, 29331827, 29331828, 56182435, 265008, 60170831, 264595, 264758, 264596, 265011, 264686, 21906766, 21906768, 55811957, 27486285, 264639, 18108385, 56526486, 60432113

1590	85319825 (3178, 3180)			UNCLASSIFIED	284489, 22278996, 284259, 29331824, 29331825, 29331826, 29331827, 285006, 60433356, 21906754, 265017, 265018, 265019, 284448, 284785, 284288, 52844229, 21906765, 21906767, 21906768, 21906769, 265021, 264692, 27486285, 35695763, 56526486, 60432113, 22279000, 22279002, 264564
1591	86877160 (3181, 3182)	Novel Protein sim. GBank		MHC	264259, 284905, 29331830, 264595, 265017, 264448, 284288, 284890, 284629, 87168518
1592	87882533 (3183, 3184)	gi 4557749 ref NP_000237.1 pMHC2 - MHC class II transactivator			
1593	84981661 (3185, 3186)			UNCLASSIFIED	65274572, 60432049, 264509, 60433356, 21906754, 21906767, 21906768, 18108370, 35686423, 22279000, 284565, 264567
1594	87773752 (3187, 3188)	Novel Protein sim. GBank gi 3877072 emb CAA87060  (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]		UNCLASSIFIED	264488, 29331827, 284905, 284906, 264807, 264908, 264909, 264910, 284592, 264593, 264757, 284602, 284604, 284760, 284681, 264288, 264766, 264768, 29148629, 35695917, 264692, 264628, 284629, 284630, 264632, 264634, 264635, 264636, 284639, 264563, 264564, 264566
1595	78918425 (3189, 3190)	Novel Protein sim. GBank gi 3152703 (AF085389) - tetraspan NET-4 [Homo sapiens]	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	UNCLASSIFIED	29331826, 284908, 55811957
1596	78933928 (3191, 3192)			UNCLASSIFIED	28146498, 264758, 263967
1597	86971857 (3193, 3194)	Novel Protein sim. GBank gi 5257114 gb AAD41244.1 AF094480 - (AF094480) cholesterol 24-hydroxylase [Homo sapiens]	Contains protein domain (PF00067) - Cytochrome P450		284092, 28331824, 284508, 264682, 264369, 284686, 284630, 264563
1598	87862939 (3195, 3196)				264259, 264634
1599	87849829 (3197, 3198)	Novel Protein sim. GBank gi 4506797 ref NP_000324.1 pSCA7 - spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	Contains protein domain (PF01581) - FMRFamide related peptide family	UNCLASSIFIED	32645080, 29331824, 29331826, 264511, 265009, 265011, 264605, 264448, 284764, 265020, 284692, 264693, 18108370, 284635, 18108385
1600	80056002 (3199, 3200)				29331826, 264603, 264691, 264563
1601	15023248 (3201, 3202)				284635
1602	86926987 (3203, 3204)	Novel Protein sim. GBank gi 5305704 gb AAD41780.1 AF128535 - (AF128535) cytoplasmic phosphoprotein PACSIN2 [Mus musculus]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	29146499, 264112, 284762, 18108351, 29148627, 263974
1603	80502072 (3205, 3206)	Novel Protein sim. GBank gi 283920 pir S27939 - tensin - chicken		collagen	264490, 29331824, 264807, 264909, 264511, 265008, 284592, 265010, 265011, 284762, 264764, 284369, 264288, 264687, 264769, 264693, 284628, 264634, 264636, 264555, 284556, 284638, 264557, 264558, 284559, 18108385
1604	80221813 (3207, 3208)	Novel Protein sim. GBank gi 4768831 gb AAD25633.1 AF116827 - (AF116827) unknown [Homo sapiens]		ATPase-associated	263977



1605	91221129 (3208, 3210)			struct	264905, 264509, 264906, 264907, 264908, 264909, 264604, 264766, 264768, 264692, 264693, 33637109, 264629, 35695855, 264635, 264636, 264637
1606	94312703 (3211, 3212)	Novel Protein sim. GBank gj14505313[ref]NP_003794.1pMYOM - UNKNOWN	Contains protein domain (PF00047) - Immunoglobulin domain	struct	22278996, 22278999, 264259, 33657402, 265017, 18108351, 264448, 21906767, 21906769, 52644150, 264691, 87168518
1607	10871805 (3213, 3214)	Novel Protein sim. GBank gj1574473[ref]NP_005888.1pPPI - Intracisternal A particle-promoted polypeptide		transcriptfactor	264689
1608	80428900 (3215, 3216)	Novel Protein sim. GBank gj12224629[db][BAA20802] - (AB002342) KIAA0344 [Homo sapiens]		UNCLASSIFIED	264094, 264906, 264907, 264908, 264910, 264591, 264603, 264768, 264693, 264634, 264635, 264637, 264639
1609	84311572 (3217, 3218)	Novel Protein sim. GBank gj1488407[emb][CAB43213.1] - (AL049934) hypothetical protein [Homo sapiens]			52644507, 52645156, 52646365, 52646842, 56182575, 22278994, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29147620, 29331826, 35696052, 33656970, 264508, 264509, 264807, 52644045, 56182435, 264510, 264511, 264512, 33657402, 21906754, 52646317, 33109954, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264769, 52644229, 21906765, 21906766, 21906767, 21906768, 21908769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 52645129, 27486261, 27486262, 35695763, 264628, 18108370, 18108376, 35696423, 264638, 52644332, 18108387, 87168518, 22279000, 264563, 264486
1610	85468200 (3219, 3220)	Novel Protein sim. GBank gj1283920[pir][S27939 - lensin - chicken]		UNCLASSIFIED	264593, 264757, 55812038, 265018, 265020, 264691, 264692, 264693, 264631, 264634, 264635, 264555, 22279000, 264564
1611	94122843 (3221, 3222)	Novel Protein sim. GBank gj107284[pir][A35415 - peroxidase (EC 1.11.1.7), thyroid (Grave's disease) - human (fragment)]	Contains protein domain (PF00008) - EGF-like domain	peroxidase	35696286, 21906765, 264691, 35696423
1612	85746031 (3223, 3224)	Novel Protein sim. GBank gj13874846[emb][CAA94337] - (Z70307) Similarity to B.subtilis tetracycline resistance protein (SW:TCR2_BACSU); cDNA EST EMBL:C09951 comes from this gene; cDNA EST EMBL:C08265 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264509, 18108370, 18108387, 264486
1613	82247354 (3225, 3226)			UNCLASSIFIED	264759

1614	91228634 (3227, 3228)	Novel Protein sim. GBank gll4680673jgblAAD27726.1IAF13295 - (AF132951) CGI-17 protein [Homo sapiens]	Contains protein domain (PF01605) - eRF1-like proteins	UNCLASSIFIED	22278995, 22278998, 22278997, 22278998, 22278999, 264259, 29331822, 264908, 264512, 265009, 265011, 265017, 265018, 265019, 18108351, 264683, 264286, 264766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 35696423, 35695855, 60170394, 58182323, 83373044, 284566
1615	86121909 (3229, 3230)	Novel Protein sim. GBank gll5689485dbjBAA33026.1] - (AB028987) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	22278998, 35696286, 22278997, 29331822, 35696052, 29331828, 284508, 264908, 284909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264691, 264828, 264632, 264635, 264555, 284556, 58182323, 284558, 22279002
1616	94311819 (3231, 3232)	Novel Protein sim. GBank gll3878260lenb[CAB01696] - (Z78418) cDNA EST EMBL:D71020 comes from this gene; cDNA EST EMBL:D73593 comes from this gene; cDNA EST EMBL:C07649 comes from this gene; cDNA EST EMBL:C09081 comes from this gene; cDNA EST yk399i2.3 comes from this gene; cDNA ...	UNCLASSIFIED	UNCLASSIFIED	284488, 52644507, 52645158, 52646365, 52646842, 22278994, 22278995, 35696286, 22278996, 22278997, 22278999, 52646080, 29331822, 29331824, 29331825, 29331827, 29331828, 35696052, 33856970, 264905, 284909, 264594, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264681, 264448, 264684, 52644229, 21906764, 264689, 21906765, 21906766, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 27486262, 33657349, 27486265, 35695763, 52645129, 33657109, 33657182, 27486281, 18108376, 35696423, 35695855, 264557, 52644332, 284558, 18108385, 87168518
1617	88090742 (3233, 3234)	Novel Protein sim. GBank gll468053jlpjP34679YO41_CAEEL - HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III	Contains protein domain (PF01529) - DHHC zinc finger domain	peptidase	35696052, 264905, 264509, 264907, 264908, 264510, 264511, 264764, 264766, 264768, 264689, 264693, 18108374, 264635, 264636, 284638
1618	86272860 (3235, 3236)	Novel Protein sim. GBank gll4240231dbjBAA74894.1] - (AB020678) KIAA0871 protein [Homo sapiens]		struct	35696286, 22278999, 264092, 29331824, 29331825, 35696052, 33657084, 21906765, 27486284
1619	95354580 (3237, 3238)	Novel Protein sim. GBank gll5031763jrefNP_005515.1pHRY] - hairy (Drosophila)- homolog	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	52646842, 65274572, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 58182435, 265007, 265008, 264910, 60170831, 60432229, 60433356, 60433438, 265019, 284448, 264288, 284686, 21906768, 265021, 50170615, 33657023, 65274820, 33657109, 18108374, 18108376, 35696423, 35695855, 58182323, 56526486
1620	87344655 (3239, 3240)	Novel Protein sim. GBank gll1351047jlpjP45843JSCRT_DROME - SCARLET PROTEIN		UNCLASSIFIED	284684

1621	87076708 (3241, 3242)				UNCLASSIFIED	264910
1622	94741739 (3243, 3244)	Novel Protein sim. GBank gij3822553 (AF098788) - nuclear calmodulin-binding protein [Gallus gallus]	Contains protein domain (PF00622) - SPRY domain		UNCLASSIFIED	18108392, 65274572, 18108398, 22278996, 22278997, 22278999, 29146498, 29146499, 264905, 264908, 264909, 264828, 52644045, 264592, 60433356, 21906754, 264602, 265017, 264389, 21906788, 55811957, 265021, 60170615, 264635, 264557, 60170394, 83373044, 18108385, 22279000, 22279002, 264566
1623	87779106 (3245, 3246)	Novel Protein sim. GBank gij731086ispj40389UV22_SCHPO - UV-INDUCED PROTEIN UVi22		ribosomalprot		18108398, 264259, 264909, 56182435, 87168474, 264448, 21906768, 35695917, 264691, 87168518, 264583
1624	87338178 (3247, 3248)	Novel Protein sim. GBank gij3875666[embjCAB05478] - (283104) cDNA EST EMBL: T00015 comes from this gene; cDNA EST EMBL: D33665 comes from this gene; cDNA EST EMBL: D36540 comes from this gene; cDNA EST yk240f8.3 comes from this gene; cDNA EST yk387c8.3 comes from this gene; cDNA ES...			UNCLASSIFIED	68714117, 29331825, 264909, 265008, 264758
1625	95354748 (3249, 3250)	Novel Protein sim. GBank gij4598622[djBAA76833.1] - (AB023206) KIAA0989 protein [Homo sapiens]		kinase		264489, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331824, 29331825, 29331827, 29331828, 264102, 264106, 264508, 33657084, 265017, 265018, 18108351, 264683, 264369, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 264691, 65274620, 18108368, 263972, 18108376, 35696423, 264631, 264634, 22279000, 22279002
1626	94734388 (3251, 3252)	Novel Protein sim. GBank gij5679070[gbjAAD46844.1]AF160904 - (AF160904) BcDNA.HL05936 [Drosophila melanogaster]				52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 60432289, 29331827, 29331828, 35698052, 264906, 66712502, 264909, 265008, 265009, 60432229, 60433356, 60433438, 21906754, 52646317, 52644296, 265011, 87168559, 264804, 265018, 264448, 264369, 264288, 264786, 52644229, 264689, 21906765, 21906768, 35695917, 265021, 265022, 52644150, 33657023, 65274620, 27486261, 27486262, 27486265, 35695763, 263972, 52644332, 60170394, 87168518, 60432113, 264567
1627	83388773 (3253, 3254)				UNCLASSIFIED	264288
1628	85708459 (3255, 3256)	Novel Protein sim. GBank gij3668087 (AC004667) - hypothetical protein [Arabidopsis thaliana]		eph		264288, 264686, 264767, 22279002

1629	84993841 (3257, 3258)	Novel Protein sim. GBank gij4240175[dbj][BAA74866.1] - (AB020650) KIAA0843 protein [Homo sapiens]		struct	264555
1630	87779027 (3259, 3260)			UNCLASSIFIED	29331822, 29331827, 285010, 284693, 264634, 22278002
1631	87758454 (3261, 3262)	Novel Protein sim. GBank gij1915892[emb][CAA69995] - (Y08740) tom-1A protein [Gallus gallus]		UNCLASSIFIED	55811957, 264259, 33657023, 284693, 29331822, 29331824, 29331827, 29331828, 264906, 264908, 55811576, 264910, 264634, 264636, 264637, 58182323, 284559, 284756, 18108385, 264563, 264764, 264766
1632	87871692 (3263, 3264)	Novel Protein sim. GBank gij2558501[dbj][BAA22886] - (D63850) hepatoma-derived growth factor [Mus musculus]		UNCLASSIFIED	264687, 264769, 264691, 264692, 29146489, 284508, 264905, 264907, 284511, 284512, 284482, 264681, 264763, 264682, 264683
1633	87773683 (3265, 3266)				284488, 264259, 264907, 264908, 264909, 264628, 264629, 264631
1634	85992817 (3267, 3268)	Novel Protein sim. GBank gij4887229[gb][AAD32244.1][AF150755] - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - Spectrin repeat	struct	265007, 264637, 22278002
1635	94232600 (3269, 3270)			UNCLASSIFIED	65274572, 22278998, 35696052, 52844045, 264511, 265008, 285009, 285010, 265011, 265018, 265019, 264448, 284369, 21906765, 21906768, 265021, 264680, 264482
1636	80413227 (3271, 3272)			UNCLASSIFIED	22278995, 264594, 264783, 265020
1637	80070435 (3273, 3274)	Novel Protein sim. GBank gij4557511[ref][NP_001339.1]pDAPK - death-associated protein kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264558
1638	87101854 (3275, 3276)	Novel Protein sim. GBank gij3420051 (AC004680) - unknown protein [Arabidopsis thaliana]			21906765, 21906767, 22278998, 35696286, 22278999, 264259, 264692, 264693, 29331824, 33657109, 264508, 264906, 18108370, 264629, 265007, 33857402, 21906754, 264602, 284604, 264764, 264683, 264566, 264288
1639	94322194 (3277, 3278)	Novel Protein sim. GBank gij5420389[emb][CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	284488, 18108394, 65274572, 56182575, 35696286, 29331824, 29331826, 29331827, 35696052, 264908, 56182435, 284112, 265006, 265008, 264757, 284758, 55811386, 264603, 264760, 18108351, 264764, 264288, 264766, 264768, 21908787, 55811957, 264691, 33657023, 65274620, 18108370, 55810764, 55811576, 284558, 264639, 83373044, 18108385, 87168518

1640	94143185 (3279, 3280)	Novel Protein sim. GBank gjl2842469[emb]CAA16847.1 - (AL021747) hypothetical protein [Schizosaccharomyces pombe]	UNCLASSIFIED	56182575, 56994075, 35696286, 60432049, 60432289, 29331827, 35696052, 52644045, 56182435, 264510, 265006, 265007, 265009, 264910, 265009, 33657402, 55812038, 265010, 265011, 265017, 265018, 264288, 52644229, 21906765, 21906766, 21906768, 35895917, 265021, 60170615, 52644150, 33657023, 33657109, 33657349, 18108374, 35896423, 65274791, 35695855, 264632, 264555, 56182323, 22279000
1641	87625160 (3281, 3282)		UNCLASSIFIED	29146489, 265006, 265007, 265008, 265009, 55812038, 265010, 265011, 264555, 264556, 264558, 18108383
1642	94312557 (3283, 3284)	Novel Protein sim. GBank gjl1575333 (U60416) - myr 6 myosin heavy chain [Rattus norvegicus]	struct	22278999, 29147620, 29331826, 29331828, 33656970, 55812038, 265010, 265018, 265019, 18108351, 264689, 265020, 265022, 264690, 33657023, 65274620, 35695763, 52644332, 18108381, 60170394, 56182323, 18108388, 87168518, 22279002, 264564
1643	94131766 (3285, 3286)			29331825, 29331827, 29331828, 21906754, 265019, 264288, 264693, 33657349, 18108370, 18108376, 264555, 83373044, 22279002, 264482
1644	88095125 (3287, 3288)		UNCLASSIFIED	264905, 264907, 264908, 264910, 265009, 264757, 264758, 264761, 264762, 264763, 264766, 264768, 264769, 264628, 264629, 264630, 264631, 264632, 264563, 264564, 264565, 264566, 264567
1645	95013858 (3289, 3290)		UNCLASSIFIED	264885, 264693
1646	95362691 (3281, 3292)	Novel Protein sim. GBank gjl1076802[pr]S49915 - extensin like protein - maize	UNCLASSIFIED	22278994, 56994075, 35696286, 264259, 29331824, 29331825, 29331826, 60432289, 264508, 60433356, 60433438, 87168559, 265018, 264687, 35695917, 264692, 33657023, 33657182, 27486261, 27486265, 33657349, 60432113, 264563, 264564
1647	94278428 (3293, 3294)	Novel Protein sim. GBank gjl5002573[emb]CAB44338.1 - (Y17466) alpha-N-acetylgalactosamine alpha-2,6- sialyltransferase [Fugu rubripes]	UNCLASSIFIED	29331822, 264906, 264908, 264369, 21906768, 60170815, 264639, 22279000
1648	87642098 (3295, 3296)		UNCLASSIFIED	265009, 264686, 55811957, 35695917, 55810764, 264556, 56182323, 264558, 18108385

1648	95347628 (3297, 3298)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]		cadherin	264488, 22278995, 35886286, 22278998, 22278997, 22278999, 60432048, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 66712502, 264908, 52644045, 264909, 56182435, 264511, 265007, 265008, 265009, 264591, 264593, 60433438, 264596, 55812038, 21906754, 265011, 264601, 284602, 265017, 265018, 265019, 264682, 264448, 264764, 264683, 264288, 264768, 264685, 264687, 264768, 264688, 264769, 52644228, 264689, 21906765, 21908768, 21906767, 21906768, 55811957, 3585917, 265021, 265022, 52644150, 264692, 33657023, 33657109, 20281149, 18106370, 264628, 18108374, 18108378, 35696423, 35695855, 264632, 264634, 264635, 264636, 18108380, 264639, 264558, 18108382, 18108384, 18108385, 18108387, 264080, 264404, 60432113, 22278000, 22278002, 264482, 264555, 264566, 264487, 265011, 264602, 21906767, 18108374, 18108377, 18108385
1650	87418539 (3298, 3300)	Novel Protein sim. GBank gi 3647335 emb CAA21059  - (AL031644) possible zinc-finger protein [Schizosaccharomyces pombe]			
1651	91639773 (3301, 3302)	Novel Protein sim. GBank gi 4884278 emb CAB43247.1  - (AL050037) hypothetical protein [Homo sapiens]		synthase	264488, 52645156, 18108397, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264508, 264908, 29331830, 264910, 60432229, 21906754, 265010, 265011, 265017, 265019, 264448, 18108354, 264288, 264688, 21906765, 21908768, 21908768, 21906769, 265022, 264692, 264693, 264629, 35695855, 264556, 264637, 264557, 264559, 83373044, 56526486, 22278000, 22278002, 264564
1652	86598622 (3303, 3304)	Novel Protein sim. GBank gi 1657837 (U73200) - p116Rip [Mus musculus]	Contains protein domain (PF00169) - struct PH domain		22278997, 29146498, 56182435, 21906754, 264389, 21906765, 21908768, 21908769, 265020, 52644150, 33657108, 22278000, 22278002
1653	94255993 (3305, 3306)	Novel Protein sim. GBank gi 3776054 emb CAA06273  - (AJ004999) Tapasin [Gallus gallus]	Contains protein domain (PF00047) - glycoprotein Immunoglobulin domain		18108398, 22278995, 22278998, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331830, 264909, 265006, 265009, 60432229, 60433356, 60433438, 21906754, 265017, 265019, 264448, 264683, 264288, 265021, 265022, 264692, 18108384, 85274781, 18108384, 60432113, 264567
1654	78756471 (3307, 3308)			UNCLASSIFIED	33657109, 264585

1655	86689346 (3309, 3310)	Novel Protein sim. GBank gij3355717[emb]CAA73496] - (Y13053) seryl-HRNA synthetase [Zea mays]		synthase	52644507, 35696286, 22278998, 22278999, 29331824, 29331825, 29331828, 33656970, 264908, 52644045, 264511, 264910, 52646317, 264288, 52644229, 33657023, 33657109, 52644332, 264557, 56182323, 56526486, 60432113
1656	79962297 (3311, 3312)	Novel Protein sim. GBank gij1890141[dbj]BAA18947] - (D83208) P24 protein [Mus musculus]		UNCLASSIFIED	29331822, 29331824, 29331825, 264563
1657	87771994 (3313, 3314)	Novel Protein sim. GBank gij4557645[ref]NP_001524.1[pHNP - heterogeneous nuclear ribonucleoprotein L	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331827, 265009, 21906766, 21906767, 265020, 265022, 33657109, 264638, 56526486, 264482
1658	87773778 (3315, 3316)	Novel Protein sim. GBank gij3877072[emb]CAA87060] - (Z48937) similarity with ribosomal protein L21 [Caenorhabditis elegans]	Contains protein domain (PF00829) - Ribosomal prokaryotic L21 protein	UNCLASSIFIED	52646365, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 264905, 264908, 52644045, 265006, 60433356, 264757, 60433438, 21906754, 265011, 18108351, 264448, 264369, 264288, 264766, 264768, 21906765, 21906767, 21906768, 21906769, 29146629, 265021, 285022, 18108362, 263969, 263971, 18108374, 35696423, 18108383, 22279000, 264482
1659	88230101 (3317, 3318)	Novel Protein sim. GBank gij539218[pir]S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	52646317, 21906766, 21906767, 21906768, 87168518, 22278996, 265020, 22278999, 87168559, 264603, 265017, 264631, 265018, 265019, 22279002, 264482, 264635, 264565
1660	94315313 (3319, 3320)	Novel Protein sim. GBank gij2497012[sp]Q10010[YSV4_CAEEL - HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III		UNCLASSIFIED	264488, 35696286, 264259, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265009, 264910, 264592, 264596, 265010, 264600, 264602, 265017, 265018, 264605, 264760, 264764, 264288, 264766, 264686, 264768, 264769, 264689, 21906766, 35695917, 264690, 33657023, 264693, 33657109, 264629, 35696423, 35695855, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264639, 264559, 18108385, 18108388, 264563, 264483, 264564, 264565, 264566, 264486, 264567

1661	94234071 (3321, 3322)	Novel Protein sim. GBank gi 4759100 ref NP_004759.1 pSFRS - splicing factor, arginine/serine-rich 11	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264488, 22278988, 264258, 29331824, 29331826, 29331827, 29331828, 264509, 66712502, 29331830, 264908, 52844045, 265007, 264512, 60433356, 60433438, 55812038, 21906754, 265019, 284448, 264766, 264768, 264769, 21906768, 21908769, 265020, 33657023, 33657109, 65274791, 87168518, 264482, 264583, 264584, 264585, 264587
1662	94135172 (3323, 3324)	Novel Protein sim. GBank gi 1730502 sp P52875 PF27_MOUSE - TRANSMEMBRANE PROTEIN PF27			18108392, 29331822, 29331828, 20281100, 264106, 285008, 265007, 265008, 18108348, 21908766, 18108365, 18108366, 18108374, 83373044, 18108385
1663	94217146 (3325, 3326)	Novel Protein sim. GBank gi 4884136 emb CAB43275.1  - (AL050107) hypothetical protein [Homo sapiens]	Contains protein domain (PF00397) - kinase WW domain	kinase	52845156, 56182575, 22278994, 22278995, 35696286, 22278998, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331826, 29331827, 29331828, 33656970, 29331830, 264908, 56182435, 264511, 60433356, 33657402, 33108954, 87168474, 87168559, 265017, 265018, 264605, 18108351, 264764, 264288, 264766, 264768, 21908765, 21908766, 21908767, 21908768, 21908769, 265021, 265022, 264691, 33657023, 264693, 263967, 33657109, 264630, 52644332, 83373044, 87168518, 60432113, 22278000
1664	94234076 (3327, 3328)	Novel Protein sim. GBank gi 3043692 gb BA25510  - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	264488, 263994, 35696286, 29331824, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 60170831, 264591, 264592, 264595, 87168474, 265011, 264600, 264601, 264604, 264605, 264760, 264762, 18108351, 264681, 264682, 264763, 264683, 264764, 264288, 264684, 264766, 264687, 264768, 264769, 21908764, 21908765, 21908767, 35695917, 265021, 264534, 60170615, 264690, 264691, 264692, 33657109, 33657182, 264628, 18108370, 264629, 35698423, 35695855, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264568, 264488



1665	81226952 (3329, 3330)	Novel Protein sim. GBank gi 1083506 pir S50065 - sialoadhesin - mouse	Contains protein domain (PF00047) - Immunoglobulin domain	264488, 29331826, 29331828, 264509, 264906, 264907, 264909, 264510, 264511, 264910, 264592, 264593, 264595, 264758, 264596, 264600, 264760, 264762, 264764, 264766, 264768, 264629, 264630, 264634, 264636, 83373044, 264564, 264566, 264567, 264486
1666	95358160 (3331, 3332)	Novel Protein sim. GBank gi 3913431 sp O42643 DDX8 - PUTATIVE PRE- MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C	Contains protein domain (PF00575) - S1 RNA binding domain	56994075, 22278999, 264259, 29331824, 29331826, 29331827, 29146498, 265009, 33109954, 87168559, 265019, 264288, 264688, 21906767, 21906769, 264691, 33657182, 18108370, 18108374, 18108385, 22279002
1667	91228655 (3333, 3334)	Novel Protein sim. GBank gi 5689535 db BAA83051.1  - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	264259, 29331822, 29331826, 264905, 264906, 264908, 264510, 265009, 264595, 264758, 265011, 87168559, 265017, 265018, 265019, 264448, 264768, 264686, 21906765, 21906767, 21906769, 265020, 265021, 60170815, 264690, 264692, 264693, 18108368, 18108370, 263972, 55810764, 264555, 83373044, 60432113, 22279000, 22279002
1668	88095135 (3335, 3336)	Novel Protein sim. GBank gi 2076894 gb AAB53983.1  - (AF002187) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE- bind), Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]	kinase	66714117, 264508, 264509, 264906, 264907, 264908, 264511, 264910, 264764, 264687, 264689, 33657109, 35696423, 35695855, 264632
1669	91227846 (3337, 3338)	Novel Protein sim. GBank gi 3875371 emb CAA85414.1  - (Z36948) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D66829 comes fr...	UNCLASSIFIED	29331825, 33109954, 264369, 264767, 264689, 33657109, 83373044
1670	87628009 (3339, 3340)		UNCLASSIFIED	264259, 29331824, 29331827, 60433438, 265022, 264636
1671	87346372 (3341, 3342)	Novel Protein sim. GBank gi 462451 sp P34244 KKK1_YEAST - PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35696286, 22278997, 29331825, 264909, 21906754, 265017, 265018, 265019, 264682, 264683, 264768, 264688, 21906766, 21906767, 21906768, 21906769, 264691, 264555, 264556, 22279000, 264566 264906, 264909, 264632, 18108381
1672	86291834 (3343, 3344)	Novel Protein sim. GBank gi 1814270 (U74586) - double- stranded RNA specific adenosine deaminase [Rattus norvegicus]	deaminase	

1673	88095137 (3345, 3348)	Novel Protein sim. GBank gjl2078894[gb AAB53983.1] - (AF002187) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG-PE-bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00130) - kinase Phorbol esters/diacylglycerol binding domain (C1 domain)	284488, 264568, 18108394, 56994075, 22278996, 264259, 35696052, 284508, 264905, 264509, 284908, 264907, 264908, 264909, 264510, 284910, 60170831, 264592, 264594, 264595, 264758, 264601, 264760, 264762, 264683, 264764, 264288, 264766, 264686, 264768, 264687, 264769, 264689, 264690, 33657023, 264692, 264693, 33657109, 264828, 264629, 18108374, 35696423, 35695855, 264631, 264632, 264634, 264635, 264637, 264556, 264638, 264639, 264563, 264482, 264564, 264565, 264566, 264567, 264486
1674	88258028 (3347, 3348)	Novel Protein sim. GBank gjl5262467[emb CAB45693.1] - (AL080062) hypothetical protein [Homo sapiens]	kinase	29331822, 29331824, 264908, 52644045, 60433356, 87168559, 264448, 264288, 264686, 264691
1675	87606466 (3349, 3350)	Novel Protein sim. GBank gjl3128366 (AF010496) - 50S ribosomal protein l9 [Rhodobacter capsulatus]	UNCLASSIFIED	56181686, 35686286, 22278997, 22278998, 264259, 29331824, 29331827, 35696052, 68712502, 264764, 264288, 264686, 264687, 35695917, 265020, 264690, 264693, 35695763, 18108370, 35696423, 35695855, 264637, 264639, 18108385, 264564
1676	85358086 (3351, 3352)	Novel Protein sim. GBank gjl4164065[gb AAD05327] - (AF111091) latrophilin 3 splice variant bbaf [Bos taurus]	UNCLASSIFIED	264259, 29331827, 29331828, 264106, 264907, 265009, 264600, 265019, 264288, 21906765, 265020, 265022, 35695855, 83373044, 18108385
1677	87408587 (3353, 3354)	Novel Protein sim. GBank gjl3327046[dbj BAA31591] - (AB014516) KIAA0616 protein [Homo sapiens]	UNCLASSIFIED	264908
1678	88868829 (3355, 3356)	Novel Protein sim. GBank gjl550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	UNCLASSIFIED	29331824, 264102
1679	91214106 (3357, 3358)	Novel Protein sim. GBank gjl550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	carboxylase	264488, 18108392, 18108394, 52646842, 18108397, 18108398, 35696286, 29331824, 265006, 265007, 265008, 265009, 18108348, 265011, 18108351, 284683, 18108354, 18108358, 18108359, 21906765, 29148627, 29148628, 264690, 18108361, 18108362, 18108364, 18108365, 18108368, 264628, 18108378, 35696423, 35695855, 264635, 18108381, 18108382, 18108383, 18108384, 18108385, 18108388
1680	91005372 (3359, 3360)	Novel Protein sim. GBank gjl2394478 (AF024500) - No definition line found [Caenorhabditis elegans]	transport	65274572, 22278994, 22278998, 68714117, 29331827, 56182435, 21906754, 265018, 264288, 21906769
1681	94324150 (3361, 3362)	Novel Protein sim. GBank gjl5689537[dbj BAA83052.1] - (AB029023) KIAA1100 protein [Homo sapiens]	UNCLASSIFIED	22278996, 29331822, 264908, 264593, 264604, 265019, 264683, 55811957, 264690, 33657023, 35696423, 83373044, 264563
1682	86042710 (3363, 3364)		UNCLASSIFIED	264909, 265017, 264605

1683	94316213 (3385, 3368)	Novel Protein sim. GBank gi 5031717 ref NP_005704.1 pGPBP - goodpasture antigen- binding protein	Contains protein domain (PF01852) - START domain	UNCLASSIFIED	263994, 35696286, 35696032, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 265007, 265009, 264910, 264593, 264758, 265010, 265011, 264760, 264761, 264762, 264763, 264784, 264369, 264766, 264768, 35695917, 264692, 33657109, 35696423, 35695855, 264634, 264635, 264636, 264638, 264639, 83373044, 264486
1684	80063409 (3367, 3368)			UNCLASSIFIED	264563, 264566
1685	94323182 (3389, 3370)	Novel Protein sim. GBank gi 1255371 (U53147) - coded for by C. elegans cDNA yk34a9.5; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase. [Caenorhabditis elegans]	Contains protein domain (PF00625) - Guanylate kinase	UNCLASSIFIED	60424179, 52646842, 22278994, 35696286, 22278998, 264259, 52645080, 29331824, 29331826, 265007, 33657084, 265018, 264881, 264448, 264683, 264369, 264689, 21908765, 21908767, 21908768, 21908769, 265021, 264692, 65274620, 33657109, 27486262, 264635, 52644332, 56182323, 22278000
1686	87820710 (3371, 3372)	Novel Protein sim. GBank gi 2244707 db BAA21115.1  - (AB005287) thrombospondin 1 [Bos taurus]		UNCLASSIFIED	56182575, 264259, 264508, 264905, 264509, 264907, 264908, 264510, 264511, 265006, 264512, 265009, 264910, 264758, 265010, 265011, 264605, 18108351, 264764, 264766, 18108357, 264768, 18108362, 264628, 264630, 264631, 264634, 264635, 264637, 264638, 264639, 264585, 264486, 264587
1687	94719400 (3373, 3374)	Novel Protein sim. GBank gi 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264906, 264907, 264908, 264510, 265006, 265007, 264910, 264558, 18108381, 18108383, 265011
1688	82158442 (3375, 3376)			UNCLASSIFIED	264905, 264910, 264760, 264629, 264555
1689	94325049 (3377, 3378)	Novel Protein sim. GBank gi 4240193 db BAA74875.1  - (AB020659) KIAA0852 protein [Homo sapiens]		UNCLASSIFIED	264569, 35696286, 22278999, 264508, 264908, 264909, 56182435, 33657402, 60433438, 55812038, 265017, 265018, 264448, 264764, 264288, 264686, 29148629, 35695917, 265020, 265021, 263972, 18108374, 65274791, 83373044, 264089
1690	83255346 (3379, 3380)	Novel Protein sim. GBank gi 3800736 (AF031572) - seven- pass transmembrane receptor precursor [Mus musculus]	Contains protein domain (PF00028) - Cadherin domain		264369, 21908766, 264692, 264639, 87188518
1691	88095223 (3381, 3382)	Novel Protein sim. GBank gi 2773208 (AF039713) - No definition line found [Caenorhabditis elegans]			264768, 33657109, 29331827, 29148629, 264510, 264106, 264910, 264109, 264508, 60170831, 264563, 264905, 264564, 264691, 264637, 264628, 264907, 264908, 33657023, 264567, 264766, 263974
1692	86106709 (3383, 3384)				264106
1693	87012775 (3385, 3386)	Novel Protein sim. GBank gi 121271 sp P02207 GLB_LAMFL - GLOBIN	Contains protein domain (PF00042) - Globin	UNCLASSIFIED	29331826, 264508, 264905, 264907, 264595, 265010, 265011, 21908768, 33657023, 264629, 263978, 264558

1694	94208168 (3387, 3388)	Novel Protein sim. GBank gi 5453932 ref NP_006225.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Contains protein domain (PF01193) - mapolymerase RNA polymerases L / 13 to 16 kDa subunit	35898288, 22278998, 22278998, 22278998, 264259, 29331822, 29331825, 29331826, 29331828, 35898052, 29148499, 264905, 264908, 52844045, 264511, 285008, 285007, 265009, 284592, 60433358, 21906754, 265010, 265011, 18108351, 264763, 264682, 264448, 264683, 264288, 264768, 264689, 21906768, 60170615, 264691, 264692, 264693, 18108370, 18108374, 263978, 35698423, 35698585, 284558, 18108381, 18108385, 87168518, 264482, 264486 264634
1695	84719325 (3389, 3390)	Novel Protein sim. GBank gi 4680679 gb AAD27729.1 AF132954 - CGI-20 protein [Homo sapiens]	UNCLASSIFIED	
1696	87824038 (3391, 3392)	Novel Protein sim. GBank gi 4220517 emb CAA229901 - (AL035356) hypophthal protein [Arabidopsis thaliana]		22278997, 284259, 265010, 18108351, 264764, 21906768, 18108370
1697	85740963 (3393, 3394)	Novel Protein sim. GBank gi 505652 (U10362) - GP36b glycoprotein [Homo sapiens]	glycoprotein	264682
1698	87445285 (3395, 3396)	Novel Protein sim. GBank gi 5052031 gb AAD38411.1 AF155739 - axotrophin [Mus musculus]		56994075, 22278998, 22278999, 264509, 33657402, 284758, 87168474, 87168559, 265017, 265018, 264448, 264687, 29148627, 21908769, 29148629, 285020, 265022, 33657023, 264558, 87168518, 22278902
1699	87424783 (3397, 3398)		UNCLASSIFIED	35698288, 264635
1700	87859161 (3399, 3400)	Novel Protein sim. GBank gi 543344 pir IS41647 - zinc finger 5 protein - mouse	Contains protein domain (PF00096) - Zinc finger, C2H2 type	29331824, 52844045, 265008, 265009, 263969, 263971
1701	86570488 (3401, 3402)		UNCLASSIFIED	264092, 264110, 263977
1702	87765082 (3403, 3404)	Novel Protein sim. GBank gi 3877439 emb CAA966521 - (Z72510) similarity to yeast UTR3 protein (Swiss Prot accession number P21374); cDNA EST EMBL:D72822 comes from this gene; cDNA EST EMBL:D75763 comes from this gene; cDNA EST yk274e3.3 comes from this gene; cDNA EST yk274e3.5 c...	MHC	22278995, 22278997, 264092, 29146488, 29146499, 264107, 264508, 264907, 264110, 264112, 265009, 60170831, 21906754, 265011, 265017, 264762, 18108351, 264288, 21908765, 35698917, 265021, 60170815, 263967, 33657109, 18108370, 263972, 263974, 18108374, 263978, 35698585, 264555, 263981, 60170394, 18108385, 56528486, 87168518, 60432113
1703	79568651 (3405, 3406)	Novel Protein sim. GBank gi 451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]	UNCLASSIFIED	264909, 265017, 264628, 264629, 264638
1704	86822878 (3407, 3408)	Novel Protein sim. GBank gi 1263289 (U47856) - fibrin-4 [Araneus diadematus]	UNCLASSIFIED	264369
1705	87795175 (3409, 3410)	Novel Protein sim. GBank gi 4519621 dbj BA75670.11 - (AB017814) OASIS protein [Mus musculus]		264569, 35698288, 264807, 265010, 264687, 264768, 264692, 264693, 264638, 264566
1706	87790967 (3411, 3412)	Novel Protein sim. GBank gi 3123034 sp Q15011 Y025_HUMAN - HYPOTHETICAL PROTEIN KIAA0025		22278996, 22278998, 264259, 264509, 265018, 264764, 264685, 264686, 21908768, 21906769, 265022, 264691, 264558, 22278900

1707	88041230 (3413, 3414)	Novel Protein sim. GBank gi 4321664 gb AA015797  - (AF055470) ZNF258 [Homo sapiens]		UNCLASSIFIED	18108398, 22278987, 264259, 29147620, 29331826, 29146498, 264905, 264906, 265008, 264593, 264595, 264758, 264596, 265018, 264760, 18108351, 264764, 264766, 264689, 264693, 18108370, 35698423, 55811578, 264558, 87168518, 60432113, 264567
1708	91220519 (3415, 3416)	Novel Protein sim. GBank gi 5174591 ref NP_005947.1 pMTuF - 5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase	Contains protein domain (PF01268) - Formate-tetrahydrofolate ligase	synthase	56182575, 22278996, 56994075, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 29146498, 29146499, 29331830, 265009, 60170831, 33657402, 33109954, 87168559, 265019, 18108351, 264448, 21908765, 21908767, 21908768, 29148627, 29148629, 29148784, 60170615, 52644150, 33657023, 33657109, 18108374, 55811576, 264559, 18108385, 22279000, 264563
1709	80222583 (3417, 3418)			UNCLASSIFIED	264107, 55811957, 263974, 263976, 263977, 263981
1710	20754572 (3419, 3420)	Novel Protein sim. GBank gi 5031735 ref NP_005760.1 pHEC - N-acetylglucosamine 6-O-sulfotransferase		UNCLASSIFIED	264556
1711	81013729 (3421, 3422)	Novel Protein sim. GBank gi 5031735 ref NP_005760.1 pHEC - N-acetylglucosamine 6-O-sulfotransferase		sulfotransferase	65274372, 29331824, 29331826, 264768, 60431528, 35696423, 60432113, 264563
1712	95330184 (3423, 3424)	Novel Protein sim. GBank gi 5454168 ref NP_006453.1 pXAP4 - HBV associated factor	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	kinase	56994075, 264093, 264259, 29331822, 264099, 29331824, 29331827, 264107, 264110, 264511, 264592, 265011, 265018, 264683, 264686, 264689, 265020, 33657023, 263967, 33657109, 263974, 35696423, 35695855, 264630, 264636, 264558, 264566
1713	94143453 (3425, 3426)	Novel Protein sim. GBank gi 160409 (M69183) - mature-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	Contains protein domain (PF00643) - B-box zinc finger.	UNCLASSIFIED	22278995, 264508, 264758, 18108351, 18108370, 263974, 18108374, 264634, 56182323, 83373044, 60432113
1714	87420048 (3427, 3428)				22278997, 264757, 21908765, 265020, 265021, 264692, 56526486
1715	94260257 (3429, 3430)	Novel Protein sim. GBank gi 5689537 db BAA83052.1  - (AB029023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	264509, 264905, 264906, 264907, 264908, 264909, 264910, 264591, 265011, 264766, 264768, 264769, 264691, 264692, 264632, 264634, 264635, 264636, 264637, 264556, 264639, 264564
1716	87400449 (3431, 3432)	Novel Protein sim. GBank gi 4589468 db BAA76761.1  - (AB012808) mBOCT [Mus musculus]		transport	56182575, 29331824, 60432289, 264109, 264909, 265007, 264600, 265019, 264686, 265020, 264693, 55811576, 264558, 60432113, 22279002

1717	87563223 (3433, 3434)	Novel Protein sim. GBank gi 2765411 emb CAA74749  - (Y14391) GTP-binding protein [Homo sapiens]		UNCLASSIFIED	264569, 264259, 29331825, 29331826, 29331828, 35696052, 264509, 264905, 264907, 264908, 264909, 264512, 265009, 264910, 264592, 264595, 264758, 264759, 265017, 264681, 264764, 264768, 264686, 18108357, 35695917, 264690, 264692, 264693, 264628, 264629, 35695423, 264630, 264631, 264635, 264636, 18108380, 264638, 264639, 18108388, 18108391
1718	87032828 (3435, 3436)	Novel Protein sim. GBank gi 2833262 sp Q14999 Y076_HUMAN - HYPOTHETICAL PROTEIN KIAA0076 (HA0936)		UNCLASSIFIED	265011, 264681, 264682, 264684, 264688, 264689, 21806785, 265021, 264691, 33657023, 264693, 18108370, 35695855, 264632, 264634, 264636, 18108388, 22278002
1719	94315259 (3437, 3438)	Novel Protein sim. GBank gi 4505197 ref NP_003473.1 pMLL2 - myeloid/lymphoid or mixed-lineage leukemia 2		UNCLASSIFIED	18108396, 65274572, 35698286, 22278997, 60432049, 56182181, 68714117, 60432289, 29331826, 35696052, 29331828, 264906, 29331830, 56182435, 264592, 60431735, 60433438, 55812038, 264759, 265010, 264600, 264601, 265017, 264448, 264764, 264288, 264768, 21906766, 21906769, 55811957, 265020, 265021, 52644150, 33657023, 33657109, 33657182, 27486262, 33657349, 35695763, 18108370, 60431528, 18108374, 35696423, 55811576, 35695855, 264631, 56182223, 264559, 264584, 264486, 56182575, 22278998, 264259, 29331824, 60432289, 29331827, 35698032, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 264758, 21906754, 265011, 264601, 264760, 264762, 264288, 264768, 264686, 18108357, 264689, 21906785, 55811957, 264693, 20281149, 264629, 18108374, 55811576, 65274791, 264630, 20281071, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 56182323, 87168518
1720	84853063 (3439, 3440)	Novel Protein sim. GBank gi 2129478 p I S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	22278994, 22278999, 29331822, 265008, 265007, 265008, 55812038, 21906754, 60174639, 265011, 87168559, 18108351, 18108354, 21906765, 21906766, 21906788, 21906769, 265020, 33657109, 18108370, 18108374, 264556, 60170394, 83373044, 18108385, 284486
1721	91722288 (3441, 3442)	Novel Protein sim. GBank gi 4886461 emb CAB43381.1  - (AL050280) hypothetical protein [Homo sapiens]		UNCLASSIFIED	56994075, 29331824, 29331828, 265009, 18108351, 21906768, 265020, 33657023, 18108374, 83373044
1722	84134549 (3443, 3444)	Novel Protein sim. GBank gi 5689375 dbj BAA82968.1  - (AB030644) tudor repeat associator with PCTAIRE 2 [(Rattus norvegicus)]	Contains protein domain (PF00567) - Tudor domain	kinase	

1723	95358181 (3445, 3446)	Novel Protein sim. GBank gij4426962[gb AAD20633] - (AF126062) Ar-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264488, 264687, 264769, 21906767, 21908768, 58182575, 55811957, 22278997, 22278998, 265020, 264259, 264692, 33657023, 29331822, 29331824, 29331825, 60432289, 33857182, 33856970, 33857349, 29146499, 264508, 264907, 18108370, 264629, 264908, 264909, 18108374, 55811576, 264510, 265008, 264511, 265007, 264910, 264632, 264591, 60432229, 264592, 60433356, 264594, 60433438, 264595, 83373044, 55812038, 33109954, 33657084, 87168518, 87168474, 265010, 265011, 87168559, 264600, 60432113, 264604, 265019, 264583, 264448, 264682, 264566, 264764, 264288, 264587, 264486, 264369, 264766
1724	87713806 (3447, 3448)	Novel Protein sim. GBank gij2340162 (AF005083) - dsRBP-ZFa [Xenopus laevis]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264905, 18108359, 264693, 264628, 264631, 264636, 264555, 264556, 264558, 264559
1725	85855191 (3449, 3450)	Novel Protein sim. GBank gij3152662 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	35696286, 264259, 29331822, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264910, 265009, 264591, 264601, 264760, 18108351, 264881, 264764, 264288, 264766, 264768, 21906769, 35695917, 264628, 35696423, 264630, 264631, 264632, 264635, 264636, 264638, 87168518, 264566
1726	85754255 (3451, 3452)	Novel Protein sim. GBank		UNCLASSIFIED	29146498, 264683, 264689
1727	85296362 (3453, 3454)	gi4689348[gb AAD27861.1 AF132562] BcDNA LD14270 [Drosophila melanogaster]		UNCLASSIFIED	264905, 265011, 264689, 21906768

1728	85348515 (3455, 3456)	Novel Protein sim. GBank g 406549 gb AA020027  - (AF131738) Unknown [Homo sapiens]	UNCLASSIFIED	60424179, 18108397, 56182575, 22278995, 56994075, 35698286, 22278997, 22278998, 22278999, 264094, 60432048, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331826, 29331827, 35696052, 264905, 264906, 264907, 29331830, 66712502, 264908, 56182435, 264511, 265008, 265009, 60432229, 60433356, 33657402, 60433438, 264759, 21908754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 5581150, 264681, 264448, 264682, 264763, 264683, 264288, 264684, 264369, 264685, 264766, 264687, 264769, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 264535, 264691, 264692, 33657023, 264693, 33657109, 18108370, 264628, 263972, 264629, 18108374, 18108376, 55810764, 65274791, 35695855, 264631, 264634, 264635, 60431850, 264636, 264638, 60170394, 264639, 83373044, 56526486, 87168518, 60432113, 22279000, 22279002, 264584, 264586
1729	91227948 (3457, 3458)	Novel Protein sim. GBank g 854065 emb CAA83337  - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	264906, 264907, 264908, 264511, 264555, 83373044, 264596, 264566
1730	85463474 (3459, 3460)		UNCLASSIFIED	29331822, 29331825, 29331828, 264907, 264908, 264909, 265011, 264764, 264629
1731	88266088 (3461, 3462)	Novel Protein sim. GBank g 631600 pir IS47094 - hypothetical protein - rabbit	UNCLASSIFIED	52646842, 264907, 264909, 56182435, 55811386, 87168459, 265018, 265019, 264760, 52844229, 55811578
1732	91218878 (3463, 3464)	Novel Protein sim. GBank g 4240231 db BAA74894.1  - (AB020678) KIAA0871 protein [Homo sapiens]	struct	56182575, 29331822, 29331824, 29331827, 66712502, 264591, 33657402, 60433356, 265019, 21908768, 21908769, 35695917, 265020, 265021, 264638, 56182323
1733	87617178 (3465, 3466)	Novel Protein sim. GBank g 1575756 (U70674) - m-Numb [Mus musculus]	Contains protein domain (PF00640) - synthase Phosphotyrosine interaction domain (PTB/PID)	264907, 264910, 33657402, 265010, 264681, 264683, 264684, 264688, 264769, 264691, 264692, 264693, 264628, 264636, 264556
1734	87795261 (3467, 3468)			264693



1735	88318638 (3469, 3470)	Novel Protein sim. GBank gi 4836807 gb AAD30566.1 AF14679 - (AF146793) PFT27 [Mus musculus]	Contains protein domain (PF01169) - Uncharacterized protein family UPF0016	264488, 18108394, 18108398, 22278998, 60432049, 264259, 29331822, 264908, 285008, 265007, 265008, 265009, 264591, 33657402, 265010, 265011, 87168559, 265017, 18108351, 264682, 18108354, 264769, 264689, 21906765, 21906768, 21906769, 29148629, 29148784, 265021, 265022, 52644150, 18108364, 18108365, 33657109, 18108370, 18108374, 18108380, 18108385, 87168518, 264563, 18108390, 264490, 264259, 66714117, 66712502, 58182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1736	95362884 (3471, 3472)	Novel Protein sim. GBank gi 4885647 ref NP_005472.1 pTRAP - thyroid hormone receptor-associated protein complex component	UNCLASSIFIED	264490, 264259, 66714117, 66712502, 58182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1737	88165549 (3473, 3474)	Novel Protein sim. GBank gi 2143607 pir S68695 - BIK protein - rat	Contains protein domain (PF00168) - C2 domain	29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1738	85788811 (3475, 3476)	Novel Protein sim. GBank gi 2225941 emb CAA69714 - [Y08460] Mdes protein [Mus musculus]	UNCLASSIFIED	264908, 264909, 265008, 264910, 264566
1739	87328576 (3477, 3478)		Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	35696052, 264603, 264557
1740	83592939 (3479, 3480)	Novel Protein sim. GBank gi 4809 emb CAA44309  - [X62462] YCR601 [Saccharomyces cerevisiae]	trafic	264604, 21908764, 18108364, 264629, 35695955, 264636
1741	95010100 (3481, 3482)	Novel Protein sim. GBank gi 4883898 gb AAD31695.1 AF13042 - (AF130420) serine protease-like protein isoform [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	60432229, 29331827, 264509, 265009, 60432229, 264759, 265017, 264767, 264688, 264689, 21908769, 265020, 33657109
1742	85788814 (3483, 3484)	Novel Protein sim. GBank gi 4505183 ref NP_003667.1 pMLD  - membrane fatty acid (lipid) desaturase	UNCLASSIFIED	264908, 264910, 264758, 265011, 264631, 264638, 264566
1743	86968475 (3485, 3486)			265017, 265020, 264692
1744	91224003 (3487, 3488)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	UNCLASSIFIED	22278998, 264508, 264907
1745	20290075 (3489, 3490)		UNCLASSIFIED	264558
1746	94326110 (3491, 3492)	Novel Protein sim. GBank gi 731756 sp P38873 YHY6_YEAST - HYPOTHETICAL 175.8 KD PROTEIN IN GND1-K11 INTERGENIC REGION	Contains protein domain (PF00400) - WD domain, G-beta repeat	65274791, 264639, 264559
1747	94324333 (3493, 3494)	Novel Protein sim. GBank gi 1658503 (U75467) - Alu [Drosophila melanogaster]	transcriptfactor	52646842, 29331824, 29331825, 52644045, 56182435, 265007, 52646317, 87168474, 265018, 18108351, 264369, 264769, 264689, 35695917, 60170615, 264691, 33657023, 65274791, 35695855, 60170394, 22279000, 264482

1748	88003580 (3485, 3498)	Novel Protein sim. GBank gi 450451 ref NP_001530.1 pHSJ2 - heat shock protein, DNAJ-like 2	Contains protein domain (PF00684) - eph DnaJ central domain (4 repeats)	264489, 56182575, 29331824, 56182435, 264112, 265007, 265019, 264764, 21908788, 265020, 264691, 55811578, 264635, 264555, 264556, 264557, 264559, 264106
1749	83363081 (3497, 3498)	Novel Protein sim. GBank gi 5650780 gb AAD45948.1 AF15196 - (AF151968) RGS protein RGS-17 [Gallus gallus]	Contains protein domain (PF00615) - oncogene Regulator of G protein signaling domain	33657402, 264288, 52644150, 263974, 83373044
1750	94321664 (3499, 3500)	Novel Protein sim. GBank gi 4989894 gb AAC28444.2  - (AF05164) hyperpolarization-activated, cyclic nucleotide-gated channel 2 [Homo sapiens]		
1751	83373058 (3501, 3502)	Novel Protein sim. GBank gi 2760161 dbj BAA24184  - (AB010054) outer arm dynein light chain 2 [Anthodidaris crassispina]	Contains protein domain (PF00560) - ATPase associated Leucine Rich Repeat	265010, 264369
1752	86456530 (3503, 3504)	Novel Protein sim. GBank gi 3915482 sp P74346 YC29_SYN3 - HYPOTHETICAL 35.0 KD PROTEIN SLR1629	Contains protein domain (PF00849) - deaminase RNA pseudouridylation synthase	264510, 264593, 264682, 21906765, 18108370
1753	94235159 (3505, 3506)	Novel Protein sim. GBank gi 2852636 (AF007155) - unknown [Homo sapiens]	Contains protein domain (PF01553) - phosphatase Acyltransferase	56994075, 22278996, 264908, 60170831, 264682, 264764, 264389, 264288, 264685, 264687, 21908788, 264692, 264693, 65274620, 65274791, 35695855, 264637, 264594
1754	88095323 (3507, 3508)	Novel Protein sim. GBank gi 731421 sp P39981 YE4_YEAST - HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION	transport	264488, 35698286, 264509, 264806, 264807, 264908, 264909, 264511, 264910, 264591, 33657402, 264594, 264757, 264758, 264600, 264604, 264762, 264763, 264685, 264766, 264691, 264628, 35696423, 264632, 264634, 264637, 264638, 263981, 264558, 264639, 264563, 264584, 264565, 264566, 264567, 264688
1755	79470282 (3509, 3510)	Novel Protein sim. GBank gi 1176422 (U43194) - rhophilin [Mus musculus]	UNCLASSIFIED	
1756	92962614 (3511, 3512)	Novel Protein sim. GBank gi 4432860 gb AAD20708  - (AC008300) putative glucose-induced repressor protein [Arabidopsis thaliana]		52648842, 22278994, 22278995, 56994075, 22278996, 22278997, 264259, 29331822, 60432289, 29331827, 33856970, 285006, 265009, 60432229, 60433356, 60433438, 33109954, 21906754, 265017, 265018, 265019, 264448, 264389, 264288, 21908785, 21908786, 21908787, 21908788, 21908789, 265020, 265021, 265022, 264692, 27486262, 27486264, 18108376, 20281152, 264596, 18108388, 87168518, 60432113, 22279000, 22279002, 264482
1757	95357380 (3513, 3514)	Novel Protein sim. GBank gi 5441615 emb CAB46856.1  - (AJ388557) zinc finger protein [Canis familiaris]	Contains protein domain (PF00096) - dna_rna_bind Zinc finger, C2H2 type	22278997, 264259, 60432289, 29331827, 264908, 52644045, 265008, 264593, 265019, 264766, 21908788, 65274620, 18108385, 60432113, 264586, 264487

1758	87612971 (3515, 3516)	Novel Protein sim. GBank gij388104[embjCAA18403] - (AL021497) predicted using Genefinder (Caenorhabditis elegans)		UNCLASSIFIED	22278994, 22278999, 29331822, 29331824, 29331825, 33656970, 264508, 265006, 265007, 265009, 264591, 33657402, 33109954, 87168474, 264600, 265017, 265018, 21908769, 265020, 265021, 33657023, 33657109, 264629, 18108374, 35695855, 264632, 52644332, 22279002, 264563
1759	36894372 (3517, 3518)			UNCLASSIFIED	264759
1760	87329716 (3518, 3520)	Novel Protein sim. GBank gij5262748[embjCAB45888.1] - (AJ133120) Proline rich synapse associated protein 2 [Rattus norvegicus]		UNCLASSIFIED	56182575, 60432049, 35696052, 264905, 264906, 264907, 264908, 264909, 265006, 265009, 264910, 60432229, 264592, 264595, 55812038, 264758, 264762, 18108351, 264764, 264766, 264768, 264769, 21906765, 55811957, 35695917, 264690, 264692, 264628, 264629, 55811576, 35696423, 264632, 264634, 264636, 264557, 264639, 60432113, 264565, 264486
1761	87409586 (3521, 3522)	Novel Protein sim. GBank gij127749[spP10569]MYSC_ACACA - MYOSIN IC HEAVY CHAIN	Contains protein domain (PF00618) - Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif	UNCLASSIFIED	29331822, 264910, 264685, 264686
1762	95319887 (3523, 3524)	Novel Protein sim. GBank gij3169158 (AC004770) - BC269730_2 [Homo sapiens]	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	desaturase	22278998, 264259, 264905, 264907, 60170831, 265010, 265011, 265017, 264448, 21906765, 21906766, 21906767, 21906768, 265021, 264690, 33657109, 18108374, 264558, 60170394
1763	91224013 (3525, 3526)	Novel Protein sim. GBank gij4809026[gbjAAD30062.1] - (AF132856) suppressor of G2 allele of skp1 homolog [Homo sapiens]			56181886, 29331825, 35696052, 264905, 264906, 264909, 264763, 264682, 264769, 35695917, 265022, 33657023, 18108374, 35696423, 264634
1764	87757697 (3527, 3528)	Novel Protein sim. GBank gij1360869[pirj]CGHU1V - collagen alpha 1(V) chain precursor - human	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	22278998, 264259, 35696052, 29331828, 56182435, 265008, 265017, 265018, 264448, 264288, 21906766, 21906767, 29148627, 35695917, 264691, 33657023, 60432113, 22279002
1765	81230091 (3529, 3530)	Novel Protein sim. GBank gij486806[pirj]JS35503 - finger protein neutralized - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	264488, 18108394, 22278995, 22278997, 22278999, 264259, 264104, 264508, 264905, 264907, 264511, 265007, 265008, 264910, 265009, 21906754, 265010, 265017, 264603, 265018, 265019, 18108351, 264682, 264448, 264369, 264288, 264766, 18108358, 21906766, 21906767, 29148627, 29148629, 35695917, 265020, 265021, 264692, 264628, 264629, 18108374, 263976, 264636, 83373044, 22279000, 22279002

1766	95081201 (3531, 3532)	Novel Protein sim. GBank gi 2499087 sp Q09332 UGG_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)		glycoprotein	52645156, 87168559, 80170815, 33657023, 264693, 33657109, 27486261, 264555, 83373044
1767	87755998 (3533, 3534)	Novel Protein sim. GBank gi 4176443 emb CAA18263.1  - (AL022238) dJ1042K10.4 (novel protein) [Homo sapiens]		UNCLASSIFIED	265017, 265019, 264686, 264768, 265020, 264692
1768	80253216 (3535, 3536)			UNCLASSIFIED	29331824, 29331825, 264591, 56182323
1769	87388988 (3537, 3538)			UNCLASSIFIED	264563
1770	95413144 (3539, 3540)	Novel Protein sim. GBank gi 115204 sp P00736 C1R_HUMAN - COMPLEMENT C1R COMPONENT PRECURSOR	Contains protein domain (PF00089) - Trypsin	complement	264488, 264768, 264769, 56182575, 55811957, 264690, 264691, 35696052, 264905, 264509, 264906, 264907, 264628, 264908, 264909, 264910, 264634, 264635, 264636, 264556, 264757, 264758, 55812038, 55274444, 264760, 264563, 264762, 264764, 264684, 264766
1771	94233542 (3541, 3542)	Novel Protein sim. GBank gi 3914191 sp P56558 OGT1_RAT - UDP-N- ACETYLGLUCOSAMINE-PEPTIDE N- ACETYLGLUCOSAMINYLTTRANSFERASE 110 KO SUBUNIT (O-GLCNAC TRANSFERASE P110 SUBUNIT)	Contains protein domain (PF00515) - TPR Domain	transferase	264758, 264600, 264369, 55811957, 265020, 83373044, 22278000
1772	87643510 (3543, 3544)	Novel Protein sim. GBank gi 4959442 gb AAD34351.1 AF12136 - (AF121360) DNZDHHHC/NEW1 zinc finger protein 11 [Drosophila melanogaster]	Contains protein domain (PF01529) - DHC zinc finger domain		22278998, 29331828, 33109954, 265018, 265019, 264764, 21906765, 265020, 265021, 264556
1773	94118824 (3545, 3546)	Novel Protein sim. GBank gi 3978464 (AF085693) - G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	potassium_channel	65274572, 56182575, 22278998, 35696286, 22278999, 264259, 29331824, 60424269, 29331825, 60432289, 35696052, 264106, 264509, 264906, 264907, 29331830, 264908, 52644045, 264511, 265006, 265007, 265008, 60170831, 60433438, 264758, 55811386, 87168559, 265017, 264604, 265019, 55811150, 264288, 56181562, 264689, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265022, 52644150, 264691, 33657023, 264692, 264693, 60431528, 35696423, 35695855, 264636, 56182323, 18108387, 56526486, 22278000, 22278002, 264563, 264564, 264565, 264566, 264567
1774	94232573 (3547, 3548)	Novel Protein sim. GBank gi 2495699 sp Q15034 Y032_HUMAN - HYPOTHETICAL PROTEIN KIAA0032	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	UNCLASSIFIED	65274572, 56182575, 35696052, 55812038, 33109954, 21906754, 265017, 21906767, 21906768, 21906769, 265020, 264691, 264636, 56182323, 22278002

1775	95359330 (3549, 3550)	Novel Protein sim. GBank gij1468199[dbj][BAA09487] - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]		UNCLASSIFIED	65274572, 56182575, 56994075, 35696286, 22278997, 29331822, 29331826, 60432289, 29331828, 35696052, 29331830, 68712502, 264828, 56182435, 284511, 285007, 265009, 60170831, 60432229, 60433438, 55812038, 21906754, 85658542, 87168559, 264601, 265017, 265018, 265019, 264762, 264448, 264288, 264689, 21906765, 21906768, 21906767, 21906768, 265020, 265021, 265022, 264691, 33657023, 264692, 33657109, 27486261, 33657349, 18108370, 18108377, 35696423, 55811576, 35695855, 264632, 264634, 264636, 264639, 56182323, 83373044, 58526486, 87168518, 60432113, 22279000, 22279002, 264482, 264486, 264910
1776	94133756 (3551, 3552)	Novel Protein sim. GBank gij4589676[dbj][BAA76857.1] - (AB023230) KIAA1013 protein [Homo sapiens]			
1777	87447171 (3553, 3554)	Novel Protein sim. GBank gij321993[sp][p87115]YDK9_SCHPO - HYPOTHETICAL 116.5 KD PROTEIN C20G8.08C IN CHROMOSOME I	nuc1_recpt		56894075, 29331826, 265008, 87168474, 265017, 265018, 264761, 55811150, 264764, 56181582, 264689, 21906765, 21906768, 21906769, 35695917, 264690, 33657023, 35695763, 60431528, 35696423, 55811576, 35695855, 22279000, 22279002, 264564
1778	94851624 (3555, 3556)	Novel Protein sim. GBank gij387564[emb][CAA91454.1] - (Z69581) Similarity to Human rab13 protein (PIR Acc. No. A49647). Contains the ATP/GTP-binding site motif (PROSITE PS00017); cDNA EST EMBL:M89412 comes from this gene; cDNA EST yk212g9.3 comes from this gene; cDNA EST yk212g9...		UNCLASSIFIED	29331826, 29331827, 35696052, 264512, 285007, 265009, 265017, 265019, 264762, 18108351, 264769, 21906765, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 264691, 264693, 18108370, 264556, 83373044
1779	94133758 (3557, 3558)	Novel Protein sim. GBank gij4589676[dbj][BAA76857.1] - (AB023230) KIAA1013 protein [Homo sapiens]		UNCLASSIFIED	29148827, 35696286, 29147620, 265006, 265007, 265008, 18108385, 65274727, 264482, 264369, 264766
1780	87023497 (3559, 3560)		Contains protein domain (PF00807) - Apidaecin	UNCLASSIFIED	264107, 33657109, 56526486
1781	84047477 (3561, 3562)			UNCLASSIFIED	264508, 284906, 264639
1782	88094607 (3563, 3564)	Novel Protein sim. GBank gij729225[sp][p41237][CTXN_RAT] - CORTEXIN			264259, 29331822, 264508, 264905, 264906, 264907, 264908, 265007, 265009, 264910, 264591, 264758, 264764, 264288, 264768, 264769, 264635, 264636, 264637, 264639, 264583
1783	85717905 (3565, 3566)	Novel Protein sim. GBank gij2257543[dbj][BAA21436] - (AB004538) protein arginine N-methyltransferase [Schizosaccharomyces pombe]	interferon		264768

1784	95197093 (3567, 3568)	Novel Protein sim. GBank gi 1755049 (U55042) - myosin X [Bos taurus]	Contains protein domain (PF00169) - struct PH domain	35698286, 264259, 35698052, 264508, 264905, 264908, 264907, 66712502, 264908, 264909, 265007, 265008, 265009, 264910, 264591, 264594, 264757, 264758, 264759, 265010, 265011, 264601, 264602, 264604, 264605, 18108351, 264762, 264763, 264764, 264369, 264768, 264687, 264768, 264688, 21908768, 35695917, 264690, 264691, 264692, 264693, 264628, 18108374, 35698423, 264631, 264632, 264635, 264637, 264638, 264639, 18108365, 22278000, 22279002, 264555, 264566, 264488
1785	95357475 (3569, 3570)	Novel Protein sim. GBank gi 4589552(dbj)BAA76788.1] - (AB023171) KIAA0954 protein [Homo sapiens]	UNCLASSIFIED	65274572, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 264905, 264906, 264908, 66712502, 56182435, 264511, 265007, 60433356, 55811150, 264683, 264369, 264687, 52644229, 21908767, 52644150, 33637023, 65274620, 33657182, 65274781, 35695855, 264555, 65274727, 22279002
1786	85296485 (3571, 3572)	Novel Protein sim. GBank gi 117788]sp P26770(CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)	UNCLASSIFIED	264908, 35696423, 264636
1787	87434784 (3573, 3574)	Novel Protein sim. GBank gi 387717]emb CAA90338.1] - (Z50028) cDNA EST yk321n8.5 comes from this gene; cDNA EST EMBL:D68896 comes from this gene; cDNA EST yk395f9.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264905, 264908, 264909, 264595, 264784, 264786, 264692, 60431528, 264629, 264636, 264564, 264568
1788	91228779 (3575, 3576)		UNCLASSIFIED	264488, 83373044
1789	88094529 (3577, 3578)	Novel Protein sim. GBank gi 2088669 (AF003130) - F55A12.9 gene product [Caenorhabditis elegans]	UNCLASSIFIED	264488, 29331828, 264909, 18108351, 264288, 265021, 264555, 264636
1790	82489734 (3579, 3580)			35695052, 264905, 264908, 264907, 264908, 264909, 265008, 264910, 264758, 265011, 265019, 264764, 264768, 264769, 264628, 264635

1781	95187259 (3581, 3582)	Novel Protein sim. GBank gi 2114321 dbj BA420037.1  - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00047) - glycoprotein Immunoglobulin domain	264488, 264686, 264687, 264768, 18108394, 264769, 18108397, 264259, 264691, 264692, 33657023, 264693, 264509, 264905, 264906, 264628, 264907, 264629, 264908, 264909, 264510, 265006, 264511, 265008, 264630, 265009, 264631, 264910, 264632, 264634, 264635, 264555, 264636, 264592, 264637, 264593, 264638, 18108381, 264639, 264758, 265010, 265011, 264602, 22279000, 264604, 264760, 264564, 264681, 264762, 264565, 264763, 264683, 264566, 264764, 264288, 264684, 264567, 18108354, 18108391, 264685, 264766
1792	87792680 (3583, 3584)	Novel Protein sim. GBank gi 4337106 gb AAD18082.1  - (AF129756) BAT4 [Homo sapiens]	Contains protein domain (PF01585) - UNCLASSIFIED G-patch domain	22278997, 264259, 264508, 265007, 33657402, 87188559, 264369, 33657023, 35695855, 20281071, 264559, 18108387, 87168518
1793	95337877 (3585, 3586)	Novel Protein sim. GBank gi 5579331 gb AAD45504.1 AF145732 - (AF145732) endoplasmic reticulum alpha-mannosidase I [Homo sapiens]	Contains protein domain (PF01532) - ATPase_associated Glycosyl hydrolase family 47	65274572, 22278995, 22278996, 22278997, 22278999, 264093, 264259, 29331824, 66714117, 60432289, 29331827, 29331828, 264103, 264105, 29331830, 265007, 264910, 265009, 60170831, 60433356, 21906754, 265010, 265017, 265019, 264681, 264682, 264288, 52644229, 21906765, 21908786, 21906767, 21906768, 21906769, 265020, 265021, 265022, 60170615, 52644150, 33657023, 33657109, 18108370, 18108374, 65274791, 20281071, 60432113, 22279000, 264482, 264564
1794	87759806 (3587, 3588)	Novel Protein sim. GBank gi 4914604 emb CAB43677.1  - (AL050369) hypothetical protein [Homo sapiens]	Contains protein domain (PF01798) - UNCLASSIFIED Putative snoRNA binding domain	18108394, 22278995, 22278999, 264259, 29331822, 29331824, 29331825, 29146498, 29146499, 264508, 264905, 52644045, 264112, 265006, 265008, 264910, 60433356, 264757, 55812038, 87168474, 265011, 265017, 18108351, 264763, 264448, 264683, 264369, 21906765, 21908766, 21908767, 21908769, 29148784, 35695917, 60170615, 33657023, 264629, 18108374, 18108376, 35696423, 35695855, 264556, 264557, 264638, 264558, 18108385, 264584
1795	79747856 (3589, 3590)		UNCLASSIFIED	264632, 264635, 264636, 264595, 264596, 264907, 264566, 264909
1796	86599486 (3591, 3592)	Novel Protein sim. GBank gi 585084 sp Q07803 IEFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)	glycoprotein	264488, 264907, 264909, 264594, 264595, 264766, 264687, 21908765, 21906767, 264628, 264630, 264559

1787	91223218 (3593, 3594)	Novel Protein sim. GBank g11842111 (U87586) - decoy (Arabidopsis thaliana)		ribosomalprol	22278996, 22278997, 22278998, 22278999, 29331822, 264910, 60170831, 21906754, 52644229, 21906785, 21906768, 21906769, 35695917, 265022, 52644150, 264691, 33657023, 263967, 33657109, 22279000
1788	91221276 (3595, 3596)	Novel Protein sim. GBank g12832906(dijlBAA24608.1) - (D89340) dipeptidyl peptidase III (Rattus norvegicus)		peptidase	22278994, 56994075, 22278997, 22278998, 22278999, 264259, 29331826, 60432289, 29331828, 33656970, 265008, 60432229, 264757, 60433438, 21906754, 33657084, 87168559, 265017, 18108351, 264682, 264448, 264288, 21906765, 21906788, 21906787, 21906768, 21906789, 35695917, 265020, 265021, 33657023, 33657182, 27486281, 27486285, 33657349, 263973, 18108374, 55811576, 35695855, 18108385, 87168518, 22279000, 264486
1789	86321713 (3597, 3598)	Novel Protein sim. GBank g15689541(dijlBAA83054.1) - (AB029025) KIAA1102 protein [Homo sapiens]		eph	264908, 21906754, 21906787, 21906769, 265020, 33657023, 264692, 264693, 264404, 22279000
1800	87080116 (3599, 3600)	Novel Protein sim. GBank g14680679(gb AAD27729.1 AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	284691, 264556, 264566
1801	95060723 (3601, 3602)	Novel Protein sim. GBank g1134920(sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			52644045, 265007, 264632
1802	87771012 (3603, 3604)	Novel Protein sim. GBank g1134920(sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			35686286, 66714117, 264508, 264509, 56182435, 264512, 18108351, 264698, 55811957, 264692, 55811576, 35695855, 264486
1803	95060725 (3605, 3606)	Novel Protein sim. GBank g14680679(gb AAD27729.1 AF132954) CGI-20 protein [Homo sapiens]			264686, 264488, 264687, 264489, 264768, 264788, 264689, 21906769, 35696286, 35695917, 264259, 264691, 264692, 264693, 20281099, 18108364, 35696052, 264508, 264509, 264905, 264908, 18108370, 264628, 264907, 66712502, 264908, 264909, 18108374, 18108376, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264631, 264632, 264634, 264635, 264591, 264636, 264637, 264592, 264638, 264593, 264639, 264594, 83373044, 264758, 264586, 18108385, 18108387, 265011, 264760, 264563, 18108351, 264762, 264564, 264448, 264585, 264763, 264683, 264764, 264566, 264288, 264486, 264567, 264765, 264766



1804	87770203 (3607, 3608)	Novel Protein sim. GBank gij3879914jembj CA498538.1 - (274043) predicted using GeneFinder; cDNA EST EMBL.C13850 comes from this gene; cDNA EST EMBL.C11575 comes from this gene; cDNA EST yk34314.5 comes from this gene [Caenorhabditis elegans]			52646365, 22278997, 22278999, 264905, 264908, 264909, 264910, 21906754, 264766, 21906765, 21906788, 35695917, 265020, 265022, 264691, 264637, 264639, 22279000, 264564, 264566
1805	95330375 (3609, 3610)	Novel Protein sim. GBank gij5453644jref NP_008461.1 pEBBP - estrogen-responsive B box protein			29331824, 29331825, 29331826, 29331827, 29331828, 87168559, 264288, 264687, 52644229, 35698423, 264636, 60432113
1806	94133782 (3611, 3612)	Novel Protein sim. GBank gij4589676jdbj BAA76857.1 - (AB023230) KIAA1013 protein [Homo sapiens]	struct		264094, 264105, 264908, 35698423, 265006, 265007, 265008, 264555, 264592, 265011, 265018, 264369
1807	86943032 (3613, 3614)				29331824, 264908, 264910, 33657023, 263978
1808	87642711 (3615, 3616)	Novel Protein sim. GBank gij4884079jembj CAB43235.1 - (AL050008) hypothetical protein [Homo sapiens]	UNCLASSIFIED		264488, 35698286, 66714117, 35696052, 66712502, 264592, 60433438, 52644296, 265010, 264683, 264369, 264689, 55811957, 35695917, 33657109, 35695763, 55810764, 18108379, 35696423, 35695855, 55812323, 264563, 264564, 264487
1809	95321468 (3617, 3618)	Novel Protein sim. GBank gij1918927 (U87965) - putative G protein [Mus musculus]	UNCLASSIFIED		264594, 55811150, 264686, 29148629, 29148784, 264690, 264629, 18108374, 264556, 264557, 264558
1810	88086316 (3619, 3620)	Novel Protein sim. GBank gij1352944jsp P47179 YJP_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR	UNCLASSIFIED		264488, 35696052, 264905, 264906, 264907, 264908, 264909, 264511, 265009, 264910, 264592, 264593, 264594, 33657402, 264757, 264595, 264758, 264596, 264759, 264600, 264601, 264762, 264683, 264784, 264288, 264684, 264768, 264767, 264688, 264768, 264687, 264769, 264689, 265021, 264690, 264691, 264693, 264628, 264629, 18108374, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264563, 264566, 264486, 264567
1811	88086272 (3621, 3622)	Novel Protein sim. GBank gij2134984jpi j137275 - death-associated protein kinase (EC 2.7.1.-) - human	kinase Ank repeat	Contains protein domain (PF00023) - Ank repeat	264488, 264259, 264508, 264509, 264905, 264906, 264907, 56182435, 264511, 264512, 264910, 264758, 265011, 264600, 264604, 18108354, 264768, 264686, 264769, 264534, 60170815, 33657023, 264629, 264631, 264639, 264563, 264482, 264483
1812	79245772 (3623, 3624)				29331822, 29331824, 265018, 18108351, 21906769

1813	88090972 (3625, 3626)	Novel Protein sim. GBank gi15051638 gb AAD38326.1 AF07372 - (AF07372) EH domain-binding mitotic phosphoprotein [Homo sapiens]	Contains protein domain (PF01417) - ENTH domain	glucoamylase	56182575, 264259, 29331824, 66714117, 29331828, 35696052, 264509, 264905, 264908, 264907, 264908, 66712502, 264909, 265007, 264910, 264591, 264593, 55812038, 265011, 265018, 264780, 264682, 264764, 264683, 264369, 264788, 264769, 264769, 21906768, 21908768, 264691, 264693, 18108374, 35695855, 264634, 264635, 264637, 264638, 264558, 22279000, 22279002, 264558
1814	88176047 (3627, 3628)	Novel Protein sim. GBank gi13643608 (AC005395) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 35696288, 22278998, 264092, 264094, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264107, 52844045, 56182435, 265009, 60432229, 60433356, 87168474, 87168559, 264369, 264288, 21906765, 35695917, 265021, 285022, 33657023, 33657109, 18108374, 35696423, 264638, 56526486, 264482
1815	85296473 (3629, 3630)	Novel Protein sim. GBank gi117788 sp P26770 CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)		struct	22278999, 264508, 264509, 264907, 264908, 264910, 265011, 264760, 264766, 264634, 264636
1816	83738845 (3631, 3632)	Novel Protein sim. GBank gi1176623 sp P41846 Y096_CAEEL - HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III		UNCLASSIFIED	18108394, 18108397, 264508, 264907, 264908, 264909, 265009, 264591, 265011, 265017, 264687, 264689, 265022, 264691, 18108362, 18108368, 18108370, 18108374, 18108379, 264635, 264557, 264584, 264587
1817	88095268 (3633, 3634)	Novel Protein sim. GBank gi13766377 emb CAA2142g  - (AL031907) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	histone	264488, 22278997, 22278999, 60432049, 29331822, 29331824, 60432289, 52844045, 60170831, 265017, 265018, 265019, 18108351, 264682, 52844228, 21906765, 21906767, 21906768, 52844150, 33657023, 33657109, 27466262, 18108370, 18108374, 60170394, 56182323, 22279002
1818	85806775 (3635, 3636)	Novel Protein sim. GBank gi13879121 emb CAA94370  - (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:TO1923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	transcript factor	35086286, 60433356, 264758, 264369, 264686, 21908789, 264693, 264632
1819	87759572 (3637, 3638)	Novel Protein sim. GBank gi15031865 ref NP_005771.1 pLHFP - lipoma HMGIC fusion partner		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331826, 264908, 265007, 265008, 265009, 60432228, 265017, 265018, 265019, 264448, 264288, 21908788, 21908789, 265020, 18108381, 18108384, 22279000, 22279002, 264587

1820	87769455 (3639, 3640)				284905, 284907, 284594
1821	80431510 (3641, 3642)				284907, 284768, 263978
1822	91221523 (3643, 3644)	Novel Protein sim. GBank gij4884130[embjCAB43272.1] - (AL050101) hypothetical protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 35686052, 29331828, 284908, 29331830, 60170831, 264591, 264593, 60433356, 264598, 265017, 265019, 18108351, 264763, 284683, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 18108364, 18108370, 35695855, 22279000, 22279002
1823	85522330 (3645, 3646)			UNCLASSIFIED	264488, 264259, 264511, 264288, 264768, 284693, 35698423, 284634, 18108385, 264486
1824	86612025 (3647, 3648)	Novel Protein sim. GBank gij477072[pirjA48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	284907, 264908, 264909, 284511, 264631, 284634, 264635, 284637, 284638, 284639, 264758, 264588
1825	87430125 (3649, 3650)	Novel Protein sim. GBank gij3036803[embjCAA18493] - (AL022373) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60432049, 264910, 264487
1826	91723612 (3651, 3652)	Novel Protein sim. GBank gij4680685[gjAAD27732.1]AF13295 - (AF132957) CGI-23 protein [Homo sapiens]		ATPase-associated	52644507, 52645156, 52646842, 22278994, 22278995, 56994075, 264259, 60432049, 52645080, 35686052, 66712502, 52644045, 265008, 265009, 60432229, 60433356, 60433438, 52646317, 52644298, 265011, 87168559, 264448, 284288, 284369, 264688, 52644229, 284689, 21906765, 21906768, 265020, 60170615, 52644150, 33657023, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 83373044, 87168518, 264404, 22279002
1827	81847212 (3653, 3654)				264758

1828	95074017 (3655, 3656)	Novel Protein sim. GBank gi14503571[ref NP_001419.1 pEN01 - endolase 1, (alpha)]	Contains protein domain (PF00113) - Enolase	oncogene	264488, 52846842, 58182575, 22278998, 3598288, 22278997, 22278998, 264091, 284093, 60432049, 284259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 284508, 264807, 66712502, 52844045, 56182435, 265006, 284511, 264512, 265007, 265008, 265009, 60170831, 60432229, 264593, 60433358, 60433438, 264758, 33108954, 21906754, 87168474, 285010, 265011, 87168558, 265017, 285019, 264761, 264782, 264448, 264764, 264683, 284288, 284389, 18108355, 264768, 18108357, 18108358, 264688, 264769, 284689, 21906768, 21906769, 35695917, 265021, 60170615, 33857023, 33857349, 283972, 55811578, 35695855, 284635, 264555, 264558, 264638, 264557, 87168518, 22278000, 22279002, 264563, 284482, 264565, 264484, 264567
1829	80187720 (3657, 3658)				264508, 264634, 264509, 264482, 29331827, 264908, 265009, 264910
1830	94312942 (3659, 3660)	Novel Protein sim. GBank gi12245532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		nuclease	52645156, 22278994, 22278995, 35698286, 22278996, 22278997, 22278998, 22278999, 29331822, 29331825, 35696052, 52846317, 52844296, 87168558, 265019, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 33857023, 52845129, 33857109, 33857182, 27486261, 27486262, 35695763, 283974, 35698423, 35695855, 52844332
1831	94138063 (3681, 3682)			UNCLASSIFIED	29331824, 35696052, 29331830, 264595, 284758, 265010, 265019, 265022, 264693, 65274791 284602
1832	84521663 (3683, 3684)	Novel Protein sim. GBank gi1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....			

1833	95314184 (3665, 3666)	Novel Protein sim. GBank gi 5174413 ref NP_006026.1 pCDC4 - CDC42-binding protein kinase beta (DMPK-like)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278994, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 35696052, 29146499, 264508, 264509, 264908, 264907, 68712502, 264908, 52644045, 264909, 264512, 265008, 264591, 264593, 60433358, 21908754, 33657084, 265011, 265017, 264604, 265018, 265019, 264681, 18108351, 264683, 264288, 264685, 264766, 264687, 21908765, 21908766, 21908767, 21908768, 21908769, 29148629, 265020, 265021, 264690, 264692, 33657023, 65274620, 33657182, 27486284, 33657349, 65274791, 264634, 264635, 264556, 264557, 264558, 264559, 18108385, 58526486, 87168518, 60432113, 22279000, 22279002, 264563
1834	80562790 (3667, 3668)				264259, 264907, 264689, 22279000, 22279002
1835	94135718 (3669, 3670)			UNCLASSIFIED	22278998, 29331822, 29331826, 87168474, 264603, 21908768, 263976, 35695855, 83373044
1836	87348450 (3671, 3672)	Novel Protein sim. GBank gi 4759286 ref NP_004268.1 pUCP4 - uncoupling protein 4	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	29331825, 264908, 265019, 264764, 264686, 21906765, 264635
1837	94234297 (3673, 3674)	Novel Protein sim. GBank gi 3334400 sp Q24574 UBPE, DROME - UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	22278995, 29146499, 265006, 265008, 265009, 265010, 264683, 21906765, 29148627, 29148629, 265020, 265021, 265022, 65274620, 18108370, 18108374, 264556, 18108385
1838	94324369 (3675, 3676)	Novel Protein sim. GBank gi 1362599 ref A56154 - Abi substrate ena (enabled) - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00568) - WH1 domain		29331822, 265017, 264760, 265020, 83373044
1839	87456508 (3677, 3678)	Novel Protein sim. GBank gi 2117310 emb CAB09116.1  - (Z95620) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	60433438, 264601, 21806765, 21908766, 265021, 33657109, 264556
1840	87391708 (3679, 3680)	Novel Protein sim. GBank gi 127560 sp P23249 MOV10, MOUSE - PROTEIN MOV-10		UNCLASSIFIED	264693
1841	85818445 (3681, 3682)	Novel Protein sim. GBank gi 4572464 gb AAD23834.1 AF12365 - (AF123653) FEZ1 [Homo sapiens]			56182575, 29331824, 29331826, 60433356, 264764, 264288, 33657023, 263967, 18108370, 18108374, 264631, 264555, 264556, 264639

1842	80892845 (3683, 3684)	Novel Protein sim. GBank gi 1326268 (U58728) - C54H2.1 gene product [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 29331822, 29331824, 29331825, 66714117, 29331826, 29331827, 284907, 284908, 52844045, 56182435, 264510, 265008, 285007, 265009, 284910, 60433356, 284757, 60433438, 55812038, 265017, 18108354, 264686, 284769, 33657023, 264693, 18108384, 33657109, 18108368, 264628, 55810764, 56182323, 18108384, 264583, 264584
1843	95292892 (3685, 3686)			UNCLASSIFIED	284488, 56182435, 264769, 29331826, 29331828, 264511, 265008, 265007, 264910, 264631, 264509, 264690, 264636, 264584, 284691, 60432229, 60432048, 264259, 284629, 33657023, 264488, 284908, 264587, 284595, 264766
1844	67444764 (3687, 3688)	Novel Protein sim. GBank gi 2496887 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	264908, 265022, 33657023, 87168518, 22279002
1845	95096673 (3689, 3690)	Novel Protein sim. GBank gi 1175494 sp Q08819 YAC5_SCHPO - HYPOTHETICAL 45.0 KD PROTEIN C16C9.05 IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger	transcriptfactor	264259, 29331824, 284907, 284908, 66712502, 264510, 265007, 265008, 55812038, 265018, 21908765, 52844150, 33657109, 264555, 264556, 264557, 56182323, 18108382, 83373044, 18108385, 284584
1846	84287872 (3691, 3692)	Novel Protein sim. GBank gi 3881080 emb CAA21739  (AL032657) similar to EGF-like domain; cDNA EST yk298a12.3 comes from this gene; cDNA EST EMBL-D35398 comes from this gene; cDNA EST yk331he.5 comes from this gene; cDNA EST yk299a12.5 comes from this gene; cDNA EST yk467g8.5 c...	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	284905, 284908
1847	87821487 (3693, 3694)	Novel Protein sim. GBank gi 5059323 gb AAD38967.1 AF151522 - (AF151522) hairy and enhancer of split related-1 [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	22278997, 264259, 29331824, 284909, 18108351, 263974, 22279002
1848	86789360 (3695, 3696)	Novel Protein sim. GBank gi 5701854 emb CAB52191.1  - (AJ245417) G5b protein [Homo sapiens]	Im7		29331825, 29331826, 29331827, 265017, 284693, 264288, 264786, 264788, 21906787, 21906788, 264692, 22279002
1849	84287874 (3697, 3698)	Novel Protein sim. GBank gi 4503665 ref NP_001989.1 pFBLN - fibulin 2 precursor	Contains protein domain (PF00008) - EGF-like domain	ATPase_associated	56182575, 265018
1850	86689650 (3699, 3700)	Novel Protein sim. GBank gi 4589582 db BAA76813.1  - (AB023186) KIAA0969 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain		60432049, 264808
1851	95410789 (3701, 3702)	Novel Protein sim. GBank gi 220637 db BAA01477  - (D10627) zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - dna_rna_bind Zinc finger, C2H2 type	dna_rna_bind	29331824, 35696052, 264910, 60433438, 284688, 35695917, 265020, 52644150, 65274620, 52644332

1852	95413170 (3703, 3704)	Novel Protein sim. GBank gi 5174629 ref NP_006090.1 pPIAS - protein inhibitor of activated STAT3		UNCLASSIFIED	56182575, 35696286, 22278996, 22278997, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 35696052, 52844045, 285007, 264910, 60432229, 60433356, 60433438, 55812038, 65274444, 265018, 285019, 18108351, 284448, 264686, 264687, 21906765, 21906767, 21906769, 265021, 265022, 52644150, 264693, 33657109, 18108370, 18108374, 55811576, 35695855, 56182323, 60432113, 22279002, 264553, 264687, 264768, 52644507, 264769, 21906765, 21906767, 21906768, 22278995, 56994075, 22278999, 52844150, 264259, 264692, 29331822, 29331824, 52845129, 29331827, 33656970, 33657349, 35695763, 264508, 264906, 264628, 264907, 264629, 264509, 35696423, 35695855, 264510, 265006, 264511, 264512, 264630, 265009, 264631, 264910, 264634, 264635, 264637, 264593, 264638, 264639, 33657402, 18108385, 52646317, 52644296, 87168518, 87168559, 264602, 265017, 22279000, 265018, 264760, 264762, 264682, 264448, 264764, 264684, 264567, 264288, 264369, 264766, 264592
1853	91222267 (3705, 3706)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	
1854	86038152 (3707, 3708)	Novel Protein sim. GBank gi 2072964 (U93569) - putative p150 [Homo sapiens]		nuclease	
1855	91221459 (3709, 3710)	Novel Protein sim. GBank gi 4539520 emb CA839994.1  - (AL035424) dA22D12.1 (novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogeneous set of other types of proteins) [Homo sapiens]	Contains protein domain (PF01344) - nucl_recpt Kelch motif		18108392, 52646385, 65274572, 56182575, 22278994, 56994075, 22278996, 35696286, 22278998, 264259, 60432049, 264908, 264510, 265007, 265008, 265009, 264595, 21906754, 87168474, 265011, 87168559, 264681, 264288, 264768, 18108359, 21906764, 21906768, 29148627, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108372, 18108374, 18108376, 35696423, 264631, 264636, 18108381, 264482
1856	94231871 (3711, 3712)	Novel Protein sim. GBank gi 3954978 emb CAA06945  - (AJ008278) acetylglucosaminyltransferase-like protein [Mus musculus]		UNCLASSIFIED	56994075, 264259, 29331828, 264511, 264910, 264758, 264693, 264637, 18108381, 83373044
1857	94324455 (3713, 3714)	Novel Protein sim. GBank gi 4322670 gb AAD16120  - (AF094508) dentin phosphoryn [Homo sapiens]		ATPase-associated	22278999, 264259, 264906, 60170831, 264448, 264686, 265020, 265022, 33657109, 60170394, 83373044

1858	87628311 (3715, 3716)	Novel Protein sim. GBank gi 4981903 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomal prot	284757
1859	84407464 (3717, 3718)	Novel Protein sim. GBank gi 4240317 dbj BAAY4937.1  - (AB020721) KIAA0914 protein [Homo sapiens]			22278986, 28331824, 265007, 33109954, 265019, 264369, 21908788, 26148784, 27488261, 52844332, 22279002 265019
1860	17829308 (3719, 3720)	Novel Protein sim. GBank gi 4009522 (AF099731) - connexin 31.1 [Homo sapiens]			
1861	88086370 (3721, 3722)	Novel Protein sim. GBank gi 2143637 pir j 8-505 - calcium- dependent actin-binding protein - rat	Contains protein domain (PF00285) - Citrate synthase		264887, 284259, 28331822, 28331824, 29331825, 265007, 265009, 264591, 33109954, 265010, 265019, 264369, 264288, 284886, 264691, 284693, 27486284, 18108370, 18108374, 263977, 55811578, 56182323, 264639, 22279000, 22279002, 264482
1862	67372923 (3723, 3724)	Novel Protein sim. GBank gi 125493 sp P07313 KMLC_RABIT - MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	35898286, 264259, 87188474, 264369, 21908766, 284558, 264563
1863	85775037 (3725, 3726)	Novel Protein sim. GBank gi 3820909 emb CA00299  - (AJ010642) Dot protein [Drosophila melanogaster]		UNCLASSIFIED	284601, 284766, 29148627, 29148629, 264692, 284629, 264635
1864	85547832 (3727, 3728)	Novel Protein sim. GBank gi 4322263 gb AAD15985  - (AF077738) metalloproteinase CPX-1 [Mus musculus]	Contains protein domain (PF00754) - F5/8 type C domain	synthase	22278989, 264259, 264907, 265018, 18108370, 284634, 284635, 264555, 264556, 284638, 18108387
1865	87740827 (3729, 3730)	Novel Protein sim. GBank gi 2485727 sp Q93073 Y256_HUMAN - HYPOTHETICAL PROTEIN KIAA0256			22278989, 264490, 29331822, 26714117, 68712502, 265006, 265007, 265008, 265009, 264591, 60433438, 285010, 265019, 264760, 284448, 284766, 28148627, 29148628, 265020, 265022, 18108385, 60432113
1866	87266816 (3731, 3732)	Novel Protein sim. GBank gi 5262617 emb CAB45748.1  - (AL080157) hypothetical protein [Homo sapiens]		kinase	18108374, 284769, 18108377, 21908765, 21908766, 35698423, 56182575, 21908769, 29148629, 35698286, 35695917, 265021, 264510, 264511, 264512, 264534, 264535, 60170831, 52644150, 284555, 284891, 264259, 264556, 264692, 284557, 33657023, 60433356, 28331822, 284559, 284595, 29331824, 18108385, 21908754, 33657182, 29331827, 35696052, 33656970, 87168518, 265017, 60431602, 22279000, 264508, 264509, 18108351, 284907, 264682, 264567, 18108372, 284765, 284486
1867	84579159 (3733, 3734)	Novel Protein sim. GBank gi 3859930 (AF078096) - forkhead/winged helix-like transcription factor 7 [Homo sapiens]		UNCLASSIFIED	2644094



1868	87357459 (3735, 3736)	Novel Protein sim. GBank gij3881525[embjCAA93884] - (Z70038) cDNA EST EMBL.D32579 comes from this gene; cDNA EST EMBL.D35254 comes from this gene; cDNA EST yk224b3.5 comes from this gene; cDNA EST yk35710.5 comes from this gene [Caenorhabditis elegans]		nuclease	264489, 22278997, 22278999, 29331825, 29331826, 265008, 265009, 33657402, 87188474, 18108351, 21906765, 21906768, 21906769, 265020, 265021, 60170615, 27486264, 264628, 18108374, 264631, 18108385, 87168518, 22279000, 22279002, 264568, 264567
1869	86977292 (3737, 3738)	Novel Protein sim. GBank gij4826772[refNP_004961.1]pIGFA - insulin-like growth factor binding protein, acid labile subunit	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264508, 264509, 264906, 264908, 264909, 264910, 264991, 264600, 18108351, 284883, 264766, 264769, 35695855, 284834, 264558, 264839, 18108385, 264583, 284486
1870	95349488 (3739, 3740)	Novel Protein sim. GBank gij1869859[embjCAB06722] - (Z80099) very large legume protein [human herpesvirus 2]		UNCLASSIFIED	29331824, 60424269, 265007, 265008, 21906754, 265017, 265018, 265019, 264288, 264766, 264886, 264688, 21906768, 21906769, 35695917, 60170615, 264692, 18108368, 35695763, 35696423, 65274791, 264638, 264639, 56526486
1871	80234464 (3741, 3742)			UNCLASSIFIED	264509, 264905, 264595, 264768, 264635, 264636, 264563, 284486
1872	80233355 (3743, 3744)	Novel Protein sim. GBank gij2460316 (AF022147) - uterus-ovary specific putative transmembrane protein [Rattus norvegicus]		protease	264510, 264594, 264565
1873	80213890 (3745, 3746)				264509, 264512, 265009, 265011, 18108351, 264887, 264691, 18108370, 18108374, 264635
1874	95351136 (3747, 3748)		Contains protein domain (PF00293) - Bacterial multi protein	UNCLASSIFIED	264488, 35695917, 264259, 264905, 264907, 264908, 264909, 263978, 264511, 264635, 264636, 264637, 264638, 33657402, 264558, 18108385, 264600, 264604, 264764, 264587, 264766
1875	87330516 (3749, 3750)	Novel Protein sim. GBank gij4589520[dbjBAA76782.1] - (AB023155) KIAA0938 protein [Homo sapiens]		UNCLASSIFIED	35696286, 264828, 264592, 264557, 264558
1876	87112950 (3751, 3752)	Novel Protein sim. GBank gij263810[bbj122920] - collagen alpha chain [Riftia pachyptila=tube worms, Peptide, 1027 aa]		UNCLASSIFIED	264359, 29331822, 60432289, 264908, 264909, 264604, 264764, 264288, 264769, 18108376, 264556, 264558, 264559, 18108385
1877	87315208 (3753, 3754)	Novel Protein sim. GBank gij3983356[gbjAAC83924.1] - (AF102545) riboflavin binding protein precursor [Scaphiopus couchii]		UNCLASSIFIED	264767, 264686, 264768, 263978, 264693, 264839, 265010, 264563, 264905, 264906, 264907

1876	95351086 (3755, 3756)	Novel Protein sim. GBank gij4510345jgb AAD21434.1  - (ACO08921) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264569, 264488, 35898286, 56994076, 264259, 28331822, 29331824, 29331825, 35698052, 29331828, 29148498, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 285009, 264910, 33657402, 264594, 264758, 55812038, 265011, 264602, 264760, 18108351, 264762, 264681, 264682, 264764, 264369, 284288, 264766, 264687, 264788, 264789, 21906766, 35695917, 265021, 60170815, 33657023, 264692, 264693, 33657109, 27486265, 284628, 18108370, 264629, 18108374, 35696423, 284634, 264635, 284555, 264638, 264639, 83373044, 18108385, 56526486, 87188518, 264563, 264564, 264566, 264488, 264567, 264905, 264907, 264908, 265007, 264565, 264566
1879	95310883 (3757, 3758)	Novel Protein sim. GBank gij4929643jgb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	
1880	91012978 (3759, 3760)	Novel Protein sim. GBank gij1550785jemb CAA69283  - (Y08026) immune associated protein 38 [Mus musculus]		UNCLASSIFIED	264766, 264691, 264692, 83373044
1881	80214949 (3761, 3762)	Novel Protein sim. GBank gij93144 pir JB40505 - hypothetical protein - suid herpesvirus 1 (strain Indiana-Funkhouser or Becker)		UNCLASSIFIED	264509, 264905, 264908, 264909, 264910, 264762, 264687, 33657023, 264632
1882	86582450 (3763, 3764)	Novel Protein sim. GBank gij2384956 (AF022985) - No definition line found [Caenorhabditis elegans]			264908, 21906766, 18108370, 263974, 87188518
1883	84216817 (3765, 3766)	Novel Protein sim. GBank gij1351218 sp P47226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	264908, 264910, 87168559, 21906766, 264638

1884	95310885 (3767, 3789)	Novel Protein sim. GBank gi 4929643 gb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108394, 58181686, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 58182435, 264510, 264511, 265007, 264512, 265009, 264910, 264592, 264593, 33657402, 55812038, 264758, 55811388, 265010, 265011, 87168559, 264600, 265017, 264604, 265019, 264603, 264760, 55811150, 264761, 264682, 264763, 264683, 264764, 264288, 264389, 264766, 264686, 264768, 264769, 29148784, 35695917, 264690, 264691, 33657023, 264692, 264693, 33657109, 18108370, 264628, 60431528, 264629, 263973, 18108374, 55810764, 55811576, 35696423, 35695855, 264631, 264634, 60431850, 264637, 264638, 58182323, 264639, 18108382, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264565, 264566, 264488, 264567
1885	87644280 (3769, 3770)	Novel Protein sim. GBank gi 2507155 sp P37370 VRP1_YEAST - VERPROLIN		UNCLASSIFIED	58182575, 284259, 264905, 264909, 265008, 264596, 264766, 265020, 264628, 60431528, 264634, 58528486, 264080, 264563
1886	86674062 (3771, 3772)	Novel Protein sim. GBank gi 2854158 gb AAC02577.1  - (AF045641) No definition line found [Caenorhabditis elegans]			22278998, 22278999, 60432049, 264910, 265018, 264766, 21906768, 29148628, 264690, 264693, 264628, 264555, 264486
1887	94139139 (3773, 3774)	Novel Protein sim. GBank gi 5174421 re NP_008023.1 PCPNE - copine VI (neuronal)	Contains protein domain (PF00168) - C2 domain	ATPase-associated	29331822, 29331824, 29331825, 29331826, 29331827, 264906, 265007, 264681, 264768, 29148627, 264693, 18108364, 35695423, 65274791, 35695855, 264632, 58182323, 264639, 264563
1888	87822804 (3775, 3776)	Novel Protein sim. GBank gi 3319931 emb CAB10841  - (Z98046) dJ1409.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens]	Contains protein domain (PF01454) - MAGE family		263978
1889	91255783 (3777, 3778)	Novel Protein sim. GBank gi 1083308 pir J1A56539 - enhancer-trap-locus-1 protein - mouse (fragment)	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	264906, 55812038, 264758, 265010, 265018, 265019, 18108351, 264288, 21908765, 21906768, 21906769, 265021, 33657023, 33657109, 58182323, 83373044, 18108385, 22279000, 22279002
1890	87626705 (3779, 3780)	Novel Protein sim. GBank gi 4240185 db BAA74876.1  - (AB020660) KIAA0853 protein [Homo sapiens]		UNCLASSIFIED	18108398, 29147620, 264907, 265009, 264600, 265018, 18108351, 264288, 264689, 21906765, 21906768, 21906769, 264691, 264692, 264693, 264628, 18108370, 264836, 264558, 264404

1891	87013895 (3781, 3782)			UNCLASSIFIED	264886, 264768, 264887, 264692, 264693, 29331822, 29331824, 264508, 264905, 264906, 18108370, 264628, 264907, 264908, 264909, 18108379, 265007, 265008, 264910, 264632, 264591, 264639, 264596, 18108384, 265010, 265011, 264601, 264605, 264563, 264369
1892	87642825 (3783, 3784)	Novel Protein sim. GBank gi 5689535 dbj BAA03051.1  - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - putative GTP-ase activating protein for Arf	struct	22278995, 264508, 87168559, 18108351, 264448, 264682, 265020, 264689, 18108374, 22279000
1893	88533826 (3785, 3786)			laminin	264569, 65274572, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331828, 264906, 265008, 265008, 265009, 264592, 265018, 264681, 264448, 264683, 18108354, 264369, 264884, 264685, 264768, 264687, 264689, 21906768, 265020, 265022, 60170815, 52644150, 264690, 264691, 264692, 33657023, 264693, 33857109, 264628, 18108374, 35695855, 264630, 264632, 264634, 264557, 264558, 60170394, 18108381, 18108385, 22279000
1894	86989120 (3787, 3788)				264508, 264905, 264908, 264907, 264594, 264684, 264690, 264692, 264830, 264635, 264636, 264639, 264583
1895	87631891 (3789, 3790)	Novel Protein sim. GBank gi 5262574 emb CAB45729.1  - (AL080133) hypothetical protein [Homo sapiens]	Contains protein domain (PF00435) - Spectrin repeat		56182575, 264259, 60432289, 29331826, 264107, 264905, 264908, 264910, 60170831, 264758, 265010, 265018, 264448, 264286, 264768, 33657109, 264828, 55810784, 18108379, 264634, 56182323, 56526488
1896	85673555 (3791, 3792)		Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	264907, 265008, 264682, 264686, 21906769, 264629, 264631, 264634, 264555, 264259
1897	80585589 (3793, 3794)	Novel Protein sim. GBank gi 728836 sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		cadherin	
1898	87617637 (3795, 3796)	Novel Protein sim. GBank gi 127560 sp P23249 MV10_MOUSE - PROTEIN MOV-10		helicase	22278996, 22278998, 22278999, 29331824, 29331825, 60432289, 29331827, 35696052, 29331828, 265008, 265019, 264681, 264682, 264448, 264369, 52644229, 21906765, 21906766, 21906768, 21906769, 60170615, 55810784, 22279000
1899	86673097 (3797, 3798)	Novel Protein sim. GBank gi 2909819 (AF031548) - erythrocyte membrane glycoprotein Rh50 [Homo sapiens]	Contains protein domain (PF00609) - Ammonium Transporter Family	glycoprotein	264259, 264508, 264909, 60432229, 264769, 21906765, 21906769
1900	87641858 (3799, 3800)	Novel Protein sim. GBank gi 4102881 (AF017250) - vitellogenin precursor [Oreochromis aureus]		UNCLASSIFIED	264683

1801	95196647 (3801, 3802)	Novel Protein sim. GBank gij585959j[P38378][S61A_RAT PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT	Contains protein domain (PF00242) - DNA polymerase (viral) N-terminal domain	transport	264488, 52644507, 52645156, 18108396, 52646365, 52646842, 18108397, 56182575, 22278994, 22278995, 56994075, 35696286, 22278997, 22278998, 264490, 60432049, 264259, 29331822, 52645080, 29331824, 29331825, 68714117, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 29146498, 264906, 264907, 29331830, 264908, 52644045, 264909, 264112, 265006, 264512, 265008, 264910, 265009, 60170831, 60432229, 60433356, 33657402, 60433438, 55812038, 264758, 33109954, 21908754, 33657084, 52644296, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 264288, 264886, 52644229, 21908765, 21908766, 21908767, 21908769, 55811957, 35695917, 265020, 265021, 52644150, 18108362, 33657023, 264693, 33657109, 33657182, 27486264, 33657349, 35695763, 18108370, 18108376, 55811576, 35696423, 35695855, 60431850, 264638, 263981, 52644332, 60170394, 83373044, 18108385, 87168518, 60432113, 264584
1802	80202013 (3803, 3804)	Novel Protein sim. GBank gij4426613jg[P4AD20451] - (AF098796) SLM-1 [Mus musculus]		dna_ma_bind	264107, 263976
1803	87778554 (3805, 3806)	Novel Protein sim. GBank gij3747107 (AF095741) - unknown [Rattus norvegicus]		UNCLASSIFIED	264259, 29331825, 29331827, 264508, 264907, 265008, 60170831, 60433356, 60433438, 264759, 21908754, 264448, 264288, 265021, 265022, 33657023, 264693, 55811576, 264555, 264556, 22279000
1804	80434213 (3807, 3808)	Novel Protein sim. GBank gij1352911j[P471471YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-NNF1 INTERGENIC REGION		struct	264509, 264905, 264908, 264907, 264908, 265007, 264910, 264686, 264768, 264687, 264769, 264693, 264628, 18108374, 264634, 264636, 264637, 264565
1805	95351140 (3809, 3810)	Novel Protein sim. GBank gij3043714jdbj[BAA25521] - (AB011167) KIAA0595 protein [Homo sapiens]	Contains protein domain (PF00293) - Bacterial mutT protein		264488, 264768, 264769, 264689, 29148629, 35695917, 35696286, 264259, 264692, 18108362, 33657023, 29331824, 33657109, 29146498, 264508, 264509, 264905, 264906, 264907, 66712502, 264908, 264909, 35698423, 35695855, 264510, 264511, 264512, 264910, 264634, 264635, 264637, 264638, 33657402, 264758, 85658542, 284602, 264760, 264761, 264482, 264563, 264762, 264483, 264764, 264566, 264288, 264768
1806	12763822 (3811, 3812)			UNCLASSIFIED	264637

1907	95351144 (3813, 3814)	Novel Protein sim. GBank gi 4929285 gb AAD34053.1 AF15181 - (AF151816) CGI-58 protein [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	hydrolase	65274572, 22278996, 35698286, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 60424268, 29331828, 35696052, 264593, 60433356, 21808754, 55811386, 95658542, 87168559, 285018, 264681, 284882, 264684, 264288, 21808785, 21806768, 21806768, 265020, 265022, 284890, 52844150, 264682, 33657023, 264693, 33657109, 35695855, 264636, 264638, 60432113
1908	95313641 (3815, 3816)	Novel Protein sim. GBank gi 3986770 (AF109906) - NC22 [Mus musculus]		UNCLASSIFIED	264488, 65274572, 58182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 60432289, 29331828, 29331827, 29331828, 29146499, 264805, 264906, 264907, 264908, 66712502, 264909, 58182435, 264510, 264511, 265008, 264910, 60170831, 264592, 60433356, 33657402, 264594, 60433436, 264596, 55812038, 33109954, 52846317, 265011, 265017, 264804, 265018, 265019, 264605, 55811150, 264681, 264448, 264288, 264686, 264688, 264769, 21806765, 21806766, 21806767, 21806768, 21806769, 55811957, 29148629, 35695917, 285020, 265022, 264691, 264692, 18108364, 65274620, 33657109, 33657349, 35695763, 18108374, 263978, 55810764, 55811576, 35698423, 65274791, 264631, 264632, 264556, 264557, 60170394, 56182323, 83373044, 18108385, 60432113, 22278000, 22279002, 284568, 264488
1909	95514505 (3817, 3818)	Novel Protein sim. GBank gi 2224653 dbj BAA20813  - (AB002354) KIAA0356 [Homo sapiens]		UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 264511, 264910, 264593, 264758, 264764, 264766, 18108370, 264634, 264637, 264486
1910	94216821 (3819, 3820)	Novel Protein sim. GBank gi 1351218 sp P47226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	35698286, 22278996, 22278999, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265007, 264512, 264810, 264758, 265011, 264601, 264602, 264604, 264605, 264761, 264764, 264288, 264768, 264768, 264687, 264769, 35695917, 265021, 52844150, 264692, 264628, 18108370, 264629, 18108372, 18108374, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 18108385, 264565, 264566, 264486

1911	91725345 (3821, 3822)	Novel Protein sim. GBank gi 4809339 gb AAD30184.1 AC008530 hypothetical protein [Homo sapiens]	Contains protein domain (PF01119) - DNA mismatch repair protein	nuclease	18108394, 56182575, 56182181, 29331826, 29331827, 33658970, 264906, 265007, 264591, 55812038, 87168559, 264448, 264369, 21906765, 21906768, 265022, 264691, 264693, 18108365, 55811576, 264556, 18108385, 18108388
1912	95413519 (3823, 3824)	Novel Protein sim. GBank gi 5689439 dbj BAA83003.1  - (AB028974) KIAA1051 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	18108397, 56182575, 56181666, 22278994, 22278995, 56994075, 22278996, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 66714117, 35696052, 264905, 264806, 264907, 264808, 52644045, 56182435, 265007, 285008, 264910, 265009, 264591, 264596, 65274444, 55811386, 87168474, 265011, 87168559, 265018, 265019, 264760, 18108351, 264681, 264369, 264684, 264288, 264686, 264768, 21906765, 21906768, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 264692, 33657023, 264693, 18108376, 55811576, 35696423, 65274791, 264637, 56182323, 83373044, 56526486, 22279002, 264563, 264568
1913	95305546 (3825, 3826)	Novel Protein sim. GBank gi 5022245 ref NP_005665.1 pZNF2 - zinc finger protein (C2H2) homologous to mouse MOK-2			56182575, 22278994, 22278995, 56994075, 22278996, 22278998, 22278999, 29331826, 29331827, 265006, 55812038, 265010, 265017, 265018, 265019, 264681, 18108351, 264683, 264764, 264369, 264288, 264685, 264686, 264769, 21906765, 21906766, 21906768, 21906769, 55811957, 265020, 265022, 264691, 55811576, 264634, 264635, 264638, 56182323, 83373044, 18108385
1914	83423982 (3827, 3828)	Novel Protein sim. GBank gi 4589604 dbj BAA76824.1  - (AB023197) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	56182575, 29331824, 35696052, 264906, 264908, 264628, 264909, 264592, 264758, 87168559, 18108351, 18108354, 264684, 264686, 33657023, 264693, 264628, 264631, 264632, 264634, 264635, 264639
1915	95340459 (3829, 3830)	Novel Protein sim. GBank gi 5689415 dbj BAA82991.1  - (AB028982) KIAA1039 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331824, 29331826, 29331827, 264508, 264909, 265009, 265017, 265019, 264768, 264769, 264689, 264628, 264635, 264637, 264639, 83373044, 264565
1916	79640761 (3831, 3832)				264693, 264639

1917	87821680 (3833, 3834)	Novel Protein sim. GBank gi15689391[dbj BA82979.1] - (AB028850) KIAA1027 protein [Homo sapiens]		struct	284769, 284689, 21908785, 21908786, 22278996, 264259, 284691, 284693, 29331824, 29331825, 29331826, 29331828, 264905, 264906, 264628, 264907, 264908, 264909, 264510, 264630, 264910, 264634, 264635, 264636, 264637, 264638, 263981, 264639, 264758, 18108365, 21908754, 265011, 264604, 264563, 18108351, 264762, 264763, 264566, 264764, 264766
1918	85302785 (3835, 3838)	Novel Protein sim. GBank gi15281517[gb AAD41524.1 AF15483] - (AF15483) PV-1 [Rattus norvegicus]		struct	264488, 18108392, 18108357, 21908765, 21908767, 21908768, 56182575, 21908769, 22278994, 35696286, 35695917, 22278996, 22278997, 285021, 285022, 264534, 264690, 264691, 264692, 33637023, 264693, 29331824, 29331825, 33657109, 29331826, 32645129, 35696052, 29331828, 27486262, 27486264, 35695763, 264508, 264905, 264509, 264906, 264628, 264907, 18108370, 264908, 264629, 264909, 18108372, 18108374, 263978, 35696423, 35695855, 264510, 264511, 285006, 265007, 264512, 265008, 264631, 285009, 264910, 264634, 264635, 264555, 264636, 264556, 264637, 264557, 264593, 264638, 264594, 60170394, 264595, 264559, 264596, 83373044, 264758, 52646317, 18108385, 52644296, 56526486, 87168518, 265010, 265011, 87168559, 264600, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 264760, 264761, 264482, 264564, 18108351, 264762, 264682, 264565, 264448, 264764, 264566, 264486, 264567, 264369, 264288, 264766, 264487, 264685
1919	94143847 (3837, 3838)	Novel Protein sim. GBank gi13876584[emb CAB01237] - (Z77687) cDNA EST EMBL:CO8125 comes from this gene; cDNA EST EMBL:CO9753 comes from this gene [Caenorhabditis elegans]		oxidase	22278997, 28331822, 265007, 60170831, 60432226, 60433438, 264448, 264682, 264286, 55811957, 33657023, 33657109, 65274791, 56182323, 22279002
1920	81229953 (3839, 3840)	Novel Protein sim. GBank gi1809231 (AC000115) - coded for by human cDNAs R76043 (NID:g850725), R65857 (NID:g838495) and H12868 (NID:g877688) [Homo sapiens]		UNCLASSIFIED	264510, 264511, 264512, 264568
1921	79555226 (3841, 3842)	Novel Protein sim. GBank gi14560997[gb AAD24571.1 AF12108] - (AF12108) cAMP Inducible 2 protein [Mus musculus]		UNCLASSIFIED	264693



1922	87641863 (3843, 3844)	Novel Protein sim. GBank gi 138595 sp P02845 VIT2_CHICK - VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP40]		UNCLASSIFIED	264686, 264688, 264480, 18108370, 264909, 18108374, 265008, 264557, 264564, 18108351
1923	94323569 (3845, 3846)	Novel Protein sim. GBank gi 119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	264488, 264489, 22278995, 264094, 264259, 35898052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 264511, 264512, 265007, 264910, 265009, 264591, 264592, 264593, 264594, 264595, 264758, 264596, 264759, 265011, 265017, 265018, 265019, 55811150, 264681, 264762, 264448, 264764, 264288, 264369, 264766, 264767, 264686, 264687, 264768, 264769, 56181562, 264689, 21908766, 264691, 33657023, 264693, 65274620, 33657109, 18108370, 264628, 264629, 35898423, 264630, 264631, 264632, 264634, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87188518, 264583, 264584, 264585, 264586, 264587, 29331826, 264906, 264908, 264595, 265017, 265018, 265019, 265021, 264891, 264893, 264637, 18108385, 264565
1924	87338925 (3847, 3848)	Novel Protein sim. GBank gi 3877655 emb CAA86657  - (Z72511) possible zinc finger protein; cDNA EST EMBL:M89115 comes from this gene; cDNA EST EMBL:D71533 comes from this gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST EMBL:D75164 comes from this gene; cDNA EST EMBL:G1...	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		
1925	87628338 (3849, 3850)	Novel Protein sim. GBank gi 4981903 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 (Thermotoga maritima)	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomal prot	22278995, 22278996, 22278997, 264259, 29331824, 66714117, 29146499, 264909, 5264045, 265008, 265009, 264758, 265011, 265017, 264605, 264448, 264288, 264692, 33657109, 18108374, 60170394
1926	88094739 (3851, 3852)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		strud	264905, 264906, 264907, 264910, 264593, 265018, 264760, 264764, 264288, 264692, 264693, 263978, 264631, 264634, 264637, 264583
1927	85654657 (3853, 3854)	Novel Protein sim. GBank gi 3043632 db BAA25480  - (AB011126) KIAA0554 protein [Homo sapiens]			264689, 264631
1928	87799054 (3855, 3856)	Novel Protein sim. GBank gi 1665761 db BAA1337  - (D87433) KIAA0246 [Homo sapiens]	Contains protein domain (PF00193) - Inf	Inf	264489, 264259, 265017, 265021, 264692
1929	86997236 (3857, 3858)	Novel Protein sim. GBank gi 5001993 gb AAD37247.1 AF13432 - (AF134321) chimeric AFGP/trypsinogen-like serine protease precursor [Dissostichus mawsoni]	Extracellular link domain	UNCLASSIFIED	264508, 264591, 33657402, 265017, 264768, 264632, 264556, 264639

1830	87889128 (3859, 3860)	Novel Protein sim. GBank gi 1709230 sp P52963 NBL4_MOUSE - NBL4 PROTEIN		phosphatase	35696286, 29331828, 264805, 264907, 264908, 264909, 264511, 264910, 264758, 264601, 265017, 265019, 264805, 264760, 264784, 264766, 264688, 264789, 265022, 35698423, 264638, 60432113
1831	87787279 (3861, 3862)	Novel Protein sim. GBank gi 404634 (U01840) - serine/threonine kinase [Mus musculus]	Contains protein domain (PF00068) Eukaryotic protein kinase domain	kinase	264906, 264908, 60432229, 264758, 264764, 264288, 265020, 264692, 264834, 264637, 264684, 264691, 264635
1832	15030972 (3863, 3864)			UNCLASSIFIED	264595
1833	11813868 (3865, 3866)	Novel Protein sim. GBank gi 4115748 dbj BAA36494) - (AB022023) nonmuscle myosin heavy chain B [Bos taurus]		struct	56182575, 56182435, 264510, 264757, 264758, 55812038, 5581388, 285018, 55811150, 21806765, 264681, 264631, 264635, 264637
1834	84428360 (3867, 3868)			UNCLASSIFIED	264688, 265011, 264511, 264905, 18108351, 264564, 264681, 264258, 18108370, 264566, 264764, 264369, 264595
1835	87752511 (3869, 3870)			UNCLASSIFIED	60432289, 265007, 265010, 265011, 265018, 33657109, 18108374
1836	95414338 (3871, 3872)	Novel Protein sim. GBank gi 4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit			
1837	94847141 (3873, 3874)	Novel Protein sim. GBank gi 543187 ref S37771 - ankyrin, erythrocyte - mouse	Contains protein domain (PF00023) - Ank repeat	kinase	85658542, 21906767, 35685917, 60170615, 264693, 33657109
1838	87403277 (3875, 3876)	Novel Protein sim. GBank gi 4544431 gb AAAD22340.1 AC006955 - (AC006955) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00888) - Cullin family	collagen	264488, 28146488, 264805, 264559
1839	91004978 (3877, 3878)	Novel Protein sim. GBank gi 500888 dbj BAA03210  - (D14168) 50kDa lectin [Bombyx mori]		UNCLASSIFIED	65274572, 22278999, 60432289, 56182435, 60433356, 265017, 21906765, 21906766, 21906788, 55811957, 27486264, 35696423, 60432113, 264564
1840	87348810 (3879, 3880)	Novel Protein sim. GBank gi 1946300 emb CAA73132  - (Y12529) hypothetical protein [Silene latifolia]	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	264488, 29331822, 264448, 264683, 264288, 285020, 33657023, 264631
1841	94147177 (3881, 3882)	Novel Protein sim. GBank gi 4206386 (AF060570) - rig-1 protein [Mus musculus]		UNCLASSIFIED	58994075, 22278998, 264259, 29331824, 29331827, 264905, 265008, 33657084, 265017, 265018, 264288, 264687, 21908785, 21906766, 21906787, 285020, 52644150, 27486284, 83373044, 18108387, 60432113, 22279002, 264565
1842	87641870 (3883, 3884)	Novel Protein sim. GBank gi 4927204 gb AAD33048.1 AF133911 - (AF133911) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	264488, 18108398, 29331825, 27486261, 264508, 18108370, 18108374, 264482
1843	94325298 (3885, 3886)	Novel Protein sim. GBank gi 3122952 sp O15736 IPD_DICD1 - TIPD PROTEIN	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	22278998, 29331822, 29331827, 35696052, 264511, 265009, 264592, 60432228, 285017, 265018, 265019, 264684, 284682, 33657109, 65274791, 264636

1944	94232958 (3887, 3888)	Novel Protein sim. GBank gi 1799570 dbj BAA13432  - (D87671) TIP120 [Rattus norvegicus]		UNCLASSIFIED	65274572, 22278994, 22278995, 22278996, 22278997, 22278998, 264259, 52645080, 29331824, 29331826, 29331827, 66712502, 56182435, 264512, 264910, 60170831, 60432229, 60433356, 33657402, 60433438, 264596, 33109954, 21906754, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264369, 264686, 264768, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 60170615, 264692, 33657023, 18108370, 18108374, 35696423, 35695855, 264634, 60170394, 264639, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264553, 264488, 22278996, 264510, 264511, 18108351, 264683, 264488, 264567
1945	87641872 (3888, 3890)	Novel Protein sim. GBank gi 4927204 gb AAD33049.1 AF13391 - (AF133911) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	60432228, 29331827, 35696052, 265007, 265008, 60433356, 60433438, 264369, 56181562, 21906767, 52644150, 264693, 27486264, 264637, 87168518, 264563
1946	87443980 (3891, 3892)	Novel Protein sim. GBank gi 2498104 sp Q27969 AD50_BOVIN - ADRENAL MEDULLA 50 KD PROTEIN		UNCLASSIFIED	22278998, 264905, 264906, 264908, 264909, 264512, 264758, 264762, 264682, 264683, 264764, 264288, 264768, 264688, 21906768, 264693, 18108374, 35695855, 264635, 264637, 264638, 18108385, 22279002
1947	85438862 (3893, 3894)	Novel Protein sim. GBank gi 3914801 sp O54888 IPA2_RAT - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)		mapolymerase	264909, 60170831, 264591, 264594, 265010, 265011, 264764, 264369, 264689, 264631, 264638
1948	95199174 (3895, 3896)	Novel Protein sim. GBank gi 5420387 emb CA46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]		struct	264369
1949	7640129 (3897, 3898)	Novel Protein sim. GBank gi 3876766 emb CAA93466.1  - (Z69637) predicted using GeneFinder. Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]	Contains protein domain (PF00857) - Isochorismatase family	UNCLASSIFIED	264488, 264768, 264688, 264689, 264258, 29331822, 33657109, 29331828, 264103, 264509, 18108370, 35695855, 264510, 265008, 265009, 33657402, 18108385, 265018, 264563, 55811150, 18108351, 264369, 264288, 18108354
1951	86988253 (3901, 3902)	Novel Protein sim. GBank gi 2626753 dbj BAA23424  - (AB008782) sulfate transporter [Arabidopsis thaliana]	Contains protein domain (PF00916) - Sulfate transporter family	transport	56182575, 22278997, 52645080, 29331824, 29331825, 29331827, 55812038, 52646317, 265018, 265019, 264369, 21906765, 21906767, 55811957, 265020, 265021, 33657023, 264693, 35695763, 58182323, 22279002
1952	87069775 (3903, 3904)	Novel Protein sim. GBank gi 4929833 gb AAD34077.1 AF15184 - (AF151840) CGI-82 protein [Homo sapiens]	Contains protein domain (PF00106) - short chain dehydrogenase	reductase	264591, 264593, 264594, 264595, 264556, 264557, 264558, 264565

1853	20470371 (3905, 3906)	Novel Protein sim. GBank g 1168715 sp P31721 C1QB_RAT - COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain		264259, 264558
1854	91226025 (3907, 3908)	Novel Protein sim. GBank g 4240271 db BAA74914.11 - (AB020698) KIAA0891 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxy-terminal hydrolase family 2	ubiquitin	264488, 263994, 18108394, 35696286, 22278998, 29331822, 68714117, 29331828, 29331827, 264508, 264509, 264905, 264806, 264907, 264908, 264909, 264510, 265008, 265007, 265008, 264910, 265008, 60170831, 60432229, 265011, 265017, 264603, 264604, 265019, 18108351, 264685, 264768, 264769, 35895917, 265020, 265021, 264891, 33657023, 264692, 33657109, 264628, 18108374, 35696423, 55811576, 35695855, 264630, 264635, 264638, 264555, 264556, 264638, 264557, 264639, 264558, 264559, 83373044, 18108385, 264563, 264564, 264566, 264486, 264587
1855	95308310 (3909, 3910)			UNCLASSIFIED	56182575, 56181886, 22278994, 22278999, 264258, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 35696052, 264508, 29331830, 265008, 265009, 264591, 55812038, 87168474, 265017, 265018, 265019, 264448, 264766, 21908765, 21906768, 21906767, 55811857, 265020, 265021, 52645129, 33657109, 27488284, 33657349, 35695763, 60431528, 18108374, 55811576, 35695855, 264635, 60431850, 264639, 83373044
1856	95092121 (3911, 3912)	Novel Protein sim. GBank g 1665821 db BAA134071 - (D87489) Similar to D.melanogaster cadherin-related tumor suppressor [Homo sapiens]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264488, 56182575, 22278996, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264508, 264906, 264908, 264909, 264511, 265007, 264910, 264591, 55812038, 265010, 265018, 18108351, 264768, 56181562, 264689, 21906768, 21906769, 265022, 264691, 264628, 18108374, 55810764, 55811576, 35695855, 264631, 264632, 264635, 264637, 264639, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002, 264563, 264564

1957	94326510 (3913, 3914)	Novel Protein sim. GBank gi 4589674 dbj BAA76856.1  - (AB023229) KIAA1012 protein [Homo sapiens]		UNCLASSIFIED	52646842, 56182575, 22278997, 22278998, 22278999, 29331824, 66714117, 29331827, 29146498, 264593, 33657402, 33109954, 87188474, 265018, 264448, 264369, 264288, 264766, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 264692, 65274620, 27486264, 33657349, 27486265, 35695855, 22279002, 264482
1958	95313902 (3915, 3916)	Novel Protein sim. GBank gi 4240227 dbj BAA74892.1  - (AB020676) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	22278999, 284092, 264094, 264259, 60432049, 29331824, 56182181, 66714117, 264107, 264109, 264908, 264511, 60170831, 60432229, 21906754, 265010, 21906769, 35695917, 265022, 65274620, 263967, 263976, 35696423, 284631, 264632, 264634, 264635, 18108385, 22279000, 22279002, 264593, 265019
1959	85701470 (3917, 3918)	Novel Protein sim. GBank gi 2281983 emb CAB10860  - (Z96056) hypothetical protein [Schizosaccharomyces pombe]		ubiquitin	
1960	80308608 (3919, 3920)	Novel Protein sim. GBank gi 2274851 dbj BAA21515  - (D64159) 3-7 gene product [Homo sapiens]		struct	264905, 264806, 264907, 264908, 264909, 265006, 265007, 264910, 264595, 265017, 264604, 265018, 18108351, 264764, 264369, 264766, 264768, 21906765, 18108368, 264629, 18108378, 264635, 264636, 264637, 264638, 264486
1961	16292607 (3921, 3922)				264635
1962	91008385 (3923, 3924)			UNCLASSIFIED	65274572, 264592, 264593, 265019, 264691
1963	90936017 (3925, 3926)	Novel Protein sim. GBank gi 3721653 dbj BAA33581  - (AB012933) acyl-CoA synthetase 5 [Rattus norvegicus]		eph	65274572, 18108398, 35696286, 29331825, 60432289, 29331827, 264828, 265006, 265009, 60433356, 60433438, 21906754, 265020, 265021, 33657023, 33657109, 27486285, 35695855, 264555
1964	94317605 (3927, 3928)	Novel Protein sim. GBank gi 5262638 emb CAB45757.1  - (AL080169) hypothetical protein [Homo sapiens]		cadherin	264488, 264092, 264259, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 265009, 264910, 264592, 264593, 264594, 264595, 264758, 264600, 264603, 264604, 264605, 264760, 264762, 264448, 264764, 264288, 264685, 264766, 264768, 264769, 21906766, 264691, 264692, 264693, 18108370, 264628, 264629
1965	94317445 (3929, 3930)	Novel Protein sim. GBank gi 4107017 dbj BAA36294  - (AB001773) PEM-6 [Ciona savignyi]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	18108374, 264630, 264631, 264634, 264636, 264637, 264638, 18108382, 83373044, 18108385, 264483, 264564, 264565, 264566, 264486, 264567
					264488, 264510, 264760, 264768, 264486

1866	94192058 (3931, 3932)	Novel Protein sim. GBank gi 4929707 gb AAD34114.1 AF151877 - (AF151877) CGI-119 protein [Homo sapiens]	Contains protein domain (PF01027) - Uncharacterized protein family	glycoprotein	22278999, 264092, 264259, 29331826, 29331828, 28146498, 264595, 265011, 264448, 18108354, 264288, 264684, 264766, 264685, 264686, 265022, 264691, 264692, 18108370, 18108377, 264555, 18108381, 18108385, 264486, 264567
1867	87396123 (3933, 3934)	Novel Protein sim. GBank gi 2957270 (AF045476) - phospholipase C PLC210 [Caenorhabditis elegans]	Contains protein domain (PF00388) - Phosphatidylinositol-specific phospholipase C, X domain	esterase	29331824, 265010, 265017, 264288, 21906764, 263981, 56526486
1868	88095641 (3935, 3936)	Novel Protein sim. GBank gi 2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	oncogene	35685286, 264805, 264509, 264806, 264907, 264908, 264909, 264511, 264512, 265008, 264910, 265009, 264594, 264757, 264758, 264604, 264605, 264760, 264762, 264682, 264764, 264685, 264766, 264767, 264689, 264691, 264683, 264628, 264629, 35698423, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 18108380, 264564, 264565, 264566, 264567
1869	84326528 (3937, 3938)	Novel Protein sim. GBank gi 2911274 (U20329) - spidroin 1 [Nephila clavipes]		UNCLASSIFIED	22278995, 22278996, 35686052, 264906, 264908, 18108351, 264482
1870	80596049 (3939, 3940)	Novel Protein sim. GBank gi 4050087 (AF109907) - S164 [Homo sapiens]		UNCLASSIFIED	264908, 264288, 264766, 264636
1871	94843814 (3941, 3942)	Novel Protein sim. GBank gi 134206 sp P09593 SANT_PLAFV - S-ANTIGEN PROTEIN PRECURSOR		collagen	264488, 264489, 22278998, 264259, 60432049, 66714117, 29331826, 60432289, 29331827, 35698052, 264508, 264905, 264509, 264805, 264807, 264908, 264909, 264510, 264511, 264512, 264910, 264591, 264592, 60432229, 60433356, 264595, 264598, 264600, 264604, 264605, 264760, 18108351, 264448, 264764, 264288, 264766, 264768, 264769, 21908785, 33657023, 264692, 18108370, 264628, 35698423, 65274791, 35695855, 264632, 264635, 264555, 264638, 264637, 264638, 264639, 18108385, 60432113, 22278000, 264583, 264584, 264585, 264586, 264486
1872	87645444 (3943, 3944)	Novel Protein sim. GBank gi 4518623 dbj BAA75671.1 - (AB017616) homologous to the yeast YGR163 gene [Mus musculus]	Contains protein domain (PF01462) - Leucine rich repeat N-terminal domain		22278999, 264259, 29331822, 56182181, 60432289, 29331827, 52644045, 264909, 265008, 264511, 265008, 52644286, 265018, 265019, 264761, 264689, 21908768, 21908769, 264691, 264893, 33657109, 33657182, 264556, 52644332, 264558, 60432113
1873	86395533 (3945, 3946)			UNCLASSIFIED	29331826, 264692, 35698423, 264631, 264555, 264556, 264557, 264558, 264559
1874	80396629 (3947, 3948)	Novel Protein sim. GBank gi 3309543 (AF036382) - MLL [Fugu rubripes]		UNCLASSIFIED	264682, 264764, 264593

1975	94316479 (3949, 3950)			UNCLASSIFIED	264488, 66714117, 26331826, 29331828, 56182435, 265006, 264757, 55812038, 265010, 265017, 264369, 55811957, 65274791, 35695855, 56182323, 60432113
1976	95358914 (3951, 3952)			UNCLASSIFIED	264259, 35696052, 265018, 265020, 265021, 33657109, 36528486
1977	94852664 (3953, 3954)	Novel Protein sim. GBank gij2499528ipic007782INASU_RAT - SODIUM/SULFATE COTRANSPORTER (NA(+)/SULFATE COTRANSPORTER)		homeobox	264908, 264596, 265021, 264566
1978	87447645 (3955, 3956)	Novel Protein sim. GBank gij103421ipij1A33471 - transcription factor NTF1 - fruit fly ( <i>Drosophila</i> melanogaster) (fragment)		transcript factor	60170831, 264566
1979	87627708 (3957, 3958)	Novel Protein sim. GBank gij2244815jemb[CAB10238.1] - (Z97336) hypothetical protein ( <i>Arabidopsis thaliana</i> )		UNCLASSIFIED	29331826, 29146498, 264805, 264907, 265007, 265009, 265010, 265018, 264686, 18108359, 21906768, 35695917, 265020, 60170615, 264693, 18108368, 18108370, 264631, 264635, 264556, 264558, 18108384, 22279000, 264565
1980	86577059 (3959, 3960)	Novel Protein sim. GBank gij4759290refNP_004642.1pUSP1 - Ubiquitin carboxyl- terminal hydrolase, X-linked (AF131849) Unknown [ <i>Homo sapiens</i> ]		ubiquitin	264489
1981	87606974 (3961, 3962)	Novel Protein sim. GBank gij4406693ipijAAD200601 - (AF131849) Unknown [ <i>Homo sapiens</i> ]		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331825, 29331828, 29148498, 29148499, 264107, 264906, 264910, 264595, 21906754, 265010, 265017, 265018, 265019, 264448, 264286, 21906767, 33657023, 27486264, 18108370, 18108374, 18108376, 264630, 264631, 264635, 18108385, 87168518, 22279000, 264482, 264564
1982	80995367 (3963, 3964)	Novel Protein sim. GBank gij5689523ipij[BAA83045.1] - (AB029016) KIAA1093 protein [ <i>Homo sapiens</i> ]			65274572, 29331825, 35696052, 33656970, 264909, 265008, 55811386, 264760, 264686, 264691, 27486264
1983	95098668 (3965, 3966)	Novel Protein sim. GBank gij3417297 (AC002310) - Unknown gene product [ <i>Homo sapiens</i> ]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	22278996, 35696286, 264259, 29331822, 20281099, 29331824, 60432289, 29331827, 264509, 264905, 264906, 264907, 66712502, 264908, 52844045, 264909, 264510, 264512, 264910, 265009, 264591, 264592, 60433356, 60433438, 264758, 265010, 264600, 264603, 264604, 264760, 264762, 264763, 264764, 264766, 264687, 264768, 264769, 21906765, 55811957, 35695917, 264690, 264692, 264693, 264628, 264629, 263978, 18108379, 35696423, 35695855, 20281071, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 83373044, 18108385, 22279000, 22279002

1984	85700899 (3967, 3968)	Novel Protein sim. GBank gij2896695jembjCAA17174.1] - (AL021897) tadD14 [Mycobacterium tuberculosis]		synthase	264688, 21908768, 55811857, 56994075, 265020, 265021, 22278999, 265022, 284259, 29331822, 33657182, 29146499, 264628, 18108370, 264908, 264629, 55811578, 35695855, 265008, 265007, 264591, 21908754, 33657084, 285010, 265017, 265019, 264288
1985	85636897 (3969, 3970)	Novel Protein sim. GBank gij5712131jgijAAD47379.1jAF12049 - (AF120499) DEM1 protein [Homo sapiens]		glycoprotein	264760, 264288, 263978, 55811578, 264637, 56182323, 18108385, 284584
1986	80200507 (3971, 3972)	Novel Protein sim. GBank gij4868443jgijAAD31319.1jAF14457 - (AF144573) Mx-interacting protein kinase PKM [Mesocricetus auratus]		UNCLASSIFIED	284488, 264629
1987	87011117 (3973, 3974)	Novel Protein sim. GBank gij4868443jgijAAD31319.1jAF14457 - (AF144573) Mx-interacting protein kinase PKM [Mesocricetus auratus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		22278999, 29331830, 265007, 265018, 21908768, 33657023, 264692, 264693, 18108377, 264835, 60170394, 22279002
1988	94122108 (3975, 3976)			UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264910, 264591, 264593, 264758, 264764, 284686, 264768, 265021, 264692, 264628, 264629, 35695855, 264630, 264635, 264636, 264637, 264638, 264639, 264483
1989	91225225 (3977, 3978)	Novel Protein sim. GBank gij2801701 (AF042379) - spindle pole body protein spc87 homolog GCP2 [Homo sapiens]		tubulin	60432049, 60432289, 52644045, 56182435, 264112, 265007, 33657402, 52644229, 21908765, 21908768, 21908769, 55811957, 33657023, 263967, 33657109, 18108370, 22279000, 22279002
1990	85698888 (3979, 3980)	Novel Protein sim. GBank gij5701727jgijBAA83074.1] - (AB024729) alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homologue [Homo sapiens]			284508, 264757, 264764, 18108381
1991	95353114 (3981, 3982)	Novel Protein sim. GBank gij4240287jgijBAA74922.1] - (AB020706) KIAA0899 protein [Homo sapiens]	Contains protein domain (PF01602) - Adaptin N terminal region	glycoprotein	18108394, 56182575, 22278994, 35698286, 56994075, 22278997, 22278999, 29331822, 29331824, 29331825, 60432289, 29331828, 284508, 264908, 264907, 264908, 56182435, 264510, 265007, 21908754, 33109954, 87168474, 265017, 265018, 265019, 264762, 18108351, 264763, 284883, 284389, 264288, 264685, 264765, 264687, 264769, 21908765, 21908768, 21908769, 55811957, 265020, 60431528, 263974, 18108378, 35695855, 264555, 264557, 264639, 83373044, 18108384, 87168518, 60432113, 22279000, 22279002, 264564, 264488
1992	95317232 (3983, 3984)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	Contains protein domain (PF00096) - struct Zinc finger, C2H2 type		29331827, 264908, 264907, 264909, 265007, 284603, 264766, 264686, 264768, 21908768, 264628, 264635, 264636, 18108385, 56526486, 264568, 264597
1993	80054763 (3985, 3986)	Novel Protein sim. GBank gij2565091 (U80761) - CTG26 alternate open reading frame [Homo sapiens]		UNCLASSIFIED	284592, 35696423



1994	94329114 (3987, 3988)	Novel Protein sim. GBank gi 5630077 gb AAD45822.1 AC006017 similar to ALR; similar to AAC51735 (PID:g2358287) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	mapolymerase 264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 264908, 265008, 60432229, 33657402, 60433356, 264757, 60433438, 264758, 33109954, 265011, 265017, 265018, 265019, 264684, 264369, 264685, 264686, 264788, 21906765, 21906767, 21906768, 21906769, 265020, 264690, 18108362, 264693, 65274620, 18108370, 264635, 264555, 264556, 264557, 58182323, 83373044, 56526486, 22279000, 22279002, 264564 264488, 18108396, 22278994, 56994075, 22278996, 35696286, 22278997, 22278999, 264259, 29147620, 58182181, 29331824, 60432229, 29331826, 29331827, 35696052, 29146499, 264905, 264907, 66712502, 58182435, 265006, 265007, 265008, 265009, 60431735, 60433356, 33657402, 264595, 55812038, 33657084, 55811386, 85658542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 56181562, 264689, 21906765, 21906766, 21906767, 29148627, 21906768, 21906769, 29148629, 29148784, 265020, 265021, 264690, 18108361, 264693, 27485262, 27486264, 27486265, 18108370, 60431528, 18108374, 18108377, 35698423, 55811578, 65274791, 35695855, 264631, 264634, 264635, 264555, 264636, 60431850, 264557, 264558, 264559, 83373044, 20798451, 87188518, 264404, 60432113, 264567 264564
1995	85414353 (3989, 3990)	Novel Protein sim. GBank gi 4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit	UNCLASSIFIED	UNCLASSIFIED
1996	80254186 (3981, 3992)	Novel Protein sim. GBank gi 791146 emb CAA60020  - (X86028) extensin-like protein [Vigna unguiculata]	UNCLASSIFIED	UNCLASSIFIED
1997	87028423 (3983, 3994)	Novel Protein sim. GBank gi 2842034 (AF034547) - protein phosphatase M130 myosin binding subunit [Ovis aries]	Contains protein domain (PF00023) - Ank repeat	phosphatase 264908, 264909, 264592, 264593
1998	85262704 (3995, 3996)	Novel Protein sim. GBank gi 4589634 dbj BAA76839.1  - (AB023212) KIAA0995 protein [Homo sapiens]	UNCLASSIFIED	264113, 264885, 264555, 264567

1999	194324803 (3997, 3998)	Novel Protein sim. GBank gi15225312 gb AAD40846.1 AF07244 - (AF072441) calcineurin binding protein cabin 1 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	UNCLASSIFIED	18108394, 18108397, 35696286, 60424269, 29331827, 29331828, 35696052, 265006, 264512, 55811388, 265010, 265018, 265019, 55811150, 18108351, 284783, 264682, 284369, 284685, 284686, 56181562, 265020, 264691, 33657023, 284693, 33657109, 27486284, 18108370, 18108379, 35695855, 284634, 284635, 284636, 284555, 284557, 56182323, 18108382, 284558, 83373044, 60432113, 22279000, 264563, 264564, 264566
2000	195413705 (3999, 4000)	Novel Protein sim. GBank gi1723232 sp Q10155 YATA_SCHPO - HYPOTHETICAL 90.6 KD PROTEIN CTD4.10 IN CHROMOSOME 1		UNCLASSIFIED	52646365, 52646842, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331826, 29331827, 29331828, 35696052, 264106, 29331830, 52644045, 265007, 265008, 60170831, 264592, 264593, 33657402, 60433438, 21906754, 52644286, 265017, 265018, 265019, 264781, 264389, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 33657023, 65274820, 52645129, 27486281, 27486282, 27486284, 35695763, 35696423, 35695855, 264631, 52644332, 56182323, 60170394, 83373044, 56526486, 22279002, 264568, 264587
2001	195072534 (4001, 4002)	Novel Protein sim. GBank gi107560 pi JB38637 - Ras inhibitor (clone JC285) - human (fragment)		UNCLASSIFIED	264769, 52644229, 65274572, 21906768, 22278996, 35696286, 35695917, 265020, 22278998, 264534, 264490, 264259, 264692, 60432289, 33657109, 35696052, 264508, 264509, 18108370, 60431528, 18108374, 35696423, 65274781, 35695855, 264510, 264511, 264512, 265009, 284634, 284636, 264555, 264558, 264638, 264557, 264558, 284559, 60433438, 83373044, 264759, 18108385, 285011, 264600, 264601, 60432113, 264603, 264604, 264605, 264448, 264288, 264765
2002	80236368 (4003, 4004)	Novel Protein sim. GBank gi1729433 sp P38657 ER60_BOVIN - PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (ERP60) (58 KD MICROSOMAL PROTEIN) (P58)	Contains protein domain (PF00085) - Thioredoxin	isomerase	264907, 265006, 264910, 264603, 264692, 264629, 18108374, 264556, 264557
2003	80074449 (4005, 4006)	Novel Protein sim. GBank gi185388 pi A27040 - neurofilament triplet M protein - chicken (fragment)		UNCLASSIFIED	264805, 264906, 264908, 264910, 264595, 265017, 18108351, 264692, 264629, 264634, 264565

2004	95317318 (4007, 4008)	Novel Protein sim. GBank gi 4864249 emb CAB43230.1  - (AL049996) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	52645156, 52646842, 52646365, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331824, 29331826, 29331827, 35696052, 29331828, 33656970, 29331830, 264908, 264592, 60433356, 33657402, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264763, 264683, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695783, 18108374, 18108376, 18108377, 35696423, 35695855, 264631, 52644332, 264558, 18108385, 56526486, 87168518, 60432113, 264483, 264488, 264908
2005	87400864 (4009, 4010)	Novel Protein sim. GBank gi 3878501 emb CAA87795  - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...		ubiquitin	
2006	95351177 (4011, 4012)	Novel Protein sim. GBank gi 4106673 emb CAA22613  - (AL035064) queuine tma-ribosyltransferase [Schizosaccharomyces pombe]	Contains protein domain (PF01702) - Queuine [RNA-ribosyltransferase]	UNCLASSIFIED	56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 56182181, 60424269, 66714117, 35696052, 264906, 66712502, 264909, 264510, 60433356, 85658542, 265010, 265018, 265019, 264682, 264448, 264288, 264768, 29148627, 21906769, 29148784, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 55810764, 55811576, 35695855, 87168518, 60432113, 264563, 264482
2007	94325556 (4013, 4014)	Novel Protein sim. GBank gi 2662161 dbj BA423712  - (AB007800) HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]		UNCLASSIFIED	264488, 263994, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265007, 264910, 264592, 264595, 264758, 265011, 264760, 264762, 264784, 264768, 264685, 264767, 264768, 264769, 55811957, 35695917, 265020, 264691, 264693, 264628, 264629, 65274791, 35695855, 264631, 264632, 264634, 264835, 264637, 264638, 264839, 264586
2008	85084428 (4015, 4016)	Novel Protein sim. GBank gi 1550783 emb CAA69257  - (Y07960) homeodomain protein [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	264809, 264768, 35695855

2009	85749240 (4017, 4018)	Novel Protein sim. GBank gij3882303dbjBAA34512.1) - (AB018335) KIAA0792 protein [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 264910, 264591, 265017, 264881, 264683, 21906788, 284691, 33857182, 33857349, 264631, 87168518, 264404, 22279002, 284583
2010	85422458 (4019, 4020)	Novel Protein sim. GBank gij5262829jembI(CAB45753.1) - (AL080164) hypothetical protein [Homo sapiens]	Contains protein domain (PF00057) - eph (Low-density lipoprotein receptor domain class A		52844507, 52845158, 52846365, 52846842, 18108397, 65274572, 22278994, 58994075, 35898286, 22278996, 22278997, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264511, 265007, 264512, 265008, 265009, 60432229, 60433356, 21906754, 52846317, 33109954, 52844296, 87168474, 87168559, 265017, 265018, 265019, 284681, 284685, 284687, 52844229, 264689, 21906765, 21906766, 21906767, 21906768, 35895917, 265020, 52844150, 264891, 284692, 33857023, 263967, 52845129, 35895763, 18108376, 35896423, 65274791, 35895855, 264631, 264634, 60431850, 264637, 284638, 52844332, 80170394, 18108385, 87168518, 22279002, 264584, 264585, 264586, 284567
2011	94328149 (4021, 4022)	Novel Protein sim. GBank gij3347953 (AF076183) - cytosolic sorting protein PACS-1a [Rattus norvegicus]		UNCLASSIFIED	56182575, 56894075, 22278999, 284259, 29331824, 29331826, 29331827, 29331828, 35896052, 264906, 66712502, 265006, 265007, 265008, 265010, 265011, 265017, 265019, 264881, 264448, 284683, 284368, 284288, 284685, 284766, 264687, 21906765, 21906767, 21906768, 21906769, 285020, 265022, 264691, 33857023, 65274620, 33857109, 264629, 264557, 264559, 93373044, 87168518, 60432113, 22279002
2012	87772137 (4023, 4024)	Novel Protein sim. GBank gij1086678 (U41020) - coded for by C. elegans cDNA yk100g4.5; coded for by C. elegans cDNA yk100g4.3; weakly similar to human SREBF-2 basic-helix-loop-helix-leucine zipper transcription factor [Caenorhabditis elegans]	Contains protein domain (PF00409) - Kinesin light chain repeat	UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29148498, 87168559, 265019, 284682, 264288, 264686, 21906764, 285020, 265022, 33857023, 264693, 33857109, 55811576, 284632, 284558, 56182323, 284639, 18108383, 18108384, 18108388, 22279000, 22279002, 284587
2013	94843842 (4025, 4026)	Novel Protein sim. GBank gij4507985jrefjNP_003427.1pZNF1 - zinc finger protein 135 (clone pHZ-17)	Contains protein domain (PF00098) - dna_ina_bind Zinc finger, C2H2 type		18108398, 264908, 265007, 265010, 265018, 265019, 264689, 21906767, 265020, 284692
2014	87347940 (4027, 4028)	Novel Protein sim. GBank gij127720jspjP20938IMYP0_HETFR - MYELIN P0 PROTEIN PRECURSOR		UNCLASSIFIED	264488, 29331826, 264907, 284636, 284555, 264639, 264558

2015	88094922 (4028, 4030)	Novel Protein sim. GBank gij181266 pir  S22687 - extensin - Volvox carteri (fragment)		UNCLASSIFIED	56182575, 35696286, 264259, 35696052, 264508, 264906, 264907, 264510, 264512, 87189474, 265010, 264681, 264288, 264689, 264628, 35698423, 35695855, 264639, 264563, 264564
2016	85298641 (4031, 4032)	Novel Protein sim. GBank gij285046 pir  S26413 - t-complex protein Tcp-10 - mouse	struct		264102, 264508, 264110, 265009, 33109954, 21906768, 265021, 33657109, 27486262, 263972, 18108374, 263976, 264555, 264564
2017	79464293 (4033, 4034)	Novel Protein sim. GBank gij124735 sp P18175 INVO_PIG - INVOLUCRIN		UNCLASSIFIED	264685, 264636
2018	79637067 (4035, 4036)	Novel Protein sim. GBank gij2143910 pir  S68216 - phosphatase-1 glycogen-binding (GL)-chain - rat	phosphatase		264107, 264110, 264112, 265017, 263976
2019	87787900 (4037, 4038)	Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycoprotein AFGP precursor [Boreogadus saiid]	UNCLASSIFIED		264259, 264508, 264591, 265018, 264682, 264288, 264688, 22279002
2020	94674476 (4039, 4040)	Novel Protein sim. GBank gij585084 sp Q07803 IEFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)			56994075, 264593, 33109954, 21906754, 21908768, 33657023, 33657109, 27486261, 87168518
2021	86718818 (4041, 4042)	Novel Protein sim. GBank gij4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]			264737, 264767, 60170615, 18108385
2022	95295665 (4043, 4044)	Novel Protein sim. GBank gij5410230 gb AAD42992.1 AF07334 - (AF073344) ubiquitin specific protease 3 [Homo sapiens]	ubiquitin		18108394, 22278999, 264259, 264905, 264906, 264908, 264595, 264762, 264769, 264634, 264636, 87168518, 60432113, 22279000, 264482, 264565
2023	87722976 (4045, 4046)	Novel Protein sim. GBank gij4755188 gb AAD29055.1 AC00701 - (AC007018) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2		60433438, 265017, 264686, 264692, 264693, 264636
2024	87896443 (4047, 4048)	Novel Protein sim. GBank gij1655699 emb CAA69032  - (Y07752) perophorin-S [Volvox carteri]	UNCLASSIFIED		22278997, 264509, 264906, 264909, 55812038, 265017, 265021, 265022, 80170815, 264556
2025	87858863 (4049, 4050)	Novel Protein sim. GBank gij1655699 emb CAA69032  - (Y07752) perophorin-S [Volvox carteri]	UNCLASSIFIED		56994075, 60432049, 264508, 66712502, 264112, 60170831, 87168559, 264288, 264688, 264689, 21906766, 33657109, 18108370, 264638, 18108385, 60432113, 22279000, 22279002, 264964, 264566, 264567
2026	84122114 (4051, 4052)	Novel Protein sim. GBank gij1655699 emb CAA69032  - (Y07752) perophorin-S [Volvox carteri]			
2027	80249001 (4053, 4054)		UNCLASSIFIED		263978, 264634, 264486

2028	94699884 (4055, 4056)	Novel Protein sim. GBank gi 1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	Contains protein domain (PF00632) - HECT-domain (ubiquitin-transferase).	ubiquitin	52644507, 52645158, 52646842, 56182575, 56994075, 35969286, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 68714117, 29331825, 29331826, 29331827, 29331828, 35896052, 264906, 264907, 264908, 29331830, 52644045, 56182435, 265008, 265009, 80432229, 33657402, 264595, 264757, 55812038, 21906754, 52646317, 52644296, 265010, 265011, 87168559, 265017, 285018, 265019, 264448, 18108354, 264288, 264389, 264766, 52644228, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35895917, 265020, 265021, 265022, 52644150, 33657023, 65274620, 33657109, 52645129, 18108368, 27486261, 27486262, 27486264, 27486265, 35895763, 264629, 55811576, 35896423, 35895855, 264635, 264636, 52644332, 264558, 83373044, 56526486, 22278000, 22279002, 264563, 265008, 264595, 85658542, 264555, 264556, 264557, 264558, 264559, 83373044
2029	95362032 (4057, 4058)	Novel Protein sim. GBank gi 3598940 (AF017368) - faclogential dysplasia protein 2 [Mus musculus]	Contains protein domain (PF00621) - RhoGEF domain	UNCLASSIFIED	264557, 264558, 264559, 83373044
2030	91213734 (4059, 4060)	Novel Protein sim. GBank gi 5630080 gb AAD45825.1 AC004890 similar to HUB1; similar to BAA24380 (PID:g2789430) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	18108394, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331828, 284108, 66712502, 264828, 265009, 265018, 265019, 264681, 264682, 264684, 264685, 56181562, 264688, 21906769, 265022, 264682, 264693, 264628, 18108370, 18108374, 264634, 264636, 264558, 18108385, 87168518, 22279002, 264565
2031	80245281 (4061, 4062)				264591, 55811957, 18108365, 264557, 264558, 18108382, 18108384
2032	91232607 (4063, 4064)	Novel Protein sim. GBank gi 5689491 db BAA83029.1  - (AB029000) KIAA1077 protein [Homo sapiens]	Contains protein domain (PF00884) - Sulfatase	hydrolase	65274572, 35896286, 29331824, 264908, 265009, 264593, 265018, 264288, 264688, 264769, 21906768, 21906767, 29148827, 264628, 35898423, 264634, 264556, 18108381, 60170394, 264558, 83373044, 18108385, 264482, 264484
2033	95000809 (4065, 4066)	Novel Protein sim. GBank gi 2494828 sp Q64886 CAG7_RAT - ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2-6-SIALYLTRANSFERASE (ST6GALNACIII) (STY)		synthase	56181562, 264628, 264632, 264555, 264556
2034	91232529 (4067, 4068)	Novel Protein sim. GBank gi 4626984 ref NP_005147.1 pROD1 - UNKNOWN	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	22278996, 22278998, 264907, 29331830, 265008, 265018, 264681, 264682, 264684, 21906767, 21906768, 21906769, 33657109, 83373044, 56526486

2035	83553451 (4089, 4070)				264369, 264686, 265022, 26526486, 264567
2036	87115833 (4071, 4072)				29331827, 29331828, 264682, 264369, 29148627, 60432113
2037	94324833 (4073, 4074)	Novel Protein sim. GBank gll2734081 (AF000185) - similar to oxysterol-binding proteins [Caenorhabditis elegans]	UNCLASSIFIED		65274572, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331824, 60432289, 29331826, 29331828, 35696052, 264907, 29331830, 66712502, 56182435, 265008, 265009, 60170831, 264594, 55812038, 33109954, 21906754, 87168559, 265017, 265018, 265019, 264782, 264369, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 35695763, 35695855, 264632, 264634, 264636, 56182323, 83373044, 60432113, 22279000, 22279002, 264563
2038	95422384 (4075, 4076)	Novel Protein sim. GBank gll3880825[emb]CAB07858] - (Z93785) predicted using GeneFinder: similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...	UNCLASSIFIED	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	22278995, 22278996, 56994075, 264259, 29331824, 35696052, 264905, 264906, 52644045, 265007, 265009, 87168559, 265017, 18108351, 264448, 264369, 264766, 264767, 264686, 18108358, 21906765, 21906769, 32644150, 33657023, 264692, 18108362, 33657109, 27486262, 18108370, 18108374, 18108378, 35698423, 65274791, 264632, 264636, 18108383, 83373044, 18108385, 87168518, 22279000, 22279002, 264563, 264564, 264566
2039	95514626 (4077, 4078)	Novel Protein sim. GBank gll2224653[cbj]BAA20813] - (AB002354) KIAA0356 [Homo sapiens]	UNCLASSIFIED	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	22278997, 264259, 29331822, 264905, 264906, 264907, 264908, 264909, 264510, 265009, 264910, 264593, 264758, 265011, 265018, 264762, 264288, 264766, 264768, 264769, 21906766, 33657023, 264692, 264693, 33657109, 35698423, 264631, 264632, 264634, 264635, 264636, 264637, 264639, 87168518, 264486
2040	95308417 (4079, 4080)		UNCLASSIFIED		264592
2041	95071736 (4081, 4082)	Novel Protein sim. GBank gll2500625[sp]P70700RPA2 MOUSE - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135)	mapolymerase		264486, 22278998, 35696052, 264905, 264907, 264908, 264910, 265018, 264605, 265019, 18108351, 264766, 264769, 21906766, 265021, 265022, 264692, 33657109, 264628, 264629, 35696423, 35695655, 264637, 264638, 264563, 264564, 264565, 264567

2042	95307447 (4083, 4084)	Novel Protein sim. GBank gi 406590 gb AAD20040  - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]	Contains protein domain (PF00568) - WH1 domain	UNCLASSIFIED	60424178, 35696286, 264259, 29331828, 35696052, 29331828, 264508, 264509, 264907, 264908, 264510, 264511, 265008, 264910, 264591, 60433356, 264595, 265017, 265019, 264681, 264784, 264369, 264765, 264684, 264288, 264766, 264688, 52644229, 264769, 21908785, 35695917, 264535, 52644150, 264691, 264692, 18108385, 27486281, 27486282, 27486285, 18108374, 35696423, 65274781, 35695855, 264555, 264558, 60170394, 18108385, 264404, 22279000, 22279002, 264482, 264563, 264584, 264586
2043	94328078 (4085, 4086)	Novel Protein sim. GBank gi 5052554 gb AAD38607.1 AF14563 - (AF145632) BcDNA, GH06032 [Drosophila melanogaster]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	264488, 52644507, 52646365, 56994075, 22278997, 22278999, 20281171, 264259, 29331822, 29331824, 66714117, 29331828, 29331828, 33656970, 29146498, 264509, 284908, 52644045, 56182435, 265006, 33657402, 21906754, 52644296, 87168559, 265017, 265018, 265019, 264681, 264288, 264766, 264685, 264686, 21908766, 21906767, 21906768, 21906769, 265020, 265021, 60170815, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 33657349, 35695763, 18108374, 55811576, 35695855, 18108380, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 56326486, 87168518, 60432113, 22279000, 264587
2044	87106927 (4087, 4088)	Novel Protein sim. GBank gi 2246532 U93872  - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	264093, 29331827, 264905, 66712502, 264592, 264689, 21908785, 21906769, 265020, 264692, 264482, 264566
2045	79635532 (4089, 4090)	Novel Protein sim. GBank gi 406698 gb AAD20062  - (AF131852) Unknown [Homo sapiens]			264582
2046	87320849 (4091, 4092)	Novel Protein sim. GBank gi 4101720 AF006466  - lymphocyte specific formin related protein [Mus musculus]			264259, 264908, 264683, 22279002
2047	84578801 (4093, 4094)				22278999, 29147620, 29331824, 29146498, 264508, 265007, 265008, 265019, 264605, 264681, 29148627, 29148628, 265021, 33657023, 18108365, 33657109, 33657182, 18108377, 264556, 264638, 264559, 18108388
2048	84606378 (4095, 4096)			UNCLASSIFIED	264909
2049	88034690 (4097, 4098)	Novel Protein sim. GBank gi 4589656 db BAA76850.1  - (AB023223) KIAA 1006 protein [Homo sapiens]		UNCLASSIFIED	264488, 264259, 29331824, 29331828, 35696052, 264906, 264907, 264908, 264909, 264910, 264603, 264763, 21906767, 21906768, 264629, 264634, 264637, 22278002, 264584, 264565, 264566, 264567



2050	79633835 (4099, 4100)			UNCLASSIFIED	264693	264488, 264259, 264509, 264908, 264907, 264769, 18108374, 35696423, 264563, 264566, 264486
2051	87780168 (4101, 4102)			UNCLASSIFIED		264488, 263994, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264369, 264766, 264686, 264768, 264769, 52644229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35698423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264556, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264486, 264567, 264488, 263994, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264369, 264766, 264686, 264768, 264769, 52644229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35698423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264556, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264486, 264567
2052	88096393 (4103, 4104)	Novel Protein sim. GBank gi 4529889 gb AAD21812.1  - (AF134728) GSA [Homo sapiens]	Contains protein domain (PF00856) - SET domain	kinase		264488, 263994, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264369, 264766, 264686, 264768, 264769, 52644229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35698423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264556, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264486, 264567
2053	87763078 (4105, 4106)	Novel Protein sim. GBank gi 2995449 emb CAA75113  - (Y14848) midline 1 protein [Mus musculus]		UNCLASSIFIED		22278996, 22278997, 264259, 29331822, 264102, 264508, 35695917, 263972, 264482, 60424179, 264094, 264259, 29331825, 60424268, 264906, 60432229, 60433356, 87168559, 265019, 264760, 264288, 264686, 21906769, 33657023, 264693, 55810764, 55811576, 264635, 56182323, 60432113
2054	95358937 (4107, 4108)	Novel Protein sim. GBank gi 3876326 emb CAB02090  - (Z79754) similar to C2 domain [Caenorhabditis elegans]	Contains protein domain (PF00168) - C2 domain			264488, 29331826, 60432289, 29331828, 60433356, 265019, 264683, 264684, 265021, 33657109, 18108374, 264637, 18108385, 87168518, 60432113, 22278000, 264564
2055	88259449 (4109, 4110)	Novel Protein sim. GBank gi 5353746 gb AAD42226.1 AF159133  SIR2-like protein [Oryza sativa subsp. indica]		UNCLASSIFIED		

2056	88177396 (4111, 4112)	Novel Protein sim. GBank gi14826960 ref NP_005042.1 pCARS - glutamine-tRNA synthetase	Contains protein domain (PF00749) - synthase tRNA synthetases class I (E and Q)	264488, 52645156, 56182575, 22278994, 3569286, 56994075, 22278996, 22278998, 22278999, 60432049, 264259, 29331824, 60432289, 29331827, 29331828, 33658970, 264104, 264908, 264908, 265006, 265008, 60170831, 264591, 60432228, 60433438, 18108348, 21908754, 33637084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 264760, 18108351, 264681, 264682, 264448, 264683, 264389, 264288, 264685, 264687, 264688, 264689, 21908765, 21908766, 21908767, 21908769, 55811937, 35695917, 265022, 33657023, 18108362, 33657109, 18108368, 33657182, 27486281, 27486284, 27486285, 33657349, 264628, 18108370, 264629, 18108374, 18108377, 18108379, 35696423, 55811576, 20281152, 264636, 264952, 18108385, 18108388, 87168518, 264482, 264565, 264568, 264567, 52648842, 52648385, 56182575, 35696286, 22278996, 22278997, 22278998, 264093, 52645080, 35698052, 29331828, 33656970, 265009, 52646317, 55811386, 52644296, 52644229, 21906769, 35695917, 265021, 60170615, 52644150, 33657109, 33657182, 27486281, 27486282, 35695763, 35696423, 35695855, 52644332
2057	87877905 (4113, 4114)	Novel Protein sim. GBank gi1728850 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)	UNCLASSIFIED	265007, 265008, 264591 29331825, 264682, 264686, 264691, 264693, 22279002
2058	86276896 (4115, 4116)	Novel Protein sim. GBank gi119714 sp P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)	UNCLASSIFIED	56182575, 29331824, 29331826, 264910, 55811957, 18108370, 55811576
2059	79666684 (4117, 4118)	Novel Protein sim. GBank gi12811122 (U87318) - NaDC-2 [Xenopus laevis]	UNCLASSIFIED	

2061	95362204 (4121, 4122)	Novel Protein sim. GBank gil2496947 sp Q09298 YQO9_CAEEL - HYPOTHETICAL 141.2 KD PROTEIN EED8.8 IN CHROMOSOME II	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278997, 22278999, 264259, 29331822, 29331824, 29331828, 29331827, 35696052, 29331828, 264906, 66712502, 29331830, 264908, 264909, 264112, 264511, 265007, 265009, 264910, 264591, 33657402, 21908754, 85658542, 265017, 265019, 264448, 264683, 264288, 264684, 264369, 264686, 264687, 18108358, 264689, 21906765, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 33657109, 20281149, 18108379, 35695855, 264634, 264556, 264557, 264558, 18108382, 264559, 83373044, 18108384, 56526486, 60432113
2062	87028440 (4123, 4124)	Novel Protein sim. GBank gil4502091 ref NP_001139.1 pANK2 - ankyrin 2, neuronal	Contains protein domain (PF00023) - Ank repeat	struct	264905, 264628, 264907, 264629, 264908, 264909, 18108374, 263978, 35695855, 264512, 264635, 60431850, 264638, 264760, 264563, 18108351, 264762, 264585, 264784, 264487, 264766
2063	87601272 (4125, 4126)	Novel Protein sim. GBank gil4589562 dbj BAA76803.1  - (A8023176) KIAA0959 protein [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	oncogene	22278994, 22278999, 264259, 29331827, 264906, 264909, 52644045, 264686, 21906767, 55811957, 264692, 18108365, 263972, 55811576, 18108384, 22279002, 264482, 264563, 264564, 264484
2064	95317253 (4127, 4128)	Novel Protein sim. GBank gil1754515 dbj BAA13413.1  - (D87515) aminopeptidase-B [Rattus norvegicus]		hydrolase	264488, 52646365, 56994075, 35696286, 22278997, 22278998, 264259, 29331826, 60432289, 29331827, 29331828, 35696052, 264509, 265007, 265008, 60432229, 60433438, 21908754, 265010, 265011, 87188559, 265017, 265018, 264761, 18108351, 264682, 264369, 264288, 52644229, 21908765, 21906767, 21906768, 35695917, 33657109, 18108368, 18108374, 35696423, 35695855, 52644332, 264559, 60432113, 22279000, 22279002, 264566, 264486
2065	95092238 (4129, 4130)	Novel Protein sim. GBank gil2507144 sp Q04205 TENS_CHICK - TENSIN		kinase	264569, 18108394, 56182181, 60432289, 29331826, 264905, 264906, 264908, 60431735, 60433356, 55811386, 85658542, 265018, 55811150, 264681, 264766, 264692, 60431528, 263974, 55810764, 35695855, 264631, 264634, 264635, 60431850, 264557, 83373044, 18108388, 22279000, 22279002
2066	85793402 (4131, 4132)	Novel Protein sim. GBank gil160171 (M58295) - circumsporozoite protein [Plasmodium yoelii]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	56182575, 264259, 264906, 264764, 264286, 56182323, 264567

2067	95303892 (4133, 4134)				35698286, 22278997, 22278998, 60432049, 264259, 60432289, 60433438, 264682, 264448, 264369, 264288, 18108355, 21906765, 21906768, 265022, 33657109, 35696423, 35695855, 264556, 264404, 264563, 264486
2068	84344754 (4135, 4136)		UNCLASSIFIED		264687
2069	84319177 (4137, 4138)	Novel Protein sim. GBank gij3152662 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat		60424179, 56182575, 22278995, 22278996, 56994075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 33658970, 264509, 264905, 56182435, 265009, 60433356, 87168559, 265017, 265018, 264604, 265019, 264448, 264764, 264766, 21906765, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 33657109, 263976, 264555, 264557, 56182323, 83373044, 87168518, 60432113, 22279000, 22279002
2070	85781380 (4139, 4140)	Novel Protein sim. GBank gij5712131 (gbjAAD47379, 1) (AF12049) DEM1 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264905, 264628, 264908, 264638
2071	86946116 (4141, 4142)	Novel Protein sim. GBank gij3551531 (dbj BAA33016) - (AB017437) avens [Gallus gallus]	Contains protein domain (PF00566) - WH1 domain		18108398, 265006, 265007, 265008, 265009, 264594, 265010, 265011, 18108351, 18108354, 18108364, 18108365, 18108368, 264634, 18108381, 18108385, 18108388, 18108391
2072	91718429 (4143, 4144)		Contains protein domain (PF00184) - Neurohypophysial hormones, C-terminal Domain		22278995, 35696286, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 265008, 33657402, 21906754, 265011, 265019, 18108351, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264680, 264692, 35696423, 264555, 264556, 264558, 22279000
2073	27925664 (4145, 4146)	Novel Protein sim. GBank gij1504026 (dbj BAA13212) - (D86976) similar to C. elegans protein (Z37093) [Homo sapiens]		UNCLASSIFIED	264556
2074	94324767 (4147, 4148)	Novel Protein sim. GBank gij4240317 (dbj BAA74937.1) - (AB020721) KIAA0914 protein [Homo sapiens]			29331822, 264909, 264511, 265009, 264594, 264595, 265010, 265011, 265017, 265018, 265019, 264448, 264683, 265020, 265021, 18108370, 264632, 83373044, 264567

2075	93414886 (4149, 4150)	Novel Protein sim. GBank gi 5138930 gb AAD40382.1  - (AF099880) transcription factor IIB [Homo sapiens]			18108394, 22278994, 22278996, 35696286, 22278998, 22278999, 264259, 29331822, 29331825, 29331827, 35696052, 29331828, 264905, 264907, 264908, 264510, 265007, 284910, 265009, 33657084, 264760, 264448, 264288, 264766, 264767, 264689, 21906766, 21906767, 21906769, 265021, 265022, 60170615, 33657023, 27486262, 27486265, 35696423, 35695855, 264631, 264634, 264639, 87168518, 22279002, 264563, 264486, 18108391
2076	87594118 (4151, 4152)				264259, 29331826, 264508, 264908, 264510, 265007, 265011, 264288, 264637, 18108385, 264592
2077	11389877 (4153, 4154)			UNCLASSIFIED	29331825, 265017, 265018, 264288, 265020, 265021, 264634, 56528486
2078	87539384 (4155, 4156)	Novel Protein sim. GBank gi 4220590 dbj BAA74579  - (D87908) nuclear protein np95 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	ubiquitin	264768, 22278997, 265021, 264690, 264259, 264692, 29331822, 264693, 29331824, 29331828, 264508, 264509, 264906, 264907, 264628, 20281068, 264909, 265007, 265009, 264632, 264636, 264591, 264592, 264639, 264758, 264759, 33109954, 264604, 265018, 265019, 22279002, 264563, 264564, 264448, 264684, 264567, 264685
2079	88095916 (4157, 4158)	Novel Protein sim. GBank gi 4240255 dbj BAA74906.1  - (AB020690) KIAA0883 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	56182575, 264092, 29331824, 29331826, 29331830, 265017, 265018, 265020, 83373044
2080	94136689 (4159, 4160)	Novel Protein sim. GBank gi 2408021 emb CAB16219.1  - (Z99162) putative vacuolar protein [Schizosaccharomyces pombe]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 33657402, 85858542, 265011, 265018, 265019, 21906767, 21906768, 264693, 18108385, 22279000, 22279002
2081	94847186 (4161, 4162)	Novel Protein sim. GBank gi 5524734 gb AAD44360.1 AF:16635 - (AF:166350) ST7 protein [Homo sapiens]	Contains protein domain (PF00431) - CUB domain	eph	264907, 265019
2082	87628629 (4163, 4164)	Novel Protein sim. GBank gi 3880558 emb CAA94234  - (Z70271) predicted using Genefinder; similar to collagen; cDNA EST yk308e7.3 comes from this gene; cDNA EST yk308e7.5 comes from this gene; cDNA EST yk385a8.3 comes from this gene; cDNA EST yk385a8.5 comes from this gene [Caeno...]		collagen	
2083	94141000 (4165, 4166)	Novel Protein sim. GBank gi 2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	56182575, 22278996, 22278997, 264259, 29331822, 29331825, 264509, 264112, 265009, 264593, 21908754, 265018, 265019, 264448, 264288, 264685, 21906769, 265020, 265022, 264691, 18108370, 65274791, 264631, 264555, 264563
2084	95199298 (4167, 4168)	Novel Protein sim. GBank gi 728836 sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		UNCLASSIFIED	265018, 264763, 264683, 264691

2085	94989476 (4169, 4170)	Novel Protein sim. GBank gi 1655699 emb CAA69032  - (Y07752) pherophorin-S [Volvox carter]		UNCLASSIFIED	56182575, 60432289, 264908, 56182435, 87168474, 264763, 264389, 264688, 264693, 18108370, 56182323
2086	91234404 (4171, 4172)	Novel Protein sim. GBank gi 3875032 emb CAA88936  - (Z49125) similarity to Trichostrongylus colubriformis 11 kd secretory protein (Swiss Prot accession number P21837); cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D37644 comes from this gene; cDNA EST EMBL:D36149 come...		UNCLASSIFIED	35696286, 264259, 35696052, 264906, 264907, 264908, 264909, 264910, 264759, 264604, 264762, 264768, 264769, 35695917, 263978, 35696423, 35695855, 264632, 264634, 264637, 264638, 264639, 56182323, 18108385, 264482, 264488
2087	21436337 (4173, 4174)			UNCLASSIFIED	264489
2088	94111527 (4175, 4176)	Novel Protein sim. GBank gi 3880330 emb CAA16334.1  - (AL021481) similar to Phosphoglucosylase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T0080...			264488, 22278994, 35696286, 22278996, 29331827, 35696052, 33657402, 21906754, 33109954, 87168474, 265017, 265018, 265019, 264448, 264683, 264389, 264685, 264687, 264689, 21906765, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264692, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35696423, 35695855, 83373044, 87168518, 22279000, 264567
2089	95422801 (4177, 4178)	Novel Protein sim. GBank gi 4758118 ref NP_004623.1 pDAP3 - Death associated protein 3	cadherin		18108392, 264488, 52644507, 18108394, 18108397, 52646842, 18108398, 56182575, 22278994, 22278995, 35696286, 22278996, 56994075, 22278997, 22278998, 22278999, 264091, 264092, 264093, 264094, 60432049, 264259, 29331822, 20281099, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33856970, 29146498, 29146499, 264102, 264106, 264107, 264109, 264508, 264905, 264509, 264906, 264907, 264908, 66712502, 284828, 52644045, 264908, 56182435, 264110, 264112, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265008, 60170831, 264592, 264593, 60433356, 33657402, 80433438, 264595, 55812038, 264758, 21906754, 33657084, 55811388, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 55811150, 264762, 18108351, 264682, 264448, 264763, 264764, 264683, 264389, 18108354, 264288, 264685, 264766, 264686, 264687, 264768, 52644229, 264688, 18108358, 56181562, 264769, 18108359, 264689, 21906765, 21906766, 21906767, 21906768, 29146627, 21906769, 55811957, 29146629, 29146784, 35695917, 265020, 265021, 265022, 60170815, 264690

2090	88222470 (4179, 4180)				22278995, 22278998, 22278999, 264259, 29331828, 35696052, 264910, 33657402, 60433438, 33109954, 87168474, 87168559, 265018, 265019, 264681, 264684, 264686, 264687, 264688, 264689, 21908765, 21908766, 21908767, 21908769, 35695917, 265022, 60170615, 33657023, 35696423, 35695855, 264952, 18108387, 22279000, 263894, 264905, 264908, 264511, 264512, 265008, 264910, 55811386, 264288, 264768, 56181562, 21906765, 21906768, 21906769, 265022, 264628, 264563, 264567
2091	95309161 (4181, 4182)	Novel Protein sim. GBank gi4580997 gb AAD24571.1 AF121081 - (AF121081) cAMP inducible 2 protein [Mus musculus]	UNCLASSIFIED		
2092	88223605 (4183, 4184)		homeobox		22278997, 22278999, 66712502, 87168559, 284683, 265021, 264486
2093	87406073 (4185, 4186)	Novel Protein sim. GBank gi2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264905, 264906, 264907, 264908, 264510, 265006, 265007, 265009, 264910, 264596, 21906754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21906767, 21906768, 21906769, 265021, 264690, 33657023, 264693, 284628, 284634, 264636, 264637, 264557, 56182323, 264564
2094	91230929 (4187, 4188)	Novel Protein sim. GBank gi4929551 gb AAD34036.1 AF15179 - (AF151799) CGI-40 protein [Homo sapiens]		MHC	35696286, 265017, 265018, 265019, 18108388
2095	95351526 (4189, 4190)	Novel Protein sim. GBank gi1363238 pir IA57284 - spermatid perinuclear RNA-binding protein Spnr - mouse	Contains protein domain (PF00035) - Double-stranded RNA binding motif	dna_mn_bind	35696286, 52644045, 265006, 265007, 265008, 87168559, 18108351, 21906769, 29148784, 265020, 33657023, 27486262, 18108374, 18108388
2096	94119760 (4191, 4192)	Novel Protein sim. GBank gi3834423 (AF070689) - cytoplasmic dynein intermediate chain isoform DIC1a [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase_associated	264486, 264489, 65274572, 56182575, 22278998, 22278997, 22278999, 264259, 60432289, 29331826, 35696052, 264107, 264508, 264509, 264905, 264906, 264907, 284908, 52644045, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264592, 60433356, 60433438, 264758, 264596, 55812038, 21906754, 264601, 264602, 264605, 264762, 264681, 18108351, 264764, 264683, 264288, 264687, 264768, 264769, 264689, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 52644150, 264691, 264692, 33657023, 264693, 27486261, 35695763, 264628, 264629, 35696423, 35695855, 264631, 264632, 284634, 264635, 264555, 264637, 263981, 284638, 264639, 264563, 264483, 264565, 264566, 264486, 264567

2097	95322772 (4193, 4194)	Novel Protein sim. GBank gi15174501[ref]NP_006051.1[plLYF1 - zinc finger protein, subfamily 1A, 1 (Ikaros)]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	65274572, 264511, 265010, 264600, 265017, 264448, 264288, 265021, 60170615, 264692, 33657109, 18108370, 264638, 264483 56894075, 264259, 264288, 265020, 264563
2098	87780340 (4195, 4196)	Novel Protein sim. GBank gi14758208[ref]NP_004081.1[plDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)]	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	
2099	95412827 (4197, 4198)	Novel Protein sim. GBank gi12695659 (AF026954) - pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDP1 [Bos taurus]		phosphatase	65274572, 264905, 65274444, 264691, 264638, 264555
2100	95332856 (4199, 4200)	Novel Protein sim. GBank gi13881189[emb]CA516514] - (Z98281) similar to ADP-ribosylation factor; cDNA EST EMBL: C08179 comes from this gene; cDNA EST EMBL: C08337 comes from this gene; cDNA EST EMBL: C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4...	Contains protein domain (PF00025) - ADP-ribosylation factor family	nucl_recp	56182575, 22278995, 22278996, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 29148498, 264909, 265008, 265009, 264910, 264591, 60432229, 60433356, 33657402, 264758, 21908754, 85658542, 87168474, 265017, 265018, 265019, 264681, 18108351, 264782, 264448, 264369, 264288, 18108355, 264886, 21908765, 21908767, 21908768, 21908769, 265020, 265021, 33657023, 18108374, 35696423, 264558, 83373044, 87168518, 60432113, 22279000, 22279002, 264091, 29331824, 264105, 265007, 265010, 18108380
2101	87782604 (4201, 4202)	Novel Protein sim. GBank gi14589468[dbj]BAA76761.1] - (AB012808) mBOCT [Mus musculus]		UNCLASSIFIED	264488, 264489, 35696286, 264259, 35696052, 264508, 264905, 264907, 264908, 264909, 264511, 264512, 264591, 264593, 60433358, 264758, 264601, 264605, 264760, 18108351, 264448, 264764, 264288, 264767, 264768, 21908769, 35695917, 18108374, 264634, 264555, 264559, 264563, 264482, 264486
2102	87770461 (4203, 4204)	Novel Protein sim. GBank gi13874149[emb]CAA97423.1] - (Z73103) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56994075, 22278998, 264259, 29331824, 29331825, 35696052, 29331828, 86712502, 265009, 60170831, 264595, 33109954, 85658542, 87168559, 265017, 265019, 264448, 21908765, 21908768, 265022, 33657023, 27486262, 33657349, 35695763, 60431528, 18108374, 55811576, 56182323, 18108387, 87168518, 60432113, 264594
2103	95413576 (4205, 4206)	Novel Protein sim. GBank gi14240159[dbj]BAA74858.1] - (AB020842) KIAA0835 protein [Homo sapiens]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcriptfactor	
2104	85776161 (4207, 4208)			UNCLASSIFIED	264592, 264604, 22279000



2105	94848080 (4209, 4210)	Novel Protein sim. GBank gii1707032 (U80445) - coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g8.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8.....		UNCLASSIFIED	264488, 56182575, 22278994, 56894075, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 264508, 264905, 264509, 264907, 29331830, 52644045, 264510, 264511, 285007, 264512, 265009, 60170831, 60432229, 33657402, 60433356, 264595, 60433438, 264758, 33657084, 87168474, 265010, 87168559, 265017, 265018, 265019, 264762, 18108351, 264684, 18108354, 264288, 264686, 52644229, 18108359, 21906765, 21906766, 21908767, 21908768, 21908789, 35695917, 265020, 265022, 60170615, 52644150, 264692, 33657023, 264693, 33657109, 60431528, 18108374, 65274791, 35695855, 264635, 60170394, 264639, 264558, 18108385, 18108387, 56526486, 87168518, 60432113, 264564, 264566, 264567, 265006, 265019, 264906, 264639
2106	83365475 (4211, 4212)	Novel Protein sim. GBank gii3881524[emb CAA93883] - (Z70038) ZK1087.4 [Caenorhabditis elegans]			
2107	79822682 (4213, 4214)	Novel Protein sim. GBank gii3176689 (AC003671) - Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gb Z35927 from S. cerevisiae. [Arabidopsis thaliana]		UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264758, 265011, 264600, 264601, 264764, 264766, 264767, 264768, 264769, 264693, 264629, 35695855, 264632, 264634, 264635, 264638, 264639, 83373044, 264486
2108	94233976 (4215, 4216)				
2109	80478719 (4217, 4218)			UNCLASSIFIED	18108348, 264769, 18108370, 18108374, 264555, 264556, 264557, 264558, 264564
2110	87729075 (4219, 4220)	Novel Protein sim. GBank gii481043[pri S37671 - bat2 protein - human		UNCLASSIFIED	
2111	87818419 (4221, 4222)	Novel Protein sim. GBank gii2143633[pri S56542 - calmodulin-binding protein - rat		UNCLASSIFIED	264766, 35695917, 264630, 264567, 264486
2112	87293783 (4223, 4224)	Novel Protein sim. GBank gii42426629[gb AAD20459] - (AF100960) protocadherin [Rattus norvegicus]	Contains protein domain (PF00069) - struct		264508, 264906, 264591, 264682, 22279002
2113	78941388 (4225, 4226)	Novel Protein sim. GBank gii42426629[gb AAD20459] - (AF100960) protocadherin [Rattus norvegicus]	Contains protein domain (PF00028) - cadherin		265006
2114	87889342 (4227, 4228)	Novel Protein sim. GBank gii3327184[db BAA31660] - (AB014585) KIAA0685 protein [Homo sapiens]	Cadherin domain		66714117, 28331826, 29331827, 60433438, 55812038, 265017, 265019, 264689, 21908769, 55811957, 265020, 265021, 33657109, 60170394, 264558
2115	90993785 (4229, 4230)	Novel Protein sim. GBank gii4757890[ref NP_004328.1]pC8OR - chromosome 8 open reading frame 1		UNCLASSIFIED	65274572, 264689, 264691, 264692, 60432113

2116	86259387 (4231, 4232)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	3568286, 22278999, 56182181, 29331824, 29331825, 29331827, 35696052, 284807, 56182435, 265008, 264591, 55812038, 55811386, 87168559, 264288, 264369, 21906769, 29148629, 33657023, 35695763, 55811576, 35698423, 18108385, 29331824, 264511, 265009, 33109954, 265017, 265018, 264288, 264689, 265020, 264692, 58526486, 284482
2117	87788904 (4233, 4234)	Novel Protein sim. GBank gij2330021 (AF019250) - kinesin-related protein; KRP; Costal2 [Drosophila melanogaster]		struct	264259, 284805, 264807, 264908, 264510, 264511, 265009, 264910, 265010, 264802, 264288, 264788, 264693, 263987, 263972, 264638, 264559
2118	87078894 (4235, 4236)	Novel Protein sim. GBank gij1079307 (p11556573) - nuclear pore complex glycoprotein p82 - African clawed frog		glycoprotein	264693, 18108385
2119	86999317 (4237, 4238)	Novel Protein sim. GBank gij4321407 (gbAA015748) - (AF047890) ATP-binding cassette protein M-ABC1 [Homo sapiens]		UNCLASSIFIED	264693, 18108385
2120	87789395 (4239, 4240)	Novel Protein sim. GBank gij4885527 (ref NP_005480.1 pNSP3 - novel SH2-containing protein 3	Contains protein domain (PF00017) - Src homology domain 2	eph	264091, 264259, 29331826, 29331828, 265017, 264604, 264288, 264685, 265020, 264691, 18108370, 55810764, 264555, 264638, 60432113
2121	80021375 (4241, 4242)	Novel Protein sim. GBank gij4757728 (ref NP_004886.1 pAGTA - angiotensin/renin receptor ALI/AVP-like		UNCLASSIFIED	264601, 264766, 263978
2122	91230831 (4243, 4244)	Novel Protein sim. GBank gij4829551 (gb AAD34036.1 AF151799) CGI-40 protein [Homo sapiens]			18108394, 56182575, 22278997, 29331822, 29331824, 29331825, 29331826, 29331828, 264907, 56182435, 265007, 264910, 265010, 265018, 264686, 265020, 55811576, 264555, 264637, 18108382, 83373044, 18108383, 18108384, 56526488, 284565, 284567, 18108386, 264757, 265011, 18108351, 264691, 264634, 18108385
2123	86787898 (4245, 4246)	Novel Protein sim. GBank gij224551 (dbj BAA20764  - (AB002303) KIAA0305 [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	struct	29331822, 264906, 264907, 264591, 264639, 264563
2124	83005951 (4247, 4248)	Novel Protein sim. GBank gij5689455 (dbj BAA83011.1  - (AB028982) KIAA1059 protein [Homo sapiens]	Contains protein domain (PF00801) - PKD domain	transport	264763, 21906765, 35695917, 264636, 264488
2125	85354041 (4249, 4250)	Novel Protein sim. GBank gij728831 (sp P39189 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII)		UNCLASSIFIED	264488, 264489, 29331827, 35696052, 264905, 264509, 264908, 264909, 264510, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264596, 264758, 264601, 264603, 265018, 264604, 264605, 264760, 264681, 264762, 264683, 264764, 264684, 264288, 264685, 264689, 60170615, 33657023, 33657109, 55810764, 264635, 264636, 264637, 264638, 264639, 83373044, 264584, 264588
2126	95084231 (4251, 4252)	Novel Protein sim. GBank gij4539264 (emb CAB39853.1  - (AL049495) conserved hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	

2127	81118652 (4253, 4254)	Novel Protein sim. GBank gi 4868435 gb AAD31315.1 AF14323 (AF143236) apoptosis related protein APR-2 (Homo sapiens)			3569286, 29331826, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 264512, 265007, 265009, 264910, 264758, 265011, 264600, 264601, 264604, 264762, 264763, 264766, 264687, 264768, 264769, 264689, 35695917, 264690, 264691, 264692, 264693, 264629, 18108374, 35695855, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264567, 56182575, 35696286, 56182181, 29331824, 60432289, 35696052, 264905, 264907, 66712502, 264908, 264909, 264510, 264512, 265009, 264910, 264591, 55812038, 265018, 264784, 264288, 264369, 264687, 264788, 55811957, 264692, 18108368, 264628, 264632, 264634, 264635, 264637, 56182323, 264639, 18108384, 18108388, 264563, 264567
2128	87414262 (4255, 4256)				66714117, 264828, 264595, 55812038, 55811150, 55811957, 264693, 18108374, 263978, 65274791, 18108381, 83373044, 22279000
2129	95102089 (4257, 4258)			UNCLASSIFIED	263981
2130	95417144 (4259, 4260)	Novel Protein sim. GBank gi 2649255 (AE001012) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	35696052, 264909, 264768, 35695917
2131	85723065 (4261, 4262)	Novel Protein sim. GBank gi 1086886 (U41276) - Similar to potassium channel protein. [Caenorhabditis elegans]	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	potassium_channel	264488, 22278999, 264259, 29331827, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265008, 264511, 265007, 264910, 264591, 264592, 264595, 264756, 21906754, 33109954, 87168474, 265011, 264600, 264601, 264605, 265019, 264760, 18108351, 264681, 264762, 264764, 264288, 264684, 264766, 264686, 264687, 264768, 264769, 264688, 21908769, 264690, 52644150, 264691, 264693, 18108370, 264628, 264629, 18108372, 18108374, 35696423, 35695855, 264631, 264634, 264635, 264636, 264558, 56182323, 56526486, 264564, 264565, 264566, 264567
2132	95361096 (4263, 4264)	Novel Protein sim. GBank gi 5689373 dbj BAA82973.1  - (AB028944) KIAA1021 protein [Homo sapiens]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase_associated	

2133	95351539 (4265, 4266)	Novel Protein sim. GBank gij4220489 (AC006069) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60421179, 52646365, 52646842, 56894075, 35696286, 22278897, 22278988, 60432049, 56182181, 66714117, 60424289, 29331826, 29331828, 35696052, 264905, 264906, 264907, 66712502, 29331830, 56182435, 285006, 284512, 265008, 60431735, 60433356, 33657402, 55812038, 33109854, 21908754, 55811386, 285010, 284603, 265017, 265018, 285019, 55811150, 18108351, 264682, 264369, 264288, 52644229, 56181582, 21908785, 21908766, 21908767, 21908768, 21908769, 55811857, 35695917, 265020, 265021, 60170615, 33657023, 33657109, 60431528, 18108374, 35696423, 65274791, 35695855, 264634, 60431850, 18108380, 56182323, 83373044, 18108385, 18108387, 60432113, 22278002, 264563, 264566
2134	95412687 (4267, 4268)	Novel Protein sim. GBank gij3875351[emb]CAB09415[- (Z96047) DY3.6 [Caenorhabditis elegans]			56181686, 35696286, 21908754, 55811386, 265011, 265017, 18108351, 264765, 264766, 264688, 21908768, 35695917, 265020, 33657023, 264628, 35695855, 264632, 264555, 264556, 264557, 264558, 18108382, 22279002
2135	86079813 (4269, 4270)	Novel Protein sim. GBank gij5689559[dij]BAA33063.1[- (AB028034) KIAA1111 protein [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	22278999, 29331828, 35696052, 264908, 264908, 264910, 265009, 264591, 264758, 52646317, 265011, 87188558, 264601, 18108351, 264448, 264683, 264684, 264689, 18108358, 264691, 33657023, 264692, 35695763, 264629, 35695855, 264631, 264635, 264636, 264637, 56182323, 264639, 22279002, 264584
2136	84346479 (4271, 4272)	Novel Protein sim. GBank gij2662167[dij]BAA23715[- (AB007903) KIAA0443 [Homo sapiens]		UNCLASSIFIED	264639
2137	87637716 (4273, 4274)	Novel Protein sim. GBank gij4884110[emb]CAB43262.1[- (AL050090) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264569, 264909, 33109954, 264763, 21908768, 60170394, 18108385, 264563
2138	87395446 (4275, 4276)	Novel Protein sim. GBank gij5174779[gib]AAD0696.1[- (U87804) 50 kDa protein [Caulobacter crescentus]		ATPass_associated	264259, 29331828, 35696052, 264908, 285006, 265017, 265018, 18108351, 264288, 21908768, 33657023, 33657109, 264628, 18108374, 35695855, 264634, 264555, 264556, 264557, 264558, 264559
2139	94843682 (4277, 4278)	Novel Protein sim. GBank gij3850821[emb]CAA77135[- (Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana glauca]]			264905, 264910, 264591, 55812038, 55811386, 55858542, 264760, 18108351, 18108359, 55811857, 265020, 265021, 33657023, 18108384, 55811576, 83373044, 18108385, 56526486, 264482

2140	87645655 (4279, 4280)	Novel Protein sim. GBank gij4417293jgb AAD20418  - (AC007019) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 264259, 29331824, 264104, 264108, 264509, 265006, 264759, 265018, 264448, 264286, 21906768, 55811957, 265021, 33657023, 27486265, 35696423, 264636, 264556, 264557, 264559, 264566
2141	79623988 (4281, 4282)			UNCLASSIFIED	265020, 264693
2142	80041222 (4283, 4284)			UNCLASSIFIED	263978
2143	94140051 (4285, 4286)	Novel Protein sim. GBank gij2135766jir j553362 - mucin SAC (clone JER47) - human (fragment)		UNCLASSIFIED	22278997, 29331827, 264907, 265020, 60432113
2144	94320114 (4287, 4288)	Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycoprotein AFGP polypeptide precursor [Boreogadus saida]		UNCLASSIFIED	65274572, 264259, 29331824, 29331827, 264906, 264908, 264591, 265011, 87168559, 264600, 265019, 264288, 264768, 21906765, 21906767, 55811576, 35696423, 65274791, 22279002
2145	20564305 (4289, 4290)			UNCLASSIFIED	263978
2146	87010515 (4291, 4292)	Novel Protein sim. GBank gij1255871 (U53341) - short region of weak similarity to bovine membrane receptor p63 (PIR:S28503) [Caenorhabditis elegans]		UNCLASSIFIED	264909, 60433356, 264686
2147	80432911 (4293, 4294)	Novel Protein sim. GBank gij3080398 emb CAA18718.1  - (AL022603) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264907, 264768, 264769, 18108365
2148	80048811 (4295, 4296)	Novel Protein sim. GBank gij728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		UNCLASSIFIED	264593
2149	87362022 (4297, 4298)	Novel Protein sim. GBank gij119863 sp P20693 FCE2_MOUSE - LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE RECEPTOR) (FC-EPSILON-RII) (CD23)	Contains protein domain (PF00059) - glycoprotein Lactin C-type domain		29331824, 29331826, 35696052, 264758, 87168474, 265018, 52644150, 33657109
2150	84140059 (4299, 4300)	Novel Protein sim. GBank gij5420387 emb CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	22278998, 29331822, 29331824, 29331828, 264764, 264769, 21906766, 264486
2151	95353241 (4301, 4302)	Novel Protein sim. GBank gij5689407 dbj BAA02987.1  - (AB028958) KIAA1035 protein [Homo sapiens]			22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 29331828, 264508, 264511, 60433356, 264758, 264596, 33109954, 60174639, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264288, 264689, 21906765, 21906766, 21906768, 265020, 60170615, 33657109, 33657182, 33657349, 18108370, 264635, 264557, 60170394, 18108385, 87168518, 22279000, 18108397, 18108398, 265007, 264591, 265011, 18108351, 18108368, 18108374, 18108388
2152	79321640 (4303, 4304)	Novel Protein sim. GBank gij3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	kinase		

2153	88313371 (4305, 4306)	Novel Protein sim. GBank gll4758704[refNP_004216.1]pMASL - MFH-amplified sequences with leucine-rich tandem repeats 1	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat	264488, 263994, 52646842, 22278996, 22278998, 22278999, 264259, 29331822, 3569032, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56162435, 264510, 264511, 264512, 264758, 87168474, 87168559, 265017, 265019, 264760, 264288, 264389, 264768, 264687, 264769, 52644229, 21906766, 21906768, 35695917, 33657023, 33657109, 35695855, 264631, 264632, 264635, 264636, 264639, 18108385, 264483, 264564, 264485
2154	87408034 (4307, 4308)	Novel Protein sim. GBank gll225150[prfj1209265U - chorion protein B11 [Bombyx mori]]	UNCLASSIFIED	56994075, 264094, 265009, 265019, 264288, 21906787, 35695917
2155	87424072 (4309, 4310)		UNCLASSIFIED	18108392, 18108398, 22278996, 264259, 29331824, 265008, 265010, 265011, 265017, 265019, 264288, 264686, 265020, 264693, 264628, 56182323
2156	84295205 (4311, 4312)	Novel Protein sim. GBank gll3970966 (AC004974) - spa-1 (like; similar to AF026504 (PID:g2555183) [Homo sapiens])		265007, 264684
2157	87316344 (4313, 4314)			
2158	86444218 (4315, 4316)	Novel Protein sim. GBank gll1076211[prj150755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii]	UNCLASSIFIED	264591, 264596
2159	80083729 (4317, 4318)	Novel Protein sim. GBank gll4650844[dbj BAA77027.1  - (AB026190) Ketch motif containing protein [Homo sapiens]]	Contains protein domain (PF00851) - dna_rna_bind	29331822, 264112, 265009, 264681, 33657023, 264634
2160	16283674 (4319, 4320)	Novel Protein sim. GBank gll2879925[dbj BAA24828  - (AB007897) KIAA0437 [Homo sapiens]]		264634
2161	87739131 (4321, 4322)			
2162	84319526 (4323, 4324)	Novel Protein sim. GBank gll1504006[dbj BAA13202  - (D86966) simliarto human ZFY protein. [Homo sapiens]]	UNCLASSIFIED	265008
2163	85417158 (4325, 4326)	Novel Protein sim. GBank gll3876537[embj CAA98270  - (Z73974) cDNA EST yk2915.3 comes from this gene; cDNA EST yk2915.5 comes from this gene [Caenorhabditis elegans]]	UNCLASSIFIED	65274572, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 265007, 264910, 264591, 264592, 264593, 55812038, 264598, 264758, 265011, 264600, 264762, 264763, 264683, 264784, 264288, 264766, 264686, 264768, 264769, 264689, 265020, 264691, 264628, 264629, 263978, 264632, 264634, 264557, 264638, 264639, 18108385, 264563, 264586, 264567
2164	80569458 (4327, 4328)		UNCLASSIFIED	56182575, 22278998, 264093, 264683, 33657023, 65274620, 60432113
			Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	264603, 264637, 264565

2165	94329169 (4329, 4330)	Novel Protein sim. GBank gi 1086794 (U41107) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	56994075, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264908, 29331830, 56182435, 285009, 21908754, 33657084, 265011, 265019, 264448, 264288, 264369, 21906765, 21906768, 21906769, 265020, 265021, 264691, 264692, 33657023, 65274620, 35695855, 264556, 60170394, 83373044, 60432113, 22278902, 264567
2166	67618934 (4331, 4332)	Novel Protein sim. GBank gi 2706522[emb]CAAT5816] - (Y15895) ubiquitin activating enzyme [Drosophila melanogaster]	ubiquitin		52645158, 22278994, 22278998, 66714117, 29331828, 52644045, 265018, 265019, 264369, 21906765, 21908767, 21906768, 21906769, 265021, 265022, 264693, 27486262, 35695763, 18108376, 56526486, 87168518, 264567
2167	87716864 (4333, 4334)	Novel Protein sim. GBank gi 2224713[dbj]BAA20840] - (AB002384) KIAA0386 [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 29331824, 29331826, 29146498, 56182435, 265008, 265009, 264592, 264593, 33657402, 33109954, 265011, 265017, 285018, 18108351, 264369, 21906764, 21906765, 21906768, 29148827, 21906769, 52644150, 33657109, 35698423, 18108381, 18108384, 18108385, 60432113, 264567
2168	86999334 (4335, 4336)	Novel Protein sim. GBank gi 4321407[gb]AAD15748] - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]	Contains protein domain (PF00664) - ABC transporter transmembrane region.	transport	66714117, 29331827, 264907, 264511, 264591, 265018, 264764, 264683, 264766, 264768, 264566
2169	87886937 (4337, 4338)	Novel Protein sim. GBank gi 5108521[gb]AAD39741.1[AF10536] - (AF105365) K-CI cotransporter KCC4 [Homo sapiens]		UNCLASSIFIED	264625, 264555, 264559
2170	94141033 (4339, 4340)	Novel Protein sim. GBank gi 5108521[gb]AAD39741.1[AF10536] - (AF105365) K-CI cotransporter KCC4 [Homo sapiens]		UNCLASSIFIED	55274572, 56182575, 22278997, 22278998, 264259, 29331825, 264509, 264906, 56182435, 60433438, 55812038, 264598, 55811386, 265019, 264762, 264763, 264448, 264764, 264684, 264288, 264766, 264685, 56181562, 264689, 55811957, 265020, 264535, 264691, 33657109, 60431528, 18108374, 35696423, 55811576, 65274791, 264634, 264639, 264558, 87168518, 60432113, 264564
2171	80194050 (4341, 4342)			UNCLASSIFIED	264369, 265020, 264558
2172	85452460 (4343, 4344)			UNCLASSIFIED	264259, 264558
2173	87036740 (4345, 4346)	Novel Protein sim. GBank gi 4309681[gb]AAD15478] - (AC006930) R33423_1 [Homo sapiens]		UNCLASSIFIED	264369
2174	95003288 (4347, 4348)	Novel Protein sim. GBank gi 2493778[sp]Q09456]Y035_CAEEL - PUTATIVE CUTICLE COLLAGEN C09G5.5			264908, 35695855, 264555, 264557

2175	94325850 (4349, 4350)	Novel Protein sim. GBank gi 1263287 (U47855) - fibroin-3 [Araneus diadematus]		UNCLASSIFIED	264488, 35696286, 20281099, 29331826, 60432289, 35696052, 264109, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264591, 264594, 264595, 264596, 264758, 55812038, 265011, 264600, 264603, 264760, 264762, 264448, 264764, 264288, 264766, 264686, 264687, 21906768, 55811957, 35695917, 265020, 265022, 264691, 264692, 33857023, 264693, 264626, 264629, 55811576, 35696423, 55274791, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264558, 18108385, 60432113, 264563, 264564, 264565, 264566, 264486, 264567
2176	88223392 (4351, 4352)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	oncogene	5264507, 52646842, 22278994, 35696286, 22278996, 22278999, 29331826, 29331827, 35696052, 29331828, 33856970, 29331830, 264910, 33857402, 264758, 52644296, 87168559, 265018, 264689, 21908765, 21906767, 21906769, 35695917, 52644150, 264690, 33857023, 33857109, 52645129, 33657182, 27486261, 27486262, 33657349, 18108376, 18108377, 35695855, 87168518, 60432113, 264404, 22279000, 264488
2177	94128942 (4353, 4354)	Novel Protein sim. GBank gi 5454072 ref NP_006416.1 pslU7 - step II splicing factor SLU7		kinase	18108392, 22278997, 22278999, 284083, 33857402, 265019, 264448, 264766, 264689, 21906767, 21908768, 21908769, 265021, 33657023, 18108370, 18108374, 60432113, 22279002
2178	87601557 (4355, 4356)	Novel Protein sim. GBank gi 473407 (U08215) - NST-1 [Mus musculus]	Contains protein domain (PF00012) - Hsp70 protein	eph	264488, 22278996, 22278999, 29331824, 29331825, 29331826, 29331827, 52644296, 87168474, 18108370, 35695855, 22279002
2179	87316275 (4357, 4358)			UNCLASSIFIED	60424269, 264760, 264628, 264632



2180	95351397 (4359, 4360)	Novel Protein sim. GBank gi 3123217 sp P90848 KMB_DICDI - MYOSIN HEAVY CHAIN KINASE B (MHCK B)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	52644507, 22278994, 35695286, 22278997, 22278998, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 33658970, 264508, 264509, 264906, 264908, 29331830, 264909, 264510, 265006, 265007, 33657402, 55812038, 21806754, 87168474, 87168559, 265017, 265018, 265019, 264763, 264682, 264683, 264684, 264288, 264686, 21906765, 21906768, 21906769, 265020, 265021, 265022, 52844150, 33657023, 33657109, 27486265, 33657349, 18108374, 35696423, 35695855, 263981, 60170394, 18108385, 56526486, 87168518, 60432113, 22279000, 264482, 264568, 264567, 264486, 29331827, 264369, 18108376, 264564
2181	85764930 (4361, 4362)	Novel Protein sim. GBank gi 3024689 sp Q15542 T2D4_HUMAN - TRANSCRIPTION INITIATION FACTOR TFIID 100 KD SUBUNIT (TAFII-100) (TAFII100)		kinase	
2182	87637731 (4363, 4364)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	22278996, 22278997, 22278999, 264259, 29331822, 58182435, 264112, 264764, 264286, 21906767, 21906768, 21906769, 33657109, 18108376, 60170394, 22279000, 22279002 264760
2183	85460649 (4365, 4366)	Novel Protein sim. GBank gi 3873406 gb AAC77482.1  - (U17129) unknown [Rhodococcus erythropolis]		inf	29331822, 29331825, 29331826, 56182435, 265011, 264685, 264686, 21906768, 18108370, 264629, 264631, 264636, 264557, 29331824, 264907, 66712502, 264757, 265019, 264288, 264692, 56526486
2184	87760690 (4367, 4368)	Novel Protein sim. GBank gi 3114713 (AF061346) - Edp1 protein [Mus musculus]			
2185	87826463 (4369, 4370)	Novel Protein sim. GBank gi 5106956 gb AAD39906.1 AF113611 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]		ATPase associated	264259, 29331822, 29331824, 29331826, 56182435, 264592, 55812038, 264760, 264766, 55811957, 33657023, 55811576, 56182323, 264563
2186	87739227 (4371, 4372)	Novel Protein sim. GBank gi 2864625 emb CAA16972  - (AL021811) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	35696052, 264905, 264906, 264907, 264908, 264510, 264511, 265008, 264910, 264758, 265019, 264762, 264681, 264766, 264769, 35695917, 264692, 35696423, 264631, 264635, 264637, 18108388, 264588, 264486
2187	87388173 (4373, 4374)				
2188	87771708 (4375, 4376)	Novel Protein sim. GBank gi 5107816 gb AAD40129.1 AF149411 - (AF149413) contains similarity to histone deacetylases; Pfam PF00850, Score=13.3, E=5e-10, N=1 [Arabidopsis thaliana]		histone	18108398, 56994075, 264259, 29331824, 29331825, 66714117, 29331827, 264906, 29331830, 265018, 265020, 265021, 56182323, 264559, 22279000, 22279002
2189	85693573 (4377, 4378)	Novel Protein sim. GBank gi 3452357 (AF075724) - unknown [Legionella pneumophila]	Contains protein domain (PF01596) - O-methyltransferase		22278996, 264259, 29331826, 21906754, 264369, 264288, 263967

2190	87639197 (4379, 4380)	Novel Protein sim. GBank gij132575[sp]29315[RINJ_RAT - RIBONUCLEASE INHIBITOR]		nucleasainhib	22278996, 22278999, 29331822, 29331824, 29331826, 265008, 264910, 60170831, 55812038, 52844298, 285010, 265018, 264685, 264688, 56181562, 21908789, 35695917, 265022, 60170394, 22279000
2191	95198928 (4381, 4382)	Novel Protein sim. GBank gij5327002[emb]CAB46272.1] - (Y18503) XAP-5-like protein [Homo sapiens]			29331825, 29331826, 29331830, 264510, 264511, 264910, 264593, 264594, 264556, 264559
2192	11126316 (4383, 4384)	Novel Protein sim. GBank gij462600[sp]P34400[Mi10_CAEEL - MIG-10 PROTEIN PH domain]	Contains protein domain (PF00169) - PH domain		264558
2193	94140073 (4385, 4386)	Novel Protein sim. GBank gij5420389[emb]CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	56181686, 29331825, 29331827, 264508, 264909, 265008, 264592, 60432228, 264288, 264684, 264766, 35695917, 33657023, 60431602, 60431528, 55810764, 55811576, 65274791, 35695955, 60431850, 56182323, 60432113
2194	21418714 (4387, 4388)	Novel Protein sim. GBank gij2773341 (AF040954) - putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]			264592
2195	88083023 (4389, 4390)	Novel Protein sim. GBank gij2832783[emb]CAA15685.1] - (AL009191) /prediction=(method: /prediction=(method: /match=(desc: /match=(desc: /molli=(desc: [Drosophila melanogaster]		UNCLASSIFIED	22278996, 22278999, 35696052, 265006, 21908754, 265017, 35695917, 265021, 265022, 35695855
2196	95091631 (4391, 4392)	Novel Protein sim. GBank gij5262487[emb]CAB45699.1] - (AL080076) hypothetical protein [Homo sapiens]		collagen	56182575, 35696286, 22278997, 22278999, 264259, 29331822, 66714117, 80432289, 29331827, 35696052, 29331828, 264508, 52644045, 56182435, 264510, 265007, 265008, 265009, 60433438, 55812038, 265010, 265011, 264448, 264288, 264686, 264687, 52844228, 21908765, 21908768, 21908767, 35695917, 285022, 264691, 33657023, 264693, 18108370, 18108376, 35696423, 55811576, 65274791, 35695955, 264636, 56182323, 18108385
2197	95073813 (4393, 4394)	Novel Protein sim. GBank gij4929567[gb]AAD34044.1]AF15180 - (AF151807) CGI-49 protein [Homo sapiens]			264768, 264769, 21906765, 21906766, 21906767, 29148627, 55811857, 35696286, 265020, 22278998, 265021, 264259, 33657023, 264693, 29331824, 35696052, 29331828, 18108370, 35695855, 264113, 265008, 264910, 60432228, 56182323, 33657402, 264758, 83373044, 21908754, 265018, 265019, 22279002, 264482, 264448, 264565, 264288, 264389
2198	88060914 (4395, 4396)	Novel Protein sim. GBank gij3548787 (AC005622) - R30953_1 [Homo sapiens]		UNCLASSIFIED	

2199	88054355 (4397, 4398)	Novel Protein sim. GBank gij2739372 (AC002505) - hypothetical protein [Arabidopsis thaliana]			264105, 264110, 264112, 264688, 55811957, 33657023, 264692, 263967, 20281071, 56526486
2200	87405385 (4398, 4400)	Novel Protein sim. GBank gij3043634[dbj BAA25481] - (AB011127) KIAA0555 protein [Homo sapiens]	struct		29331824, 264763, 264768
2201	94316872 (4401, 4402)	Novel Protein sim. GBank gij3913470[sp O57314 DHBX_ANAPL - PUTATIVE STEROID DEHYDROGENASE SPM2	Contains protein domain (PF00106) - dehydrogenase short chain dehydrogenase		29331824, 35696052, 264905, 264907, 33857402, 55811386, 265017, 265018, 265019, 264288, 21906768, 35695917, 265020, 265022, 33657023, 33657109, 27486261, 18108370, 35696423, 35695855, 264555, 264556, 83373044, 87168518, 60432113
2202	91672385 (4403, 4404)	Novel Protein sim. GBank gij5262665[emb CAB45767.1] - (AL080186) hypothetical protein [Homo sapiens]	UNCLASSIFIED		264489, 264259, 29331824, 60432289, 35696052, 264905, 264909, 264592, 265017, 265018, 265019, 18108351, 264762, 264448, 264368, 264288, 264766, 21906765, 21906766, 264690, 264691, 264692, 33657109, 264634, 264636, 264555, 264639, 264558, 264559, 83373044, 18108385, 264404, 22279002, 264482
2203	87761832 (4405, 4406)	Novel Protein sim. GBank gij1172845[sp P46629 RB25_RABIT - RAS-RELATED PROTEIN RAB-25	Contains protein domain (PF00071) - glycoprotein Ras family		52646365, 56994075, 264259, 29331822, 29331826, 29331827, 29331828, 264910, 265010, 265011, 87168559, 265018, 265019, 264605, 264288, 21906769, 35695917, 33657023, 264692, 33657109, 35695763, 18108376, 264638, 22279000, 264566, 264567
2204	8808671 (4407, 4408)	Novel Protein sim. GBank gij121036[sp P29348 GRT3_RAT GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-3 SUBUNIT (GUSTOUCIN ALPHA-3 CHAIN)	UNCLASSIFIED		
2205	94147589 (4409, 4410)	Novel Protein sim. GBank gij459480[dbj BAA76768.1] - (AB023141) KIAA0924 protein [Homo sapiens]	dna_rna_bind Zinc finger, C2H2 type		18108394, 18108397, 56182575, 60432049, 264259, 29331822, 29331824, 29331825, 29331828, 29331827, 264906, 265007, 265008, 265009, 80432229, 265010, 265011, 265018, 264683, 264288, 264369, 264686, 21906766, 21906768, 21906769, 264690, 264691, 264693, 18108388, 55811576, 65274791, 264634, 18108381, 18108384, 60432113, 22279002, 264563, 264566, 264591
2206	20620008 (4411, 4412)	Novel Protein sim. GBank gij4557753[ref NP_000372.1 pMID1 - midline 1 protein	UNCLASSIFIED		29331822, 56182181, 29331827, 35696052, 52644045, 265006, 265019, 56181562, 55811957, 265021, 33657023, 35695763, 35695855, 60170394, 60432113, 264566
2207	87787970 (4413, 4414)	Novel Protein sim. GBank gij4557753[ref NP_000372.1 pMID1 - midline 1 protein	Contains protein domain (PF00622) - SPRY domain		264906, 265019, 18108351, 21906769
2208	86100830 (4415, 4416)	Novel Protein sim. GBank gij3966746 (AF105226) - lutealin	struct		264112, 265009, 264691, 18108385, 18108374, 264634, 20281166
2209	87800420 (4417, 4418)	Novel Protein sim. GBank gij3966746 (AF105226) - lutealin [Bos taurus]			

2210	57152407 (4419, 4420)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	284603	
2211	87341720 (4421, 4422)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		oncogene	264685, 264686, 18108365, 22278002, 264482	
2212	91223824 (4423, 4424)	Novel Protein sim. GBank gi 3776027 emb CAA09214  - (AJ010475) RNA helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278895, 22278997, 22278998, 264092, 264094, 29331822, 66714117, 29331826, 29331828, 284907, 52644045, 265009, 60170831, 21906754, 87188559, 265017, 265019, 18108351, 264683, 18108354, 264389, 264766, 264687, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 33657109, 18108370, 18108374, 264638, 56182323, 18108384, 18108387, 87168518, 264585	
2213	91219309 (4425, 4426)	Novel Protein sim. GBank gi 5420387 emb CA846679.1  - (AJ243459) proteophosphoglycan [Leishmania major]			56182575, 22278896, 22278997, 35696052, 264905, 66712502, 264908, 264828, 56182435, 264112, 265008, 60431735, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 18108351, 264765, 21906765, 21906766, 21906769, 265020, 265021, 264693, 264629, 263974, 263976, 18108379, 55811576, 264556, 264637, 264558, 83373044, 22278002, 264482, 264483	

2214	95361453 (4427, 4428)	Novel Protein sim. GBank gi 4504325 ref NP_000173.1 pHADH - hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	Contains protein domain (PF00725) - dehydrogenase 3-hydroxyacyl-CoA dehydrogenase	264488, 52644507, 18108394, 56182575, 22278994, 22278995, 35696288, 56994075, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 52645080, 28331822, 29147620, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 20281100, 264509, 264907, 66712502, 264908, 29331830, 52644045, 56182435, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 60170831, 264593, 60433356, 60433438, 33109954, 33657084, 52644298, 87168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 18108351, 264448, 264682, 264763, 264288, 264687, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 264532, 60170615, 264690, 52644150, 264691, 33657023, 264692, 18108384, 33657109, 33657182, 27486262, 27486284, 27486285, 35695763, 18108370, 264629, 60431528, 18108374, 18108376, 55810764, 35696423, 35695855, 264634, 264636, 52644332, 264638, 264558, 60170394, 18108381, 56182323, 83373044, 18108385, 18108387, 18108388, 56526486, 87168518, 60432113, 22279002, 264482, 264564, 264565, 264566, 264909, 265006, 264555, 264558, 87168518
2215	95418206 (4428, 4430)	Novel Protein sim. GBank gi 1947160 (AF000288) - weak similarity to collagens; glycine- and proline-rich (Caenorhabditis elegans)		
2216	87614046 (4431, 4432)	Novel Protein sim. GBank gi 1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]	UNCLASSIFIED	264693
2217	80589404 (4433, 4434)	Novel Protein sim. GBank gi 5031707 ref NP_005503.1 pGARP - glycoprotein A repetitions predominant	Contains protein domain (PF00560) - Leucine Rich Repeat	264288, 33657109, 264556
2218	85518254 (4435, 4436)	Novel Protein sim. GBank gi 3878636 emb CAA88953  - (Z49128) similar to cAMP-dependent protein kinase; cDNA EST EMBL:T00719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk492f4.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35696423, 264563
2219	87614046 (4437, 4438)	Novel Protein sim. GBank gi 1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]	Contains protein domain (PF01963) - TraB family	264682, 264683, 264688, 264689, 264693, 18108370, 18108376

2220	95354165 (4439, 4440)	Novel Protein sim. GBank gi 4507281 refNP_003145.1 pSTAT - stattherin			264486, 18108394, 18108395, 35695286, 264259, 264097, 60432289, 264508, 264805, 264905, 264907, 29331830, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 264593, 264594, 60433358, 264595, 55812038, 264758, 85858542, 265010, 264601, 264603, 265019, 264605, 264760, 264762, 264448, 264764, 264368, 264766, 18108357, 264768, 264687, 18108358, 264769, 55811957, 264690, 264691, 33857023, 264692, 18108362, 18108368, 264628, 264629, 18108374, 263978, 264634, 264635, 264636, 264637, 264638, 18108385, 264483, 264566, 264486, 264587
2221	88060927 (4441, 4442)	Novel Protein sim. GBank gi 3549154 (AC005625) - R27328_1 [Homo sapiens]			
2222	84425892 (4443, 4444)			UNCLASSIFIED	264908, 265020, 35695855
2223	95091649 (4445, 4446)			UNCLASSIFIED	265010, 264685, 264690, 264693, 264628, 263974, 263976, 55811576, 264555, 264638, 83373044, 264483
2224	87388515 (4447, 4448)	Novel Protein sim. GBank gi 3876005 emb CAA84799  - (Z35719) cDNA EST EMBL:D67419 comes from this gene; cDNA EST EMBL:C13853 comes from this gene; cDNA EST EMBL:C11578 comes from this gene; cDNA EST yk234a7.3 comes from this gene; cDNA EST yk234a7.5 comes from this gene; cDNA ES...	Contains protein domain (PF01958) - Domain of unknown function	UNCLASSIFIED	264259, 264509, 56182435, 265006, 265008, 265009, 264757, 21808754, 18108351, 264693, 18108374, 18108385
2225	85749484 (4449, 4450)	Novel Protein sim. GBank gi 1255847 (U53338) - C05E11.1 [gene product] [Caenorhabditis elegans]		transport	22278994, 22278995, 22278999, 52844045, 264600, 265019, 21808785, 21808769
2226	86878953 (4451, 4452)	Novel Protein sim. GBank gi 4826524 emb CAB42852.1  - (AL049848) hypothetical protein [Homo sapiens]			264259, 29331822, 29331824, 29331825, 29331827, 264508, 264908, 265007, 264691, 264634, 264486
2227	87721135 (4453, 4454)			UNCLASSIFIED	22278999, 265006, 265008, 18108354, 29148629, 29148784, 27486281, 18108374, 264637, 18108384
2228	91227337 (4455, 4456)	Novel Protein sim. GBank gi 606976 (U16800) - ribonucleoprotein [Xenopus laevis]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	264091, 264092, 264094, 29331822, 29331825, 66714117, 264693, 263972, 264639, 83373044, 264563
2229	88060931 (4457, 4458)	Novel Protein sim. GBank gi 3549155 (AC005625) - R27328_2 [Homo sapiens]		UNCLASSIFIED	

2230	95342915 (4459, 4460)	Novel Protein sim. GBank gij226154jiprj11412350A - DNA polymerase [Human adenovirus type 2]		UNCLASSIFIED	264488, 264768, 52644507, 264769, 21906765, 21906766, 21906767, 21906769, 22278995, 22278996, 22278997, 22278998, 22278999, 265021, 264259, 52645129, 29331827, 264508, 264509, 264907, 18108370, 18108374, 35696423, 35695855, 265007, 264910, 264555, 33657402, 21906754, 18108387, 265010, 265018, 265019, 264760, 264288, 264587, 264563
2231	88060937 (4461, 4462)	Novel Protein sim. GBank gij3549154 (AC005625) - R27328.1 [Homo sapiens]		UNCLASSIFIED	
2232	87762581 (4463, 4464)	Novel Protein sim. GBank gij5281316jgb/AAD41478.1 [AF133124] transcription factor IIC63 [Homo sapiens]		transcript factor	18108394, 56182575, 22278995, 35696286, 22278997, 22278999, 264259, 29331827, 35696052, 264907, 56182435, 265006, 265007, 265008, 264910, 264758, 55812038, 264603, 265018, 265019, 18108351, 264682, 264764, 264683, 264368, 264288, 264686, 264687, 264689, 21906765, 21906768, 21906767, 21906769, 29148829, 35695917, 264690, 52844150, 264691, 33657023, 264693, 18108370, 18108374, 55811576, 35695855, 264639, 18108385, 264564, 264906, 33657402, 265018, 264288, 264686, 265020, 264635, 18108385
2233	87755292 (4465, 4466)	Novel Protein sim. GBank gij4249733jgb/AAD13780j - (AF109377) dIBp [Mus musculus]		kinase	56182435, 264369, 264688, 21906765, 265020, 264693, 264556, 56526486
2234	87771817 (4467, 4468)	Novel Protein sim. GBank gij1706559jipP54352IEAS_DROME - ETHANOLAMINE KINASE (EASILY SHOCKED PROTEIN)		UNCLASSIFIED	22278997, 264563
2235	91012316 (4469, 4470)	Novel Protein sim. GBank gij4972734jgb/AAD34762.1j - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat		284569, 264687, 264769, 265022, 264259, 60432049, 264691, 29331826, 60432289, 20281149, 264906, 264907, 264511, 265008, 265009, 264634, 264635, 264636, 264555, 264556, 264557, 264558, 60433356, 264595, 264559, 60433438, 60432113, 264761, 264762, 264763, 264764
2236	88003131 (4471, 4472)	Novel Protein sim. GBank gij1082675jiprj1853814 - p20 protein - human	Contains protein domain (PF00011) - eph Hsp20/alpha crystallin family		264488, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 22278995, 22278996, 22278997, 22278998, 265020, 265021, 22278999, 264259, 29331824, 29331826, 29331827, 35695763, 18108376, 35695855, 265007, 60432229, 33657402, 60433356, 60433438, 83373044, 18108385, 21906754, 18108387, 60432113, 22279000, 265018, 22279002, 264482, 18108351, 264288
2237	91012318 (4473, 4474)	Novel Protein sim. GBank gij4972734jgb/AAD34762.1j - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	

2238	84998857 (4475, 4476)		Contains protein domain (PF00286) - Viral coat protein	264509, 264907, 264629, 264634, 264564
2239	87798688 (4477, 4478)			29331825, 265009, 264369, 33657109, 18108370, 18108374, 264557, 264539, 264488, 65274572, 56182575, 35698286, 22278997, 22278999, 264259, 29331827, 35696052, 264508, 52644045, 56182435, 264511, 265007, 265008, 265009, 60433356, 60433438, 55812038, 21906754, 33657084, 55811386, 265018, 265019, 18108351, 264683, 264288, 264768, 264687, 264688, 264769, 21908765, 21908768, 21908769, 35695917, 265021, 265022, 60170615, 52644150, 33657023, 33657182, 33657349, 35695763, 18108370, 35698423, 35695855, 87168518, 22279000
2240	94121471 (4479, 4480)	Novel Protein sim. GBank gij2982311 (AF051240) - probable ubiquitin-conjugating enzyme E2 [Picea mariana]	ubiquitin	
2241	80091951 (4481, 4482)			
2242	91228075 (4483, 4484)	Novel Protein sim. GBank gij2484312 (spjP7054) IE2BG RAT - TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)	UNCLASSIFIED synthase	22278995, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 264509, 265007, 265009, 264596, 21908754, 265010, 265011, 265017, 265018, 265019, 264448, 264369, 264288, 52644229, 21908765, 21908768, 21908767, 21908768, 21908769, 265020, 265021, 33657109, 27486262, 27486264, 18108374, 35695855, 264634, 264637, 56182323, 83373044, 56526486, 87168518, 264564
2243	78902026 (4485, 4486)			
2244	85723527 (4487, 4488)	Novel Protein sim. GBank gij2291143 (AF016417) - Similar to BZIP transcription factor [Caenorhabditis elegans]	UNCLASSIFIED	265008 264604
2245	95318545 (4489, 4490)	Novel Protein sim. GBank gij470340 (U00043) - similar to beta-mannosyltransferase [Caenorhabditis elegans]	Contains protein domain (PF00534) - Glycosyl transferases group 1	52645156, 22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331827, 264907, 264512, 60433438, 264758, 21908754, 265011, 264603, 264764, 264687, 21908767, 21908768, 21908769, 55811857, 265022, 264691, 264629, 35698423, 264638, 18108387, 60432113, 22279000, 22279002, 264566



2246	94948710 (4491, 4492)	Novel Protein sim. GBank gij4996096[dbj BAA78326.1] - (AB028089) activator of S phase Kinase [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	Transport	65274572, 22278995, 35696286, 22278996, 22278997, 22278999, 264259, 35696052, 264108, 264905, 264907, 265006, 265007, 265008, 60433438, 33109954, 87168559, 265018, 265019, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265022, 27486284, 18108370, 18108374, 65274791, 35695855, 60432113
2247	87862542 (4493, 4494)	Novel Protein sim. GBank gij854065[emb CAA58337] - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	UNCLASSIFIED	35696970, 52646317, 33637084, 265017, 21908768, 21908769, 35695917, 33657109, 52645129, 33657182, 27486261, 27486262, 33657349, 27486265, 18108387
2248	95412996 (4495, 4496)	Novel Protein sim. GBank gij4758502[ref NP_004123.1]pHABP - hyaluronan-binding protein 2	Contains protein domain (PF00089) - Trypsin	calhepsin	284488, 264259, 264907, 29331830, 264909, 265007, 265009, 264595, 21906754, 65274444, 264603, 265019, 264762, 264448, 264288, 264689, 21906766, 55811957, 265021, 264691, 18108374, 264634, 264635, 264636, 264555, 264638, 264557, 264558, 264559, 18108383, 83373044, 18108385, 264486
2249	94685662 (4497, 4498)	Novel Protein sim. GBank gij4038461 (AF107772) - TcST11 [Trypanosoma cruzi]	Contains protein domain (PF00515) - TPR Domain	eph	264766, 264628, 264636, 264637
2250	79827508 (4499, 4500)	Novel Protein sim. GBank gij3738140[emb CAA2124.1] - (AL031852) valyl-tRNA synthetase, mitochondrial precursor [Schizosaccharomyces pombe]	UNCLASSIFIED	UNCLASSIFIED	264908, 18108374
2251	87385863 (4501, 4502)	Novel Protein sim. GBank gij3218467[emb CAA07090.1] - (AJ006529) putative phosphatase [Gallus gallus]	UNCLASSIFIED	UNCLASSIFIED	264259, 35696052, 264508, 56182435, 265009, 264592, 264593, 264760, 264448, 264684, 264288, 264690, 264628, 55811576, 264555, 264556, 264557, 264558, 264559, 264568
2252	87735867 (4503, 4504)	Novel Protein sim. GBank gij4929325[gb AAD33953.1]AF14531 - (AF145316) vacuolar ATP synthase subunit D proton pump della polypeptide [Homo sapiens]	Contains protein domain (PF01813) - ATP synthase subunit D	synthase	264092, 264094, 264259, 29331822, 66714117, 29331828, 264102, 264103, 264104, 264105, 264109, 264112, 264511, 265007, 60433356, 265010, 18108351, 21906767, 21906768, 264691, 263974, 263977, 264486, 264567
2253	91010703 (4505, 4506)		UNCLASSIFIED	UNCLASSIFIED	65274572, 265019

2254	95320031 (4507, 4508)	Novel Protein sim. GBank gij4502847[re]NP_001271.1]pCIRB - cold inducible RNA- binding protein	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	284569, 18108394, 18108398, 56182575, 56994075, 35698266, 22278999, 284094, 60432049, 284259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 35698052, 284106, 284508, 284509, 284906, 284907, 29331830, 66712502, 284908, 284909, 284510, 265006, 284511, 265007, 265008, 265009, 60170831, 60432229, 60433358, 60433438, 284758, 85858542, 265010, 265011, 87188559, 265017, 265018, 265019, 264448, 284764, 284286, 284369, 284766, 284686, 284768, 284769, 21908765, 21908767, 55811857, 284691, 33657023, 284692, 18108362, 65274820, 283969, 284628, 18108370, 60431528, 263972, 264629, 18108372, 18108377, 18108379, 55811576, 35698423, 35698555, 264630, 264634, 264635, 264636, 284556, 263981, 264638, 56182323, 60170394, 264558, 18108381, 18108382, 83373044, 18108385, 87188518, 60432113, 22279002, 284482, 284564, 284565, 284488, 284587, 18108391
2255	91010546 (4509, 4510)	Novel Protein sim. GBank gij5541865[emb]CAB51072.1] - (AL096858) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	struct	65274572, 56182575, 22278997, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 284508, 284905, 264906, 264907, 66712502, 264908, 56182435, 284510, 284511, 265008, 284593, 284595, 21906754, 33109954, 87168474, 285011, 265017, 265019, 284682, 284764, 284369, 284288, 284766, 284685, 284686, 284768, 21906765, 21906766, 21906768, 21906769, 285020, 60170815, 52844150, 284690, 284692, 284693, 33657109, 33657349, 264632, 284636, 52844332, 56182323, 22279000, 22279002
2256	87020531 (4511, 4512)	Novel Protein sim. GBank gij3327174[db]BAA31655] - (AB014580) KIAA0680 protein [Homo sapiens]		UNCLASSIFIED	264768, 264689, 18108374
2257	80088235 (4513, 4514)			UNCLASSIFIED	22278996, 22278999, 284681, 21908765, 21908768, 284587
2258	88090516 (4515, 4516)	Novel Protein sim. GBank gij3025446 (AC004528) - R32184_2 [Homo sapiens]	Contains protein domain (PF00050) - Ligand-gated ion channel	misc_channel	284908, 284592, 284764

2259	95364155 (4517, 4518)	Novel Protein sim. GBank gi 4884140 emb CAB3278.1 - (AL050110) hypothetical protein [Homo sapiens]	UNCLASSIFIED	18108396, 65274572, 58182575, 22278997, 22278998, 264259, 29331822, 29331827, 264905, 66712502, 264908, 264909, 56182435, 265007, 265008, 60432229, 33657084, 87188559, 18108351, 264448, 264883, 264288, 264369, 58181582, 265021, 60170815, 264690, 33657109, 60431528, 18108374, 52644332, 56182323, 18108385, 22278900, 22278902, 264482
2260	88084119 (4519, 4520)	Novel Protein sim. GBank gi 3080663 (AC004614) - similar to f-spondin proteins AB006086 (PID:g2529225) [Homo sapiens]	oxidase	56182575, 265020, 264905, 264906, 264908, 35596423, 264511, 264635, 55812038, 264758, 265018, 265019, 264805, 264760, 264563
2261	88074157 (4521, 4522)	Novel Protein sim. GBank gi 3334526 emb CAA16138 - (AL021306) predicted using FGENEH [Homo sapiens]	UNCLASSIFIED	
2262	91639282 (4523, 4524)	Novel Protein sim. GBank gi 4877759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]		56182575, 22278999, 29331822, 29331825, 60432228, 29331827, 35596052, 264508, 66712502, 52644045, 56182435, 265008, 265009, 60433356, 55812038, 265010, 265017, 265019, 264288, 264369, 21906765, 21906767, 55811957, 35595917, 52844150, 33657023, 33657109, 55811576, 65274791, 56182323
2263	87602495 (4525, 4526)	Novel Protein sim. GBank gi 3341697 (AC003672) - hypothetical protein [Arabidopsis thaliana]		22278994, 22278997, 264907, 264828, 52644150, 18108351, 264693, 18108374
2264	87756525 (4527, 4528)	Novel Protein sim. GBank gi 1657801 (U66220) - unknown [Nannocystis exedens]	UNCLASSIFIED	264686, 264488, 264768, 264769, 264691, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 35695855, 264510, 264511, 264512, 265007, 265009, 264638, 264639, 264757, 264758, 18108385, 265011, 264760, 264584, 264565, 264764, 264566, 264486, 264766
2265	86918683 (4529, 4530)	Novel Protein sim. GBank gi 477072 pr A48018 - mucin 7 precursor, salivary - human	UNCLASSIFIED	264689, 264910, 264764
2266	8773458 (4531, 4532)	Novel Protein sim. GBank gi 3150479 (AF067212) - partial CDS [Caenorhabditis elegans]	ribosomal prot	22278995, 22278997, 22278999, 264259, 265008, 265007, 265009, 60433438, 21906754, 265010, 265011, 265017, 264448, 264683, 264288, 264689, 21906765, 21906768, 35695917, 265021, 18108374, 264638, 22278900, 22279002, 264566, 264487

2267	87395838 (4533, 4534)	Novel Protein sim. GBank gl 3560229 emb CAA20697.1  - (AL031530) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35698286, 264259, 29331824, 29331825, 35698052, 29331828, 264905, 264509, 264907, 264908, 264909, 264512, 265009, 264910, 264593, 33657402, 265010, 265018, 264762, 264448, 264288, 264369, 264768, 52644229, 35695917, 264691, 33657023, 18108382, 33657109, 35698423, 264634, 18108381, 87168518, 264568
2268	85883887 (4535, 4536)	Novel Protein sim. GBank gl 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	cadherin		264488, 264259, 264509, 264595, 265010, 265017, 264766, 18108385, 264486
2269	88177677 (4537, 4538)	Novel Protein sim. GBank gl 103418 pir S17885 - Tcd37 protein - fruit fly (Drosophila melanogaster)	UNCLASSIFIED		56182575, 60432049, 265007, 265009, 264591, 87168559, 264605, 18108351, 21906764, 265020, 264628, 60431528, 264638, 18108385, 18108387, 60432113
2270	80410327 (4539, 4540)				264763
2271	91010392 (4541, 4542)		cyto450		264609, 56182435, 285008, 55812038, 55811957, 33657023, 264693, 33657109, 55810764, 55811576, 56182323
2272	84208220 (4543, 4544)		UNCLASSIFIED		264905, 264908
2273	95014271 (4545, 4546)	Novel Protein sim. GBank gl 4176370 (AC005058) - similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	Contains protein domain (PF00462) - Glutaredoxin		52645156, 22278996, 22278999, 60432048, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264909, 265006, 264593, 60433438, 21906754, 265018, 264688, 21908765, 21908766, 21908767, 21908769, 265021, 265022, 60170815, 264691, 33657023, 264693, 33657109, 27486284, 18108376, 35696423, 35695855, 264630, 52644332, 264558, 56182323, 22279002
2274	91640217 (4547, 4548)	Novel Protein sim. GBank gl 1480112 emb CAA67961  - (X99842) HP1-BP74 protein [Mus musculus]	Contains protein domain (PF00538) - linker histone H1 and H5 family	histone	52645156, 22278997, 22278999, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 52644045, 264511, 265008, 265009, 60170831, 264591, 21908754, 33109954, 265011, 265016, 18108351, 264448, 264288, 264684, 264768, 21908765, 21906766, 21906767, 21906768, 52644150, 264693, 18108384, 35695783, 18108374, 35698423, 264634, 264557, 264638, 52644332, 83373044, 18108385, 56528486, 87168518, 22279002
2275	88082501 (4549, 4550)	Novel Protein sim. GBank gl 3165406 (AC004755) - fos37502.2 [Homo sapiens]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	
2276	11287447 (4551, 4552)		UNCLASSIFIED		264555, 264556

2277	88084123 (4553, 4554)	Novel Protein sim. GBank gll2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369906) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278999, 35696052, 265008, 265019, 264389, 265020, 265022, 55810764, 264404, 22279002
2278	94133078 (4555, 4556)	Novel Protein sim. GBank gll2618702 (AC002510) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	18108394, 22278997, 29331826, 60433356, 60433438, 21906754, 265018, 33657023, 264639, 83373044, 264565
2279	80419375 (4557, 4558)	Novel Protein sim. GBank gll19714 (sp P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	264766, 264565
2280	94239723 (4559, 4560)	Novel Protein sim. GBank gll424029 (db BAA74928.1  - (AB020712) KIAA0805 protein [Homo sapiens])	Contains protein domain (PF00400) - WD domain, G-beta repeat	transport	265008, 33109954, 265010, 265019, 265020, 264092, 264259, 29331822, 29331824, 29331826, 35696052, 264107, 264906, 264909, 52844045, 265008, 33657402, 60433356, 264758, 265011, 265019, 264881, 264883, 264684, 264686, 21906765, 21906767, 21906768, 21906769, 60170615, 264690, 52644150, 18108382, 264692, 18108368, 18108374, 283978, 264631, 18108381, 264559, 18108385, 56526486, 22279000, 264566, 264567
2282	87602829 (4563, 4564)	Novel Protein sim. GBank gll1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]		UNCLASSIFIED	264488, 264259, 29331822, 29331824, 29331827, 29331828, 29331830, 33657402, 60433438, 87169474, 265019, 18108351, 21906767, 21906769, 55811957, 33657023, 52845129, 33657109, 33657182, 27466262, 263972, 55811576, 87168518, 20281169
2283	95362386 (4565, 4566)	Novel Protein sim. GBank gll2495729 (sp Q92556 Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)		UNCLASSIFIED	60424179, 56182575, 22278994, 35696286, 22278997, 22278999, 29331822, 29331824, 58182181, 29331825, 29331827, 35696052, 29146499, 264905, 66712502, 264908, 265007, 265009, 60432229, 264593, 60431735, 60433356, 33109954, 33657084, 55811386, 87169474, 265010, 265011, 265018, 265019, 55811150, 264683, 264369, 264288, 264688, 21906765, 21906767, 21906768, 23146627, 21906769, 55811957, 265020, 265022, 33657182, 27466261, 18108370, 264628, 18108374, 55810784, 18108379, 55811576, 35696423, 35695855, 264630, 60431850, 263981, 18108382, 83373044, 18108385, 18108387, 60432113, 22279000, 264482, 264567

2284	95414955 (4567, 4588)	Novel Protein sim. GBank gi2498797 sp O6431.1 PNAO_MOUSE - PROTEIN N- TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN- AMIDASE) (PNAO) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAO)			60424178, 52644507, 18108394, 52848842, 22278994, 35686288, 22278996, 22278997, 22278999, 264259, 60432049, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35686052, 29331830, 52644045, 56182435, 33657402, 60433438, 33109954, 21906754, 85858542, 87188559, 265018, 265019, 55811150, 264682, 284369, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 33657023, 33657182, 27486262, 27486264, 27486265, 18108376, 55810764, 35696423, 35695855, 60431850, 87188518, 60432113, 284482, 264584
2285	87781484 (4568, 4570)	Novel Protein sim. GBank gi3342234 (U93909) - nuclear antigen EBNA-1 [Cercopithecine herpesvirus 15]		collagen	35696052, 264905, 264907, 264908, 264909, 264512, 265009, 264910, 264595, 284760, 18108351, 264682, 264763, 264685, 264766, 264686, 264768, 264693, 264629, 35695855, 264631, 264634
2286	87737825 (4571, 4572)	Novel Protein sim. GBank gi3873414 (U00043) - similar to D. melanogaster trithorax protein [Caenorhabditis elegans]		kinase	35696286, 56182435, 60170831, 264591, 60432229, 264592, 264593, 264594, 264595, 55812038, 264596, 87188474, 35695917, 264692, 55811576, 264555, 264557
2287	82986696 (4573, 4574)	Novel Protein sim. GBank gi630905 pi S42731 - collagen alpha 1 chain - sea urchin (Hemicentrotus pulcherrimus) (fragment)	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	UNCLASSIFIED	264682
2288	94133083 (4575, 4576)	Novel Protein sim. GBank gi728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		im7	22278995, 56894075, 22278997, 22278999, 264259, 60432289, 264508, 264512, 265008, 33657402, 265017, 265018, 265019, 18108351, 264448, 21906765, 21906766, 21906767, 21906768, 33657023, 264557, 22279000, 22279002
2289	88084133 (4577, 4578)	Novel Protein sim. GBank gi2887497 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	
2290	88084137 (4579, 4580)	Novel Protein sim. GBank gi2887497 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264683
2291	84293281 (4581, 4582)	Novel Protein sim. GBank gi3253120 (AC003175) - R31449_3 [Homo sapiens]		struct	18108394, 284907, 265006, 265008, 33109954, 52846317, 265010, 18108351, 264681, 264686, 264692, 18108370, 18108374, 18108385

2292	94328834 (4583, 4584)	Novel Protein sim. GBank gi 4803672 emb CAB42643.1  - (AJ133769) nuclear transport receptor [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 56994075, 29331824, 29331825, 35696052, 56182435, 60433438, 55812038, 33109954, 87168474, 87168559, 265018, 18108351, 264763, 264448, 264369, 264288, 56181582, 264769, 21908765, 21908766, 21908767, 21908769, 265021, 265022, 33657023, 264693, 65274620, 33657109, 27486264, 264629, 55810764, 55811576, 35695855, 56182323, 56526486, 87168518, 22279000, 264567
2293	87759213 (4585, 4586)	Novel Protein sim. GBank gi 3252981 (AF068921) - Ras-binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00360) - Leucine Rich Repeat	struct	264488, 18108397, 35696286, 264092, 264259, 29331822, 29331826, 264906, 264908, 264511, 264512, 265009, 264910, 18108351, 264764, 264369, 264288, 264885, 264766, 265020, 265022, 264534, 35696423, 264631, 264637, 18108381, 56182323, 264639, 18108385, 264404, 264563, 264565
2294	86693560 (4587, 4588)	Novel Protein sim. GBank gi 2062680 (U88964) - HEM45 [Homo sapiens]	Contains protein domain (PF00929) - Exonuclease	nuclease	22278997, 22278998, 22278999, 264259, 29331822, 60432289, 29331828, 35696052, 265018, 264684, 264288, 264688, 21908765, 21908766, 21908767, 21908768, 21908769, 265020, 265021, 264692, 33657109, 18108376, 35696423, 35695855, 264634, 22279000, 22279002, 264563, 264486
2295	95312200 (4589, 4590)			UNCLASSIFIED	22278996, 60432289, 264682, 264683, 264689, 18108374
2296	80030781 (4591, 4592)				263974, 263978
2297	94321251 (4593, 4594)	Novel Protein sim. GBank gi 5689501 dbj BAA83034.1  - (AB029005) KIAA1082 protein [Homo sapiens]		transcriptfactor	264488, 65274572, 56182575, 22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 35696052, 264907, 264808, 52644045, 56182435, 264112, 265006, 265007, 264910, 265009, 60433356, 33657402, 264595, 55812038, 21908754, 265011, 265018, 265019, 264448, 264764, 264288, 264766, 21908765, 21908767, 21908768, 21908769, 55811957, 265020, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 55811576, 56182323, 60170394, 83373044, 18108385, 56526486, 264564, 264486

2298	95312207 (4595, 4596)	Novel Protein sim. GBank gij3875051[embjCAB02849] - (281050) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D65564 comes from this gene; cDNA EST EMBL:D69046 comes from this gene; cDNA EST yk366b12.3 comes from this gene; cDNA EST yk366b12.5 comes from this gene ...		collagen	60424179, 56181686, 22278995, 35696286, 22278998, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 60424268, 35698052, 29331828, 66712502, 56182435, 284510, 265006, 60433438, 21906754, 33109954, 55811386, 265010, 265018, 55811150, 264762, 18108351, 264682, 264683, 264288, 264684, 264686, 264688, 56181562, 264689, 21906768, 21906767, 29148629, 55811957, 29148784, 35695917, 265020, 18108362, 33657023, 18108384, 33657109, 60431802, 18108370, 60431528, 18108374, 55810784, 35696423, 35695855, 264630, 264634, 60431850, 18108380, 56182323, 264558, 83373044, 18108385, 60432113, 22279000, 264482, 264567, 264486
2299	80193720 (4597, 4598)			UNCLASSIFIED	264369
2300	94124346 (4599, 4600)	Novel Protein sim. GBank gij2443886 (AC002294) - Unknown protein [Arabidopsis thaliana]			264488, 22278998, 22278999, 264259, 29331824, 66714117, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 285008, 264910, 285009, 264758, 285010, 87168559, 264600, 265018, 264760, 264762, 18108351, 264764, 264766, 264768, 264769, 21906766, 21906767, 35695917, 285021, 264691, 33657023, 35695763, 18108370, 18108374, 35696423, 35695855, 264631, 264636, 264638, 18108385, 22278002, 264583
2301	91235725 (4601, 4602)	Novel Protein sim. GBank gij2143637[pirj184505 - calcium-dependent actin-binding protein - rat]		struct	264908, 264758, 265017, 21906785, 83373044, 264563
2302	88084141 (4603, 4604)	Novel Protein sim. GBank gij2867497 (AC004144) - R34001_1 [Homo sapiens]		UNCLASSIFIED	52644045, 265019, 264288, 33657023, 18108370, 18108385
2303	94141439 (4605, 4606)	Novel Protein sim. GBank gij4884194[embjCAB43220.1] - (AL049946) hypothetical protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	- struct	264259, 60432049, 264907, 264909, 264810, 60432229, 33657402, 285011, 285018, 264762, 264448, 264769, 264637, 264638, 83373044, 264486
2304	94840434 (4607, 4608)	Novel Protein sim. GBank gij2494162[spjQ10005]VRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR		UNCLASSIFIED	264259, 29331824, 21906767, 33657182, 33657348
2305	80935911 (4609, 4610)	Novel Protein sim. GBank gij4972686[gbjAAD34736.1] - (AF132150) unknown [Drosophila melanogaster]			65274572, 22278998, 264908, 265006, 21906768, 264891, 264486



2306	85334840 (4611, 4612)	Novel Protein sim. GBank gi 4929565 gb AAD34043.1 AF15180 - (AF15180) CGI-48 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	Kinase receptor	264488, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 284508, 264905, 264907, 29331830, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 33657402, 21908754, 85658542, 265010, 265011, 264601, 265017, 265018, 264604, 265019, 18108351, 264448, 264288, 264766, 264769, 21908785, 21908766, 21908767, 21908768, 29148629, 29148784, 35695917, 265020, 265021, 265022, 33657023, 264692, 18108370, 18108374, 18108376, 35696423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108382, 18108385, 18108387, 264563, 264568, 264486
2307	79415283 (4613, 4614)			UNCLASSIFIED	264828
2308	87608409 (4615, 4616)	Novel Protein sim. GBank gi 4758732 ref NP_004522.1 pMOCs - molybdenum collator synthesis 2		synthase	35696286, 264259, 29331822, 29331824, 284112, 264512, 264757, 21906754, 264288, 264690, 27486264, 264631, 264634, 264404
2309	95357218 (4617, 4618)	Novel Protein sim. GBank gi 3878059 emb CAB17070  - (Z99942) cDNA EST EMBL:D73444 comes from this gene; cDNA EST EMBL:D70905 comes from this gene; cDNA EST EMBL:D72208 comes from this gene; cDNA EST EMBL:D75030 comes from this gene; cDNA EST EMBL:D72944 comes from this gene; cDN...		glycoprotein	18108387, 22278998, 22278997, 22278998, 22278999, 60432049, 29331822, 29331826, 60432289, 66712502, 60432228, 60433356, 60433438, 65274444, 265010, 264600, 264681, 264448, 264683, 264288, 21908766, 21908768, 265020, 264691, 264692, 264693, 65274620, 65274791
2310	79601668 (4619, 4620)			UNCLASSIFIED	264508
2311	87721189 (4621, 4622)	Novel Protein sim. GBank gi 2137337 pir I48281 - gene mCBP protein - mouse	Contains protein domain (PF00013) - KH domain	transcript factor	18108397, 56182575, 22278996, 56994075, 264259, 29331824, 29331827, 264508, 264907, 56182435, 264510, 264511, 265006, 264512, 265007, 265008, 265009, 60433438, 33109954, 265010, 265011, 264603, 265017, 18108351, 264762, 264683, 264288, 264369, 264686, 33657023, 20281149, 20281069, 264628, 263972, 55811576, 35696423, 20281071, 264632, 264636, 18108385, 18108387, 87168518, 22279000, 264563, 264486

2312	87549881 (4623, 4624)	Novel Protein sim. GBank gii2911264 (AC002550) - Unknown gene product [Homo sapiens]			56182575, 56994075, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 52644045, 60432228, 60433356, 55812038, 33109954, 21906754, 87168474, 265018, 18108351, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 60170815, 33657023, 27486261, 27486264, 35696423, 35695855, 18108385, 22279000, 22279002, 263981
2313	80042533 (4625, 4626)	Novel Protein sim. GBank gii3043626(dbj BAA25477) - (AB011123) KIAA0551 protein [Homo sapiens]			
2314	94313401 (4627, 4628)	Novel Protein sim. GBank gii5598714(jemb CAB51401.1) - (AL035398) dJ79617.2 (CGI-51) [Homo sapiens]		UNCLASSIFIED	52644507, 52646365, 52646842, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 33658970, 52644045, 265008, 264593, 60433356, 60433438, 264758, 33109954, 265010, 285017, 265018, 265019, 264288, 264369, 21906765, 21906766, 21906768, 35695917, 52644150, 33657023, 33657109, 52645129, 33657349, 35695763, 18108374, 35696423, 35695855, 52644332, 22279000, 22279002, 264563, 264567
2315	80430119 (4629, 4630)			UNCLASSIFIED	264905, 264906, 264767, 264768, 264693, 55811578, 264835, 86182323, 18108385
2316	94312191 (4631, 4632)	Novel Protein sim. GBank gii5531827(jgb AAD44488.1) - (AF078856) p47 [Homo sapiens]	Contains protein domain (PF00789) - glycoprotein UBX domain		52644507, 52645158, 52646365, 22278994, 22278995, 22278996, 56984075, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264906, 264907, 29331830, 52644045, 56182435, 264511, 265007, 265008, 265009, 60170831, 60433438, 21906754, 52646317, 33109954, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264681, 264763, 264448, 264683, 264368, 52644229, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 18108362, 52645129, 33657182, 33657348, 35695763, 18108370, 18108378, 35696423, 35695855, 264831, 264556, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113, 22279000, 264568, 264567

2317	87020571 (4633, 4634)			UNCLASSIFIED	22278998, 60432049, 264910, 60432229, 264686, 264687, 264688, 264689, 264558, 18108385
2318	79959879 (4635, 4636)			UNCLASSIFIED	264488, 264569, 18108396, 52646365, 22278994, 22278995, 22278996, 58994075, 35696286, 22278997, 22278998, 264259, 52645080, 29331825, 29331826, 29331827, 29331828, 29331830, 56182435, 60170831, 60432229, 60431735, 33657402, 21908754, 52644298, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 264369, 52644229, 21908764, 21908765, 21908766, 21908767, 21908768, 21908769, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 27486264, 33657349, 35695763, 18108370, 18108376, 18108379, 35696423, 264558, 83373044, 18108385, 58526486, 87168518, 264564, 264565, 264566
2319	95101781 (4637, 4638)	Novel Protein sim. GBank gi 5262613 emb CAB45746.1  - (AL080155) hypothetical protein [Homo sapiens]			
2320	91622426 (4639, 4640)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	kinase		22278994, 60432049, 60432289, 29331827, 264511, 265008, 52646317, 265017, 265018, 21908765, 18108372, 18108387, 22279002
2321	94320377 (4641, 4642)	Novel Protein sim. GBank gi 3873837 emb CAB02700  - (Z81028) Similarity to S.pombe hypothetical protein C1D4.09C (SW-Q10154); cDNA EST EMBL:T00543 comes from this gene; cDNA EST EMBL:T01062 comes from this gene; cDNA EST EMBL:T01321 comes from this gene; cDNA EST EMBL:T02288 com...	UNCLASSIFIED		264488, 264687, 18108394, 264689, 21908765, 18108397, 18108398, 21908767, 21908768, 65274791, 22278995, 35695855, 22278998, 265021, 265022, 264510, 265006, 264511, 264512, 265008, 60170815, 264555, 264636, 264556, 18108361, 264259, 60432229, 33657023, 264557, 264558, 264693, 60433356, 264559, 60433438, 29331824, 18108365, 18108348, 18108384, 29331825, 18108385, 33109954, 29331827, 56526486, 29146499, 265011, 60432113, 265017, 265018, 264508, 264563, 264482, 264509, 18108351, 264448, 264907, 264682, 18108370, 264683, 264908, 264288, 264909, 18108354, 264486, 264567
2322	87803165 (4643, 4644)	Novel Protein sim. GBank gi 5678957 emb CAB51685.1  - (AL109830) BACRTA4.y [Drosophila melanogaster]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	22278996, 264907, 264511, 264757, 18108351, 264788, 264638

2323	94840445 (4645, 4646)	Novel Protein sim. GBank gi 2494162 sp Q10005 YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR	Contains protein domain (PF00226) - eph DnaJ domain	22278994, 22278995, 22278997, 60432049, 264259, 29331822, 33856970, 264509, 58182435, 264511, 265008, 60433358, 60433438, 55812038, 33109954, 21906754, 85658542, 87168474, 265011, 87168559, 265017, 265018, 264760, 264681, 18108351, 264369, 264288, 18108355, 264687, 264688, 21908765, 21908767, 21906768, 55811957, 33695917, 265021, 33657023, 18108362, 27468262, 55811576, 264631, 264555, 83373044, 87168518, 60432113, 22278002 264592, 264593, 265020 265020
2324	86633607 (4647, 4648)	Novel Protein sim. GBank gi 5419865 emb CAB46377.1  - (AL096732) hypothetical protein [Homo sapiens]	ATPase-associated	
2325	88165074 (4649, 4650)	Novel Protein sim. GBank gi 231865 sp P29881 CP4C_BLADI - CYTOCHROME P450 4C1 (CYPIVC1)	Contains protein domain (PF00067) - Cytochrome P450	265006, 264759, 35695855, 56182323
2326	84390962 (4651, 4652)	Novel Protein sim. GBank gi 231865 sp P29881 CP4C_BLADI - CYTOCHROME P450 4C1 (CYPIVC1)	UNCLASSIFIED	
2327	88081648 (4653, 4654)	Novel Protein sim. GBank gi 4240227 dbj BAJ74892.1  - (AB020876) KIAA0869 protein [Homo sapiens]	UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 265007, 264512, 264910, 264758, 265010, 264786, 264768, 264789, 33657023, 264693, 264628, 264631, 264634, 264638, 264639, 264486
2328	83388428 (4655, 4656)	Novel Protein sim. GBank gi 1245105 (U46463) - glutamine repeat protein-1 [Mus musculus]	UNCLASSIFIED	264629, 264635, 264638, 264639, 56182323, 60432113, 264586
2329	87604478 (4657, 4658)	Novel Protein sim. GBank gi 1169343 sp P42209 DIF6_MOUSE - DIFF6 PROTEIN	Contains protein domain (PF00735) - Cell division protein	265017, 264685, 60432113, 264088 265009
2330	67335396 (4659, 4660)	Novel Protein sim. GBank gi 5679136 gb AAD46874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]	transport	
2331	85990463 (4661, 4662)	Novel Protein sim. GBank gi 2104452 emb CAB08779  - (Z85397) unknown [Schizosaccharomyces pombe]	ATPase-associated	35696286, 22278998, 29331824, 60424269, 265008, 265008, 265018, 264448, 264764, 21908765, 35695917, 35695855, 264638, 22279000, 264566
2332	87784182 (4663, 4664)	Novel Protein sim. GBank gi 4966270 gb AA82691.1  - (Z68318) cDNA EST CEMSD62F comes from this gene; cDNA EST EMBL:C07930 comes from this gene; cDNA EST EMBL:C08493 comes from this gene; cDNA EST yk415e8.3 comes from this gene; cDNA EST yk415e8.5 comes from this gene; cDNA EST ...	UNCLASSIFIED	56182575, 56994075, 28331826, 29331828, 264107, 33657402, 87168559, 264683, 35695917, 265021, 33657023, 263976
2333	88206958 (4665, 4666)	Novel Protein sim. GBank gi 4966270 gb AA82691.1  - (Z68318) cDNA EST CEMSD62F comes from this gene; cDNA EST EMBL:C07930 comes from this gene; cDNA EST EMBL:C08493 comes from this gene; cDNA EST yk415e8.3 comes from this gene; cDNA EST yk415e8.5 comes from this gene; cDNA EST ...	UNCLASSIFIED	56182575, 56994075, 28331826, 29331828, 264107, 33657402, 87168559, 264683, 35695917, 265021, 33657023, 263976
2334	94319788 (4667, 4668)	Novel Protein sim. GBank gi 4966270 gb AA82691.1  - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh), Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E- value=1e-13, N=1 [C...]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	56182575, 29331825, 21906768, 264638, 83373044

2335	80046103 (4669, 4670)	Novel Protein sim. GBank gi 3283350 (AF062378) - calmodulin-binding protein SHA1 [Mus musculus]	Contains protein domain (PF00612) - IQ calmodulin-binding motif	struct	18108351, 21906769, 264555
2336	95196121 (4671, 4672)	Novel Protein sim. GBank gi 1929056 (emb CAA72805) - (Y12080) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]		kinase	264907, 35695917, 18108379
2337	95345810 (4673, 4674)	Novel Protein sim. GBank gi 4495063 (emb CA3181.1) - (Z65986) dJ108K11.3 (similar to yeast suppressor protein SRP40) [Homo sapiens]		UNCLASSIFIED	35696286, 22278999, 56182181, 29331825, 60424268, 56182435, 33657402, 55812038, 55811386, 265017, 265018, 285019, 21906788, 35695917, 264691, 33657023, 33657109, 263972, 35696423, 35695855, 60432113
2338	87634045 (4675, 4676)	Novel Protein sim. GBank gi 2224689 (db BAA20829) - (AB002372) KIAA0374 [Homo sapiens]	Contains protein domain (PF00323) - Mammalian defensin	UNCLASSIFIED	18108394, 29331822, 66714117, 60432289, 264906, 56182435, 265009, 60433438, 264596, 265010, 265019, 18108354, 264288, 264369, 55811957, 265021, 33657023, 263976, 55811576, 264632, 56182323, 264639
2339	85663319 (4677, 4678)	Novel Protein sim. GBank gi 3873550 (emb CAA22127) - (AL033534) serine-rich protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35696286, 264592, 264369, 264691, 264558
2340	80937716 (4678, 4680)				65274572, 22278994, 35696286, 22278997, 22278999, 264259, 29331822, 60432289, 29331826, 29331830, 265009, 33657402, 33109994, 265017, 265018, 264786, 264685, 21906769, 35695917, 264691, 264692, 35696423, 87168518, 22279000
2341	8775281 (4681, 4682)	Novel Protein sim. GBank gi 3874563 (emb CA802797) - (Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264259, 264908, 264909, 264682, 22279000
2342	95334068 (4683, 4684)				264488, 65274572, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 35696052, 264905, 264509, 29331830, 265006, 60170831, 60432229, 60433356, 87168474, 265017, 265018, 265019, 264448, 264389, 264288, 21906765, 21906766, 55811957, 35695917, 265020, 265022, 52644150, 33657023, 65274620, 33657109, 18108370, 18108378, 55810764, 35696423, 55811576, 264556, 264558, 18108385, 60432113, 264563, 264584, 264585, 264566, 264567
2343	8775448 (4685, 4686)	Novel Protein sim. GBank gi 4929741 (gb AAD34131.1) (AF151894) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	264907, 264512, 265011, 264683
2344	79953188 (4687, 4688)	Novel Protein sim. GBank gi 2506307 (sp P13944) (CA1C - COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR (FIBROCHIMERIN)	Contains protein domain (PF00092) - von Willebrand factor type A domain	UNCLASSIFIED	264758
2345	94319799 (4689, 4690)			collagen	264488, 264259, 66712502, 264759, 83373044, 264566

2346	94131820 (4691, 4692)	Novel Protein sim. GBank gll1255411 (U53153) - one short region of weak similarity to <i>S. cerevisiae</i> protease A inhibitor 3 (SP:P01094) and another short region of weak similarity to <i>S. cerevisiae</i> glucose repression mediator protein (SP:P14922) [ <i>Caenorhabditis elegans</i> ]	Contains protein domain (PF00515) - TPR Domain	proteaseinhib	35696286, 22278998, 264259, 35696052, 29331828, 33657402, 60433356, 33109954, 87188559, 264603, 265019, 18108351, 264681, 264685, 21906766, 265021, 33657109, 55811576, 35695855, 264637, 52644332, 264557, 83373044, 22279000, 22279002
2347	85330367 (4693, 4694)				22278997, 264511, 264683, 264694, 264768, 264687, 264688, 264691, 264692, 55811576
2348	95186133 (4695, 4696)	Novel Protein sim. GBank gll1929056 (emb CAA72805  - (Y12080) putative 3,4-dihydroxy-2-butanone kinase [ <i>Lycopodium obscurum</i> ])		kinase	18108394, 35696286, 264259, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265011, 264601, 264762, 18108351, 264764, 264286, 264768, 264768, 264689, 35695917, 264693, 264628, 18108370, 264629, 18108374, 35698423, 264631, 264635, 264636, 264637, 264638, 264639, 83373044, 18108385, 264587, 264488
2349	87776502 (4697, 4698)	Novel Protein sim. GBank gll4884105 (emb CAB43254.1  - (AL050062) hypothetical protein [ <i>Homo sapiens</i> ])			35696052, 28146499, 264909, 264369
2350	88260594 (4699, 4700)				22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 33109954, 21906754, 265010, 87188559, 265018, 265019, 264761, 264681, 264288, 18108357, 21906768, 21906767, 264691, 264692, 35695855, 87188518, 22279000, 22279002, 264482
2351	86968042 (4701, 4702)	Novel Protein sim. GBank gll728632 (sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII)		kinase	56182575, 264909, 265006, 264558
2352	87337196 (4703, 4704)	Novel Protein sim. GBank gll731637 (sp P38760 YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION)	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264259, 264448
2353	91638784 (4705, 4706)	Novel Protein sim. GBank gll1346955 (sp P48809 RB27_DROME - HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1))	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331826, 55812038, 265019, 264692, 264636
2354	87337199 (4707, 4708)	Novel Protein sim. GBank gll731637 (sp P38760 YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION)	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	29331824, 264908, 265006, 265008

2355	91638786 (4709, 4710)	Novel Protein sim. GBank gjl4938503[embjCAB43861.1] - (AL078465) hnRNP-like protein [Arabidopsis thaliana]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	56994075, 22278996, 35696286, 22278999, 264259, 29331825, 29331826, 29331828, 29146498, 284905, 264908, 265006, 264758, 87168474, 265010, 265017, 264687, 21906765, 21906767, 21906769, 264691, 264692, 263967, 18108370, 87168518, 22279000
2356	95327688 (4711, 4712)	Novel Protein sim. GBank gjl5138920[gblAAD40377.1] - (AF092135) PTD014 [Homo sapiens]			52644507, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35696052, 29331828, 264908, 66712502, 264512, 265007, 265008, 60170831, 60432229, 60433356, 60433438, 264758, 52646317, 33109954, 21906754, 55811386, 87168474, 265017, 265018, 264605, 265019, 264681, 264682, 264448, 264369, 264288, 264686, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170615, 33657109, 27486264, 35695763, 55810764, 18108379, 35696423, 55811576, 35695855, 60170394, 56182323, 83373044, 18108385, 56526486, 264404, 60432113, 22279000, 264482, 264563, 264566, 264486, 264567
2357	87775458 (4713, 4714)	Novel Protein sim. GBank gjl4929741[gblAAD34131.1]AF15189 - (AF151894) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	264488, 264769, 18108394, 264259, 29331822, 18108370, 18108374, 264510, 265017, 264482, 264563, 264762, 264565, 264566, 264369, 18108354
2358	87777078 (4715, 4716)	Novel Protein sim. GBank gjl4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 22278999, 264509, 264905, 264592, 18108351, 264681, 264682, 264769, 32833986, 18108374, 264556, 18108385, 264482
2359	87755659 (4717, 4718)	Novel Protein sim. GBank gjl1086830 (U41264) - coded for by C. elegans cDNA yk2018.5; coded for by C. elegans cDNA yk44g1.5; coded for by C. elegans cDNA yk12b7.5; coded for by C. elegans cDNA yk36g6.5; coded for by C. elegans cDNA yk2018.5; coded for by C. elegans cDNA yk16g12....		UNCLASSIFIED	35696286, 22278998, 264905, 264511, 265007, 265008, 60433438, 264288, 264686, 21906769, 265020, 264692, 35695855, 264558, 56526486, 264563
2360	80046125 (4719, 4720)	Novel Protein sim. GBank gjl3881545[embjCAA93779] - (Z69904) cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	22278997, 29331826, 263981, 22279000
2361	84232181 (4721, 4722)	Novel Protein sim. GBank gjl746487 (U23514) - No definition line found [Caenorhabditis elegans]			22278995, 22278999, 264512, 265009, 264757, 21906765, 65274620, 18108370, 60431528, 18108374, 264635, 60170394, 264482

2362	91721183 (4723, 4724)	Novel Protein sim. GBank gii1171093jsp19708 MYSB_ACACA - MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)		UNCLASSIFIED	22278999, 264259, 29331822, 29331824, 60432289, 264509, 284512, 60432228, 60433356, 264448, 264682, 264683, 264369, 21906765, 21906768, 21906769, 60432113, 22279000, 22279002
2363	95006635 (4725, 4726)	Novel Protein sim. GBank gii854065 emb CAA58337  - (X83413) U88 Human herpesvirus 6		UNCLASSIFIED	264807, 264629, 264635
2364	94827104 (4727, 4728)	Novel Protein sim. GBank gii5639830 gb AAD45866.1 AF14601 - (AF14601B) hydroxypyruvate reductase [Homo sapiens]	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases	reductase	264488, 18108394, 264887, 18108398, 22278998, 56994075, 35696288, 22278997, 22278998, 264259, 66714117, 29331825, 35696052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 264511, 265008, 264512, 265007, 265008, 33657402, 264758, 21906754, 87168474, 265010, 87168559, 264603, 285017, 265018, 285019, 284760, 264762, 18108351, 264448, 264764, 264683, 264684, 264288, 18108355, 264766, 18108358, 264689, 18108359, 21906765, 21906766, 21906767, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 18108368, 18108370, 18108374, 35696423, 35695855, 264635, 264556, 264557, 264639, 60170394, 83373044, 18108383, 18108384, 18108385, 18108386, 56526486, 264482, 264564, 264488
2365	94140746 (4729, 4730)	Novel Protein sim. GBank gii1840045 (U49082) - transporter protein [Homo sapiens]		transport	22278998, 22278998, 22278999, 264907, 264909, 264910, 33657402, 264758, 264600, 264766, 264687, 264689, 21906765, 21906767, 21906768, 21906769, 285021, 33657023, 33657109, 83373044, 264566
2366	94312388 (4731, 4732)			UNCLASSIFIED	52644507, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264907, 29331830, 264909, 264511, 265008, 33657402, 264595, 52646317, 265017, 265018, 265019, 264605, 264685, 264768, 264689, 21906766, 21906769, 35695917, 265020, 265021, 265022, 52644150, 35695855, 52644332, 18108385, 18108387, 264564, 264566
2367	94140910 (4733, 4734)	Novel Protein sim. GBank gii1065457 (U40410) - C54G7.4 gene product [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	35696286, 21906768, 55810764, 65274791, 284587
2368	94322190 (4735, 4736)				264628



2369	94314334 (4737, 4738)	Novel Protein sim. GBank gij5360901[dbj BAA82158.1] - (AB029343) a-helix coiled-coil rod homologue [Homo sapiens]		struct	52844507, 52846842, 35696286, 264092, 264094, 52845080, 35696052, 264107, 29331830, 52644045, 265006, 265007, 265009, 52644298, 52644229, 264689, 21906765, 21906766, 35695917, 265020, 52644150, 263987, 33657109, 27486285, 35695763, 18108370, 263974, 18108374, 18108376, 52644332, 263981, 18108385, 264508, 264909, 264596, 264369
2370	79804120 (4739, 4740)			UNCLASSIFIED	
2371	57280406 (4741, 4742)			UNCLASSIFIED	
2372	87642413 (4743, 4744)			UNCLASSIFIED	
2373	87418611 (4745, 4746)	Novel Protein sim. GBank gij4589582[dbj BAA76813.1] - (AB023186) KIAA0969 protein [Homo sapiens]		UNCLASSIFIED	29331826, 265010, 265019, 35695917, 264634, 60432113
2374	94123665 (4747, 4748)	Novel Protein sim. GBank gij5105131[dbj BAA80445.1] - (AP000061) 246aa long hypothetical ribonuclease PH [Aeropyrum pernix]	Contains protein domain (PF01139) - 3' exonuclease family	UNCLASSIFIED	265006, 265007, 265008, 265009, 265011, 264766, 35695917, 35695855, 263981, 264557, 264555
2375	87731355 (4749, 4750)	Novel Protein sim. GBank gij1351115[sp P47758 SRPB_MOUSE - SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)]		UNCLASSIFIED	60432049, 29331824, 264907, 52644045, 264512, 60433356, 21906754, 52644298, 87168559, 264448, 21908765, 21906768, 21906769, 33657023, 18108368, 55811576, 52644332
2376	87613744 (4751, 4752)	Novel Protein sim. GBank gij2645435 (AF007780) - CHD3 [Drosophila melanogaster]	Contains protein domain (PF00629) - PHD-finger	ATPase-associated	264259, 29331830, 264909, 264910, 265009, 60433438, 21906754, 265017, 265018, 265019, 264682, 264288, 264685, 21906767, 263972, 35695855, 87168518, 60432113
2377	95319689 (4753, 4754)	Novel Protein sim. GBank gij5257005[gb AAD41239.1] - (AF083249) Rb binding protein homolog [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	UNCLASSIFIED	18108394, 65274572, 22278997, 22278999, 264095, 29331822, 29147620, 29331824, 66714117, 29331825, 29331826, 29331828, 33656970, 29146498, 29148499, 264509, 265006, 265007, 265008, 265009, 60170831, 265010, 265011, 265018, 55811150, 18108351, 264764, 264288, 21906767, 21906768, 29148627, 29148629, 265021, 33657023, 33657109, 18108370, 18108374, 18108379, 35696423, 264556, 83373044, 18108385, 18108388, 56526486, 22279000, 22279002, 264553
2378	94137032 (4755, 4756)	Novel Protein sim. GBank gij1072198 (U40942) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56182575, 35696286, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 60432289, 29331827, 56182435, 264510, 265009, 60433356, 87168474, 265011, 265018, 264288, 21906765, 33657023, 264557, 56182323, 83373044, 18108385, 22279002, 264482, 285017, 264288, 21906768
2379	65444324 (4757, 4758)	Novel Protein sim. GBank gij3337357 (AC004481) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - kinase WD domain, G-beta repeat	kinase	

2380	86923062 (4759, 4760)	Novel Protein sim. GBank gi 4502839 ref NP_001845.1 pCOL1 - collagen, type XI, alpha 1	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	264908, 264910, 265011
2381	87608241 (4761, 4762)	Novel Protein sim. GBank gi 4455609 emb CAB36555  - (AL031848) dJ742C18.5 (novel Chromobox protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHR)romatin Organization Modifier domain	helicase	56182575, 264081, 264093, 264259, 29331825, 264105, 264906, 60433356, 21906754, 265017, 265019, 264883, 264288, 264685, 264686, 264687, 264681, 264682, 264693, 55811576, 264636, 264567
2382	81225982 (4763, 4764)	Novel Protein sim. GBank gi 4325130 gb AAD17276  - (AF119716) dMI-2 protein [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	transport	29331824, 60432289, 264905, 264586, 21906754, 264769, 265022, 264693, 263987, 33657109, 264629, 264631, 264558, 83373044, 60432113, 264482
2383	87442841 (4765, 4766)	Novel Protein sim. GBank gi 1902982 dbj BAA19005  - (D89049) lecithin-like oxidized LDL receptor [Bos taurus]	Contains protein domain (PF00059) - Lectin C-type domain	glycoprotein	265009, 21906765, 21906766
2384	95354766 (4767, 4768)	Novel Protein sim. GBank gi 2462851  (AF016252) - Spinophilin [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	struct	264488, 52644507, 52645156, 52646365, 35698286, 22278999, 52645080, 29331824, 29331826, 35698052, 29331828, 264906, 264828, 52644045, 265006, 265008, 265009, 33109954, 33657084, 52644296, 285011, 285017, 265018, 264683, 52644229, 21906765, 21906767, 21906768, 265020, 52644150, 33657023, 264693, 65274620, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108374, 35695855, 264634, 264555, 264556, 264557, 52644332, 264558, 264559, 18108385, 22279000, 22278002
2385	95419485 (4769, 4770)		UNCLASSIFIED		264488, 52644507, 52645156, 264887, 52646365, 22278995, 22278998, 22278997, 22278999, 264259, 52645080, 29331822, 29331826, 35698052, 52644045, 265006, 265007, 265008, 265009, 264910, 60432229, 60433356, 52646317, 21906754, 265019, 264448, 264683, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 265021, 265022, 264690, 264681, 264692, 65274620, 33657109, 18108370, 264631, 52644332, 22279000, 22279002, 264563, 264565, 264567
2386	94742649 (4771, 4772)	Novel Protein sim. GBank gi 4929699 gb AAD34110.1 AF15187 - (AF15187) CGI-115 protein [Homo sapiens]		glycoprotein	264488, 22278995, 22278996, 22278997, 264259, 29146498, 264112, 264511, 60170831, 60432229, 264595, 60433438, 87168474, 87168559, 264682, 21906765, 21906766, 21906767, 21906769, 29148829, 35695917, 265021, 264690, 33657109, 264628, 18108376, 83373044, 60432113, 22279000, 264564, 264566, 264487

2387	14997890 (4773, 4774)			UNCLASSIFIED	264634
2388	11424604 (4775, 4776)			UNCLASSIFIED	264595
2389	95310650 (4777, 4778)	Novel Protein sim. GBank gi 4758058 ref NP_004372.1 pCREB - cAMP responsive element binding protein-like 1	Contains protein domain (PF00170) - bZIP transcription factor		264488, 22278998, 22278999, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 264511, 264512, 264910, 264591, 21908754, 264601, 264604, 264761, 18108351, 264764, 264288, 264766, 264768, 264769, 21906765, 21906768, 264692, 264693, 35696423, 284635, 264638, 264555, 83373044, 22279000, 264486
2390	94320912 (4779, 4780)	Novel Protein sim. GBank gi 1644239 dbj BAA12223  - (D84103) mitochondrial DNA polymerase gamma [Homo sapiens]	Contains protein domain (PF00476) - DNA polymerase family A	polymerase	52644507, 56182575, 22278995, 35696286, 22278996, 22278997, 22278999, 29331822, 29331825, 29331826, 35696032, 284905, 52644045, 265009, 264758, 264759, 33109954, 52844296, 85658542, 265011, 265017, 265018, 264605, 52644229, 21906765, 21906767, 21906768, 21906769, 35695917, 52844150, 33657023, 33657109, 33657349, 35695763, 18108370, 18108374, 18108376, 35696423, 35695855, 264555, 52644332, 56182323, 60170394, 83373044, 56526486
2391	80036194 (4781, 4782)			UNCLASSIFIED	263976
2392	94245016 (4783, 4784)	Novel Protein sim. GBank gi 4240169 dbj BAA74863.1  - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nuclease	35696286, 35696052, 264508, 264905, 264509, 264908, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 265009, 264591, 264758, 264600, 264604, 264762, 264448, 264764, 264369, 264766, 264768, 264769, 264689, 35695917, 264629, 18108374, 263978, 35696423, 35695855, 264631, 264634, 264635, 264638, 264637, 264638, 60170394, 264639, 264565, 264486

2393	85302633 (4785, 4786)	Novel Protein sim. GBank gi 4508667 ref NP_000993.1 pRPLP - ribosomal protein, large, P0	Contains protein domain (PF00466) - ribosomal prot Ribosomal protein L10	18108392, 60424179, 264489, 18108394, 18108397, 22278995, 56994075, 35696286, 22278996, 22278997, 22278998, 284093, 60432049, 264259, 29331822, 29147820, 20281099, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 35696052, 29148499, 284508, 264508, 264805, 264907, 284908, 66712502, 52844045, 264828, 284809, 56182435, 264112, 264113, 284510, 285006, 264511, 265007, 265008, 265009, 264910, 264591, 264593, 60433356, 264595, 60433438, 52646317, 33109954, 21906754, 55811388, 265010, 265011, 265017, 265018, 265019, 264681, 264762, 18108351, 264763, 264682, 264764, 264683, 264369, 264288, 18108354, 264766, 264686, 264687, 264688, 264689, 18108359, 21906785, 21908766, 21908767, 21908768, 21908769, 55811957, 29148829, 29148784, 35695917, 265021, 285022, 33657023, 264692, 264693, 18108364, 33657109, 18108368, 27486261, 27486262, 33657349, 35695763, 18108370, 263972, 264629, 18108374, 263977, 18108376, 263978, 55810764, 35696423, 35695855, 264634, 60431850, 264555, 264637, 264557, 263981, 264558, 18108381, 60170394, 35696286, 22278997, 22278998, 56182181, 35696052, 265006, 264592, 55811386, 265010, 265011, 265017, 265019, 264448, 264683, 264288, 21908785, 21908788, 21908789, 55811957, 35695917, 33657023, 65274620, 33657182, 33657349, 35695763, 18108374, 18108378, 55810764, 55811576, 35696423, 60170394, 18108385, 264564, 264566, 264567
2394	84323266 (4787, 4788)	Novel Protein sim. GBank gi 4159888 (AC004908) - zinc finger protein from gene of uncertain exon structure; similar to Q99676 (PID:g3025333) [Homo sapiens]	Contains protein domain (PF00086) - dna_ma_bind Zinc finger, C2H2 type	264259, 29331824, 264910, 264288, 265021, 83373044, 18108387, 264563, 264568
2395	95287212 (4789, 4790)	Novel Protein sim. GBank gi 5712756 gb AA047638.1 AF16079 - (AF160798) calcium transporter CaT1 [Rattus norvegicus]	dna_ma_bind	

2398	95086700 (4791, 4792)	Novel Protein sim. GBank gij106322(pir  B34087 - hypothetical protein (L1H 3' region) - human	Contains protein domain (PF00580) - Leucine Rich Repeat	nuclease	52646365, 18108397, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264106, 264907, 29331830, 65712502, 264110, 60170831, 264591, 33657402, 60433438, 55812038, 33109954, 21908754, 33657084, 87168474, 265017, 265018, 265019, 264760, 264448, 264288, 264766, 52644229, 21906768, 21906767, 265020, 265021, 60170615, 264692, 33657023, 65274620, 52645129, 33657182, 27486262, 27486264, 27488265, 264629, 18108374, 35696423, 35695855, 264631, 264556, 52644332, 264558, 83373044, 18108388, 87168518, 22279002, 264482
2397	87280854 (4793, 4794)				52644507, 52645156, 56182575, 264259, 29147620, 264905, 264907, 264908, 264909, 264910, 264758, 52644296, 264603, 264604, 264762, 264681, 264764, 18108357, 264769, 21906768, 264693, 264628, 264635, 264638, 264639, 264564
2398	88047689 (4795, 4796)	Novel Protein sim. GBank gij3258609 (AC005178) - H53_GS1 [Homo sapiens]		UNCLASSIFIED	
2399	87738965 (4797, 4798)	Novel Protein sim. GBank gij786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 60432289, 264906, 29331830, 56182435, 264112, 264910, 33109954, 21906754, 87168474, 264600, 285017, 285018, 265019, 264764, 264765, 21906765, 21906768, 21906767, 21906769, 35695917, 265020, 265022, 60170815, 33657023, 18108370, 18108374, 264556, 60170394, 264558, 87168518, 22279000, 22279002, 264564, 264566, 264487
2400	91214116 (4799, 4800)	Novel Protein sim. GBank gij2352822(gbjAA869285.1) - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]		phosphatase	21906766, 52646842, 56994075, 33657182, 27486262, 52644296, 265017

2401	91214118 (4801, 4802)	Novel Protein sim. GBank gij2352822[gijAA869285.1] - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]	phosphatase	52644507, 52645156, 52644228, 264688, 21908784, 21908785, 52646385, 52646842, 21906786, 21906787, 21906788, 22278995, 35695917, 56984075, 35696286, 22278996, 22278997, 265020, 22278998, 22278999, 264259, 33657023, 52645080, 264693, 29331824, 33657109, 52645129, 29331826, 33657182, 29331827, 35696052, 27486261, 27486262, 33656970, 33657349, 27486265, 35695763, 264108, 264905, 35696423, 35695855, 265006, 265007, 265008, 265009, 264637, 52644332, 55812038, 52646317, 18108385, 52644296, 87168474, 265010, 87168559, 60432113, 265017, 265018, 265019, 264563, 264288, 264907, 264908, 264909, 264566
2402	91221408 (4803, 4804)	Novel Protein sim. GBank gij4689258[gijAAD27832.1]AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]		
2403	94135432 (4805, 4806)	Novel Protein sim. GBank gij4929575[gijAAD34048.1]AF15181 - (AF151811) CGI-53 protein [Homo sapiens]	Contains protein domain (PF00082) - C-type lysozyme/alpha-lactalbumin family	22278999, 35696052, 265018, 264688, 264693, 83373044, 264567
2404	95312605 (4807, 4808)	Novel Protein sim. GBank gij2315796 (AF016685) - similar to short chain-type dehydrogenases [Caenorhabditis elegans]	Contains protein domain (PF00106) - short chain dehydrogenase	35696286, 29331826, 35696052, 265008, 265018, 21906769, 264564
2405	94311851 (4809, 4810)	Novel Protein sim. GBank gij464178[dbj]BAA03581 - (D14853) polyprotein [Hepatitis C virus]	UNCLASSIFIED	35696286, 29331822, 265007, 21906754, 265017, 265018, 265019, 264763, 264369, 21908785, 35695917, 285020, 265021, 52644150, 264693, 35695855, 264632, 52644332, 22279002
2406	88094501 (4811, 4812)	Novel Protein sim. GBank gij2773363 (AF041382) - microtubule binding protein D-CLIP-190 [Drosophila melanogaster]	Contains protein domain (PF01302) - CAP-Gly domain	52646842, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264093, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264102, 264106, 264906, 52644045, 285007, 265008, 265009, 284910, 264592, 60433356, 60433438, 33109954, 265010, 285011, 265018, 265019, 264369, 264685, 264686, 21906768, 21906769, 52644150, 264693, 52645129, 264628, 35696423, 264632, 56182323, 264639, 22279000, 22279002, 264563
2407	79465005 (4813, 4814)			264685, 264686
2408	87391503 (4815, 4816)	Novel Protein sim. GBank gij423442[pir]S33513 - gene F1f protein - mouse	UNCLASSIFIED	264910, 265010, 264448, 264557

2409	94741770 (4817, 4818)	Novel Protein sim. GBank gil1176801[sp]P45966[YNZ6_CAEEL - HYPOTHETICAL 20.8 KD PROTEIN T09A5.6 IN CHROMOSOME III		UNCLASSIFIED	22278995, 22278996, 22278997, 264097, 29331822, 29331824, 29331827, 29146498, 52644045, 60433438, 33657084, 87168474, 264760, 21906767, 29148627, 29148629, 52644150, 33657023, 263967, 20281069, 18108374, 20281071, 56182323, 83373044, 18108385, 87168518 22278998, 264259
2410	87604860 (4819, 4820)	Novel Protein sim. GBank gil4966262[gb]AAC48052.2] - (UB4849) Contains similarity to Pfam domain: PF00646 (F- box). Score=28.7, E-value=4.3e-05, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00080) - Copper/zinc superoxide dismutase (SODC)		
2411	87534633 (4821, 4822)	Novel Protein sim. GBank gil3114713 (AF061346) - Edp1 protein [Mus musculus]		Inf	29331824, 29331827, 29331828, 264764, 264389, 33657109, 56182323
2412	87778332 (4823, 4824)	Novel Protein sim. GBank gil5410336[gb]AADX3038.1] - (AF106685) myelin gene expression factor 2 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	22278998, 29331827, 264907, 265011, 265017, 265018, 265019, 18108351, 21906766, 265020, 33657109, 264559, 18108385
2413	94133820 (4825, 4826)	Novel Protein sim. GBank gil5262705[emb]CAB45778.1] - (AL080214) hypothetical protein [Homo sapiens]	Contains protein domain (PF00038) - Intermediate filament proteins	strut	264488, 264259, 29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264510, 264511, 264512, 285008, 265009, 264910, 265011, 264682, 264764, 264766, 264686, 264768, 264689, 265021, 33657023, 18108370, 264628, 35695855, 264632, 264634, 264635, 264636, 83373044, 264563, 264564, 264565, 264566, 264567, 264486
2414	94312590 (4827, 4828)	Novel Protein sim. GBank gil1082340[pi]j1S52863 - DNA- binding protein R kappa B - human		ubiquitin	52645156, 52646842, 52646365, 18108398, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 29331830, 264909, 60433356, 33657402, 264594, 52646317, 21906754, 33657084, 265010, 87168559, 265017, 265018, 265019, 264369, 264684, 264687, 264688, 56181562, 21906764, 264688, 21906765, 21906766, 21906767, 29148627, 21906769, 265020, 265021, 60170615, 33657023, 264693, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 18108370, 60431528, 264628, 18108374, 18108376, 55810764, 264636, 52644332, 264638, 264556, 56182323, 83373044, 18108385, 87168518, 22279002

2415	88089002 (4829, 4830)	Novel Protein sim. GBank gij423915 pir A45439 - myosin I heavy chain - rat	Contains protein domain (PF00063) - struct	Myosin head (motor domain)	264259, 264908, 60433356, 33657402, 21906754, 265018, 264887, 264889, 21906769, 55811957, 265021, 264690, 264691, 33657023, 264693, 35696423, 56182323, 56526488
2416	94118356 (4831, 4832)	Novel Protein sim. GBank gij3025445 (AC004528) - R32184_1 [Homo sapiens]			264638
2417	87733334 (4833, 4834)	Novel Protein sim. GBank gij1084944 pir S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) -	Mitochondrial carrier proteins	264094, 29331822, 29331824, 29331827, 264369
2418	84234348 (4835, 4836)	Novel Protein sim. GBank gij1176572 sp P45895 YNA4_CAEEL - HYPOTHETICAL 91.0 KD PROTEIN PAR2.4 IN CHROMOSOME III	UNCLASSIFIED	Contains protein domain (PF00411) - Ribosomal protein S11	56994075, 264091, 264259, 29331824, 29331825, 60432289, 29331828, 264905, 264907, 264511, 265009, 60432229, 21906754, 87168559, 265019, 264682, 21906768, 21906769, 265020, 265021, 33657023, 65274620, 18108370, 55811576, 264634, 60170394, 18108365, 22279000, 22279002, 264568
2419	82374248 (4837, 4838)	Novel Protein sim. GBank gij284006 pir S18732 - autoantigen, 64K - human	struct		264569, 264762, 264448, 264691, 264631, 264634, 264555, 264558, 264638, 264558
2420	94844244 (4839, 4840)	Novel Protein sim. GBank gij107621 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii	UNCLASSIFIED		29331824, 29331825, 29331828, 60432229, 33109954, 85658542, 87168474, 265018, 264288, 265020, 264564
2421	87805345 (4841, 4842)		UNCLASSIFIED		264909, 284768, 284638
2422	88084714 (4843, 4844)	Novel Protein sim. GBank gij2224567 dbj BAA20772  - (AB002311) KIAA0313 [Homo sapiens]	transport	Contains protein domain (PF00617) - RasGEF domain	18108392, 18108394, 18108398, 264906, 265006, 265010, 18108351, 18108374, 18108385
2423	88058390 (4845, 4846)	Novel Protein sim. GBank gij4505153 ref NP_002392.1 pMEKK - MAP/ERK kinase kinase 3	kinase	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	264259, 60432049, 29331822, 29331828, 60432289, 29331828, 265008, 265009, 60433356, 21906754, 265017, 265018, 265019, 21906766, 21906768, 21906769, 265020, 265021, 20281149, 263971, 60432113
2424	94854047 (4847, 4848)	Novel Protein sim. GBank gij2988398 (AC004381) - Unknown gene product [Homo sapiens]	UNCLASSIFIED		56182575, 35686286, 22278997, 60432049, 264259, 29331828, 29331828, 264905, 66712502, 29331830, 60433356, 265011, 285019, 264768, 21906768, 55811957, 264692, 33657023, 33657109, 55811576, 56182323, 83373044, 18108365, 18108388, 60432113, 22278900
2425	87415981 (4849, 4850)	Novel Protein sim. GBank gij2077832 dbj BAA19879  - (D86556) Protein Kinase [Rattus norvegicus]	kinase	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	264634
2426	87613945 (4851, 4852)	Novel Protein sim. GBank gij2039368 gb AA833003.1  - (U94619) circulating cathodic antigen [Schistosoma mansoni]	UNCLASSIFIED		22278996, 22278998, 264259, 264102, 264512, 265008, 21906767, 18108370, 18108374, 263976



2427	87822693 (4853, 4854)	Novel Protein sim. GBank gi 4680695 gb AAD27737.1 AF132962 CGI-28 protein [Homo sapiens]	Contains protein domain (PF00573) - Ribosomal protein L4/L1 family	ribosomalprot	264259, 20281099, 35696052, 265008, 264594, 265011, 264760, 18108351, 264682, 264683, 264369, 264684, 264686, 264687, 264689, 21906766, 264691, 264692, 18108374, 18108377, 264557, 264639, 18108385
2428	85732889 (4855, 4856)	Novel Protein sim. GBank gi 1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]			22278996, 22278999, 35696052, 21906754, 264288, 21906765, 21906768, 21906769, 35695917, 265020, 263972, 22279002
2429	87769276 (4857, 4858)	Novel Protein sim. GBank gi 601931 (M94316) - neurofilament-H [Oryctolagus cuniculus]	Contains protein domain (PF00711) - Beta defensins	UNCLASSIFIED	22278999, 29331824, 264906, 264909, 264511, 265009, 21906754, 265017, 265018, 265019, 264448, 264683, 264288, 21906765, 21906768, 265021, 264693, 18108381
2430	86948827 (4859, 4860)	Novel Protein sim. GBank gi 3860729 emb CAA14630  (AJ235270) CELL DIVISION PROTEIN FTSJ (ftsJ) [Rickettsia prowazekii]	Contains protein domain (PF01728) - FisJ cell division protein	UNCLASSIFIED	264112, 264691
2431	87849884 (4861, 4862)	Novel Protein sim. GBank gi 3876367 emb CAA93287  (Z69360) Weak similarity to Eimeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89266 comes from this gene; cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans]		protease	22278996, 29331827, 35696052, 29146489, 264905, 264906, 264681, 264288, 264689, 21906765, 264692, 35696423
2432	80083033 (4863, 4864)	Novel Protein sim. GBank gi 2224593 dbj BAA20784  (AB002324) KIAA0326 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264569, 264905, 265018, 264762, 264683, 264691, 264556, 264557, 264639, 264558
2433	80055092 (4865, 4866)	Novel Protein sim. GBank gi 1263289 (U47856) - fibroin-4 [Araneus diadematus]			264563
2434	19520148 (4867, 4868)	Novel Protein sim. GBank gi 3641352 (AF091234) - putative transcription factor [Mus musculus]		UNCLASSIFIED	264555
2435	20759044 (4869, 4870)	Novel Protein sim. GBank gi 3860014 (AF091088) - unknown [Homo sapiens]	Contains protein domain (PF01256) - Uncharacterized protein family UPF0031	UNCLASSIFIED	265008, 264758, 265010, 264689, 27486261, 263972, 18108374, 18108381
2436	88044008 (4871, 4872)			UNCLASSIFIED	29331828, 265007, 265009, 265017, 264760, 264685, 264693, 264565
2437	83363424 (4873, 4874)			UNCLASSIFIED	29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 264910, 265009, 264591, 33657402, 21906754, 265011, 264760, 264764, 264685, 264686, 264768, 35695917, 33657023, 264693, 264631, 264632, 56182323, 264558, 83373044, 264563, 264564, 264565, 264566, 264567

2439	94850550 (4877, 4878)	Novel Protein sim. GBank gij4263519igb/AAD153451 - (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]	Contains protein domain (PF01423) - Sm protein	UNCLASSIFIED	60424179, 18108397, 56182575, 56181686, 56994075, 22278996, 35696286, 22278997, 22278998, 264259, 52645080, 29331822, 56182181, 29331824, 80424269, 68714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 29146498, 264509, 264905, 264906, 52644045, 80431735, 33109954, 21908754, 33657084, 55811386, 52644296, 87168474, 265017, 265018, 285019, 18108351, 264448, 264288, 264768, 52644229, 56181562, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 33657109, 33657182, 27486282, 27486264, 33657349, 27486265, 35695763, 18108370, 80431528, 263977, 55810784, 35696423, 65274791, 35695855, 60431850, 56182323, 60432113, 22278000, 22278002, 264567
2440	87641733 (4879, 4880)			UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264907, 264510, 265018, 265019, 264448, 264369, 265020, 265021, 56182323, 264639, 22278002
2441	87623914 (4881, 4882)	Novel Protein sim. GBank gij3024889spIP565241Y288_HUMAN - HYPOTHETICAL PROTEIN KIA0288 (HA6116)		UNCLASSIFIED	264488, 264629, 18108374, 264564
2442	87273590 (4883, 4884)	Novel Protein sim. GBank gij4506013jreflNP_002703.1pPPP1 - protein phosphatase 1, regulatory subunit 7	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	22278996, 22278998, 29331822, 264768, 264693
2443	84305949 (4885, 4886)	Novel Protein sim. GBank gij170858spIQ02975(KID1_RAT1 - RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17)	Contains protein domain (PF01352) - KRAB box	transcript factor	264906
2444	88086345 (4887, 4888)	Novel Protein sim. GBank gij4758824jreflNP_004280.1pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	transcript factor	264259, 18108382, 18108383, 18108385, 22278000
2445	87338636 (4889, 4890)	Novel Protein sim. GBank gij2135550jpiri[S58222 - PQ-rich protein - human			264259, 35696052, 264369, 18108361
2446	88059293 (4891, 4892)	Novel Protein sim. GBank gij4753887jemb[CAA05409.2] - (AJ002424) p65 protein [Rattus norvegicus]	Contains protein domain (PF00095) - WAP-type (Whey Acidic Protein) 'four-disulfide core'	proteaseinhib	265011, 264689, 33657023, 263981, 18108385
2447	94845149 (4893, 4894)	Novel Protein sim. GBank gij4865613jreflNP_005409.1pST51 - suppression of tumorigenicity 5	cadherin		56182575, 264259, 29331824, 29331825, 29331827, 60433356, 60433438, 264759, 265018, 264692, 65274620, 60431528, 65274791, 56182323

2448	87749680 (4895, 4896)			UNCLASSIFIED	22278996, 22278997, 22278998, 29331826, 35896052, 264107, 264110, 87168474, 87168559, 18108351, 21906767, 21906769, 27486262, 263976
2449	87869075 (4897, 4898)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!		cadherin	264259, 264828, 265007, 264595, 265021, 56528486
2450	86597784 (4899, 4900)	Novel Protein sim. GBank gi 1710021 sp P35290 R824_MOUSE - RAS-RELATED PROTEIN RAB-24 (RAB-16)	Contains protein domain (PF00071) - Ras family	UNCLASSIFIED	264906
2451	91014563 (4901, 4902)				264093, 29331822, 29331824, 29331825, 66714117, 29331826, 29331828, 35896052, 264907, 66712502, 29331830, 284910, 265009, 284758, 265017, 265018, 264762, 264448, 284288, 21906767, 265021, 33657023, 264693, 33657109, 263969, 83373044, 18108385
2452	91230509 (4903, 4904)	Novel Protein sim. GBank gi 1504034 dbj BAA13216  - (D86980) KIAA0227 [Homo sapiens]		isomerase	264102, 264112, 264888, 263972, 18108374, 83373044, 264563
2453	84201088 (4905, 4906)	Novel Protein sim. GBank gi 2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:gi1369906) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	ngf/recep	264509, 264512, 18108385
2454	95310691 (4907, 4908)	Novel Protein sim. GBank gi 1076802 pir S49915 - extensin like protein - maize	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	263994, 66714117, 29331827, 264508, 284509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 264591, 264758, 264759, 265010, 265011, 264603, 264604, 264760, 264761, 264762, 18108351, 264764, 264765, 264766, 264688, 264768, 264769, 264534, 264691, 264692, 33657023, 264693, 33657109, 284628, 263978, 35695855, 264634, 264635, 264637, 264638, 264639, 83373044, 18108385, 264563, 264564, 264488
2455	95288301 (4909, 4910)	Novel Protein sim. GBank gi 543817 sp P35585 AP47_MOUSE - CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)	Contains protein domain (PF00928) - Adaptor complexes medium subunit family	glycoprotein	264488, 22278998, 264259, 35696032, 264905, 264908, 264907, 264908, 264909, 264510, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264758, 265019, 284760, 264681, 18108351, 264683, 264764, 18108354, 264766, 264768, 264769, 264699, 21908766, 21908767, 21908789, 29148629, 35695917, 265020, 265022, 33657023, 33657109, 18108370, 264628, 264629, 284631, 264632, 264635, 56182323, 60170394, 18108385, 264563, 264564, 264566, 264567
2456	88166700 (4911, 4912)	Novel Protein sim. GBank gi 2588630 (AC003079) - Ankyrin like; 54% similar to 2022340A (NID:gi1092123) in exons spanning 43974 to 11551 of clone. [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	264693

2457	94118375 (4913, 4914)	Novel Protein sim. GBank gij3025447 (AC004528) - R32184_3 [Homo sapiens]		UNCLASSIFIED	55181688, 264905, 264907, 264511, 264598, 55811386, 264682, 264684, 264685, 264687, 264691, 33657023, 264693, 35695855, 264636, 264555, 56182323, 264558, 56526488, 264563
2458	85875304 (4915, 4916)	Novel Protein sim. GBank gij2384942 (AF022985) - Similar to collagen [Caenorhabditis elegans]		UNCLASSIFIED	264691, 264693, 264634, 264559
2459	87551913 (4917, 4918)	Novel Protein sim. GBank gij5441942 [AAD3187.1] (AC004997) supported by mouse EST AA538043 (NID:q2284036) [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transport	27486265
2460	94315289 (4919, 4920)	Novel Protein sim. GBank gij4929701 [gbjAAD3411.1] (AF15187) - (AF151874) CGI-116 protein [Homo sapiens]		kinase	55274572, 35696288, 22278996, 22278997, 60432049, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33856970, 29146499, 284102, 264109, 60433438, 265017, 265018, 265019, 264288, 21906765, 21906766, 21906769, 35695917, 265020, 264691, 33657023, 27486281, 18108374, 35695855, 87168518, 60432113
2461	87645147 (4921, 4922)	Novel Protein sim. GBank gij4428962 [gbjAAD20633] - (AF126062) Arf-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264259, 29331828, 264910, 18108351, 18108370, 18108374
2462	86988002 (4923, 4924)	Novel Protein sim. GBank gij5420387 [embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			264809, 264758, 264684, 18108374, 264637, 18108385
2463	84386543 (4925, 4926)	Novel Protein sim. GBank gij5032516 [gbjAAD38588.1] (AF14561) - (AF145613) BcDNA GH03108 [Drosophila melanogaster]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	UNCLASSIFIED	264681, 264566
2464	91219957 (4927, 4928)	Novel Protein sim. GBank gij5410300 [gbjAAD3021.1] - (AF100757) COP9 complex subunit 4 [Homo sapiens]	Contains protein domain (PF01399) - PCI domain	protease	264489, 52646842, 22278995, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 29331828, 264509, 52644045, 264510, 264511, 264512, 285008, 60170831, 264593, 52846317, 33109954, 33657084, 265017, 265018, 265019, 264762, 264448, 264764, 264288, 264766, 21906765, 21906768, 21906769, 21906767, 21906768, 21906769, 265021, 33657023, 33657109, 18108370, 18108381, 60170394, 18108385, 22279002, 264486

2465	95357483 (4928, 4930)	Novel Protein sim. GBank gi4508401ref NP_002871.1 pRAF1 - v-raf-1 murine leukemia viral oncogene homolog 1	Contains protein domain (PF00069) - oncogene Eukaryotic protein kinase domain	18108392, 52644507, 52645156, 52646365, 22278994, 22278995, 35696288, 22278996, 22278998, 264259, 29331822, 29331824, 29331825, 60424269, 60432289, 29331827, 35696052, 29331828, 264907, 29331830, 52644045, 264909, 56182435, 264511, 265007, 265008, 265009, 264910, 33657402, 60433438, 55812038, 21906754, 33109954, 265010, 265011, 87188559, 264600, 265017, 265018, 265019, 18108351, 264369, 264288, 264685, 264767, 21908785, 21906767, 21908788, 55811957, 35695917, 265020, 265021, 60170815, 52644150, 33657023, 52645129, 33657109, 27486261, 27486264, 35695763, 264628, 263972, 18108374, 35695855, 264638, 264637, 60170394, 56526486, 87188518, 60432113, 264563, 264564, 264566, 264487 264369
2466	85881386 (4931, 4932)	Novel Protein sim. GBank gi4321619 gb AAD15788.1  - (AF051098) seven transmembrane domain orphan receptor [Mus musculus]		
2467	88059465 (4933, 4934)	Novel Protein sim. GBank gi3513300 (AC005595) - F16801_1, partial CDS [Homo sapiens]	UNCLASSIFIED	56994075, 264908, 21906768, 33657023
2468	87614696 (4935, 4936)	Novel Protein sim. GBank gi2143455 pi 58106 - gene DMR-N9 protein - mouse (fragment)	Contains protein domain (PF00400) - WD domain, G-beta repeat	29331824, 52644045, 265008, 264910, 265019, 21908785, 21908789, 265021, 264288, 264628
2469	86294397 (4937, 4938)	Novel Protein sim. GBank gi420389 emb CAB46680.1  - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	264592, 264692, 264555, 264556, 264557, 264558, 264559, 18108385, 264482
2470	80223631 (4939, 4940)	Novel Protein sim. GBank gi4519882 emb CAB46424.1  - (AL098749) DKFZp434G153 [Homo sapiens]	UNCLASSIFIED	65274572, 35696286, 29331827, 265007, 264592, 33109954, 265018, 265019, 264288, 55811957, 265020, 264693, 55811576, 56182323
2471	91013681 (4941, 4942)	Novel Protein sim. GBank gi4929747 gb AAD34134.1 AF15189 - (AF151897) CGI-139 protein [Homo sapiens]	UNCLASSIFIED	264092, 60432049, 29331825, 60433356, 265010, 265011, 18108351, 264784, 264288, 264692, 65274620, 18108370, 18108372, 18108374, 264634, 18108385
2472	95060811 (4943, 4944)	Novel Protein sim. GBank gi4929747 gb AAD34134.1 AF15189 - (AF151897) CGI-139 protein [Homo sapiens]		60424179, 65274572, 22278999, 60424269, 29331826, 265008, 60433356, 60433438, 265010, 18108351, 264448, 264288, 264687, 264689, 265021, 264692, 65274620, 60431528, 65274791, 264556, 56182323, 60432113
2473	95421509 (4945, 4946)	Novel Protein sim. GBank gi4539009 emb CAB39630.1  - (AL049481) putative protein [Arabidopsis thaliana]		
2474	94315616 (4947, 4948)	Novel Protein sim. GBank gi3252827 (AC004382) - Unknown gene product [Homo sapiens]		65274572, 56994075, 264259, 29331826, 60170831, 265017, 265018, 265019, 264683, 284369, 265020, 264693, 264563, 264564

2475	94321693 (4949, 4950)	Novel Protein sim. GBank gi1216486 (U48852) - HT protein [Cricetulus griseus]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	284259, 29331822, 265006, 265007, 265010, 265011, 264448, 264288, 264389, 264685, 264686, 18108357, 264768, 18108362, 264693, 18108370, 18108374, 18108379, 35698423, 83373044, 18108383, 18108385, 264564, 264565, 264567
2476	94315618 (4951, 4952)	Novel Protein sim. GBank gi3252827 (AC004382) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	UNCLASSIFIED	284259, 60424289, 66714117, 264805, 265006, 264511, 265008, 265009, 264758, 265010, 265011, 18108351, 264681, 264369, 264288, 264689, 21906767, 265020, 18108374, 264639, 18108382, 83373044, 18108385, 87168518
2477	20718974 (4953, 4954)		UNCLASSIFIED	UNCLASSIFIED	263978
2478	17659165 (4955, 4956)		UNCLASSIFIED	UNCLASSIFIED	265017
2479	94314569 (4957, 4958)	Novel Protein sim. GBank gi1644232[db][BAA11082] - [D67066] N-WASP [Bos taurus]	Im7	UNCLASSIFIED	58994075, 22278998, 21906754, 264682, 21906765
2480	95295605 (4959, 4960)	Novel Protein sim. GBank gi5689469[db][BAA83018.1] - (AB028989) KIAA1068 protein [Homo sapiens]	collagen	UNCLASSIFIED	264905, 264907, 264765
2481	84718481 (4961, 4962)				65274572, 56182575, 22278997, 264094, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 56182435, 265008, 264810, 33657402, 55812038, 264758, 265010, 265011, 265017, 265018, 264760, 264762, 18108351, 264764, 264288, 264766, 264686, 264768, 21908768, 55811957, 265020, 264691, 264692, 264693, 264629, 55811576, 264630, 264634, 264635, 264636, 264637, 264556, 264558, 56182323, 83373044, 60432113, 22279002
2482	87393165 (4963, 4964)	Novel Protein sim. GBank gi321249[pi][S28407] - guanine nucleotide-exchange activator CDC25 homolog - mouse	UNCLASSIFIED	UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 264508, 264905, 264509, 264906, 264907, 264908, 264511, 264591, 264788, 264693, 264631, 264632, 264636, 264638, 264639, 264563
2483	87731583 (4965, 4966)		UNCLASSIFIED	UNCLASSIFIED	264488, 22278995, 264093, 264095, 60432049, 60433356, 60433438, 264448, 264288, 263967, 18108370, 18108385, 18108388, 264482
2484	94187774 (4967, 4968)	Novel Protein sim. GBank gi728831[sp][P39188]ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	kinase	UNCLASSIFIED	264563
2485	87786556 (4969, 4970)	Novel Protein sim. GBank gi1185397 (U25281) - SH3 domain binding protein [Rattus norvegicus]	UNCLASSIFIED	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 60432289, 29331827, 265007, 264910, 264593, 264600, 264603, 264604, 265019, 264448, 264288, 264685, 264686, 264769, 264688, 35685917, 265022, 264692, 264693, 56182323

2486	87748976 (4971, 4972)	Novel Protein sim. GBank gi 2662167 dbj BAA23715  - (AB007803) KIAA0443 [Homo sapiens]	Contains protein domain (PF00071) - Ras family		265017, 264555
2487	95343105 (4973, 4974)	Novel Protein sim. GBank gi 464559 sp P35287 RB14_RAT - RAS-RELATED PROTEIN RAB-14		glycoprotein	22278996, 35696286, 22278997, 22278998, 22278999, 284092, 284259, 28331822, 35696052, 284106, 284905, 284907, 29331830, 264909, 265006, 264511, 265008, 265009, 60433438, 21908754, 33109954, 87188559, 265018, 264681, 264288, 264687, 21908785, 21908766, 21908767, 21908768, 21908769, 35695917, 265021, 265022, 264534, 33657023, 264692, 33657109, 263972, 18108377, 35698423, 35695855, 60170394, 18108385, 56526486, 22279000, 22279002, 264563, 264482, 264565, 20281169, 18108391
2488	87652451 (4975, 4976)			UNCLASSIFIED	264910, 264448, 264288, 264684, 264691, 264634
2489	82990585 (4977, 4978)	Novel Protein sim. GBank gi 4886439 emb CAB43355.1  - (AL050253) hypothetical protein [Homo sapiens]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complementrecept	264685, 264693, 55811576, 22279002
2490	88069609 (4979, 4980)	Novel Protein sim. GBank gi 2588624 (AC003083) - Rap2 interacting protein-like; similar to U73941 (PID:g1916018) [Homo sapiens]		UNCLASSIFIED	284907, 265008, 22279002
2491	91242116 (4981, 4982)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		Im7	284259, 29331826, 265008, 264762, 18108370, 18108376, 18108379
2492	95308202 (4983, 4984)	Novel Protein sim. GBank gi 3355303 (AF001549) - Unknown gene product [Homo sapiens]		transcriptfactor	264488, 22278998, 22278999, 29331828, 264591, 33109954, 265017, 55811150, 21908764, 21908768, 264692, 60431528, 87168518, 60432113, 22279000

2483	95422415 (4985, 4986)	Novel Protein sim. GBank gi 4240307 dbj BAA74932.1  - (AB020716) KIAA0909 protein [Homo sapiens]	Contains protein domain (PF01424) - Struct RH domain	18108394, 264687, 65274572, 56182573, 22278995, 56994075, 60432048, 29331822, 29331824, 29331825, 29331826, 29331827, 29146498, 264508, 264905, 264508, 264908, 264907, 29331830, 264908, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 264910, 21908754, 265011, 264600, 265017, 265018, 264604, 264605, 265019, 55811150, 264762, 18108351, 264681, 264448, 264683, 264369, 264288, 18108355, 18108357, 264687, 21908765, 21908766, 21908767, 21908768, 21908769, 265020, 264691, 264692, 33657023, 33657348, 18108370, 18108374, 18108376, 55810764, 18108379, 65274791, 264630, 264632, 264634, 264635, 264636, 264555, 264637, 264557, 264558, 264639, 264559, 83373044, 18108385, 87168518, 60432113, 22279000, 22279002, 264482, 264566, 264486
2484	30783118 (4987, 4988)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1  - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED collagen	263894, 22278997, 35696052, 264509, 264905, 264908, 264907, 264908, 264909, 265006, 265009, 264595, 264604, 264448, 264682, 264764, 264288, 264685, 264766, 264769, 264689, 265020, 264692, 65274620, 264629, 55810764, 35696423, 55811578, 264636, 264637, 18108385, 22278000, 264564, 264587, 264486
2495	84234551 (4989, 4990)			29147620, 264905, 265006, 265007, 18108348, 18108362, 18108370, 18108374, 264555, 264556, 18108381, 18108383, 18108388
2496	80018765 (4991, 4992)	Novel Protein sim. GBank gi 4808220 emb CAB42832.1  - (AL022315) dJ11715.1 (PUTATIVE novel protein) [Homo sapiens]	struct	52644507, 22278996, 22278999, 29331824, 29331828, 33657402, 21908754, 87168474, 265019, 264389, 264689, 21906765, 21906766, 21906767, 21906768, 265020, 33657023, 18108376, 18108387
2497	91723554 (4993, 4994)	Novel Protein sim. GBank gi 1200503 (U47824) - B [Homo sapiens] Novel Protein sim. GBank gi 3510234 (AC005581) - R31237.1, partial CDS [Homo sapiens]	UNCLASSIFIED	29331827, 264512, 264610, 264288, 18108374, 35695855
2498	87724633 (4995, 4996)		UNCLASSIFIED	264909, 55812038, 264631, 264637, 264558
2499	94685125 (4997, 4998)		Contains protein domain (PF00069) - Eukaryotic protein kinase domain	



2500	94648324 (4989, 5000)	Novel Protein sim. GBank gij3881275 emb CAA21725  - (AL032655) predicted using GeneFinder: similar to Inositol monophosphatase family; cDNA EST yk255e11.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00459) - Inositol monophosphatase family	transport	52644507, 52645156, 22278995, 56994075, 35696286, 22278998, 264259, 52645080, 29331824, 29331825, 66714117, 60432289, 29331828, 29331827, 35696052, 29331828, 264508, 264509, 264510, 264512, 33657402, 60433438, 21906754, 52644296, 87168474, 87168559, 264603, 264681, 264448, 264683, 264288, 264369, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264683, 33657182, 35695763, 35696423, 35695855, 52644332, 83373044, 18108387, 87168518, 22279002
2501	94303896 (5001, 5002)	Novel Protein sim. GBank gij4929615 gb AAD34068.1 AF15183 - (AF151831) CGI-73 protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_ma_bind	65274572, 56182575, 35696286, 22278996, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264910, 264591, 60432229, 33657402, 60433356, 264595, 55812038, 264758, 264596, 87168474, 87168559, 264600, 264601, 264602, 265017, 264604, 265018, 264805, 265019, 18108351, 264448, 264369, 264288, 264766, 18108357, 21906765, 21906766, 21906787, 21906788, 29148629, 35695917, 264692, 33657023, 264629, 35696423, 55811576, 35695855, 264630, 264634, 264635, 264555, 264636, 264638, 264558, 60170394, 83373044, 18108385, 18108387, 87168518, 60432113, 22279002, 264566
2502	90893716 (5003, 5004)	Novel Protein sim. GBank gij3041847 (AC004542) - OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID:g129308) [Homo sapiens]	Contains protein domain (PF01237) - Oxyesterol-binding protein	UNCLASSIFIED	65274572, 264907, 56182435, 265007, 264592, 264760, 18108351, 264448, 264369, 264288, 264684, 264686, 55811957, 265021, 264692, 33657109, 263973, 55811576, 264635, 264555, 264556, 264557, 264558, 56182323, 264559, 87168518, 264563, 264482
2503	87878345 (5005, 5006)	Novel Protein sim. GBank gij2196874 emb CAA72638  - (Y11896) BRX protein [Mus musculus]			264905, 264907, 264512, 265008, 265011, 18108351, 264448, 264288, 29148627, 264693, 18108370, 18108374, 18108385

2504	87868706 (5007, 5008)	Novel Protein sim. GBank gj550420[emb]CAA48220] - (X68101) tlg [Rattus norvegicus]			284488, 52644507, 52645156, 52646842, 22278994, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 35696032, 264906, 264908, 52644045, 265009, 60433358, 33657402, 60433438, 264595, 33109954, 87168474, 265017, 265019, 264448, 264288, 264768, 52644229, 21906765, 21906766, 21906767, 21906768, 52644150, 264692, 27486261, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 52644332, 56182323, 18108367, 87189518, 60432113, 22279002, 264564
2505	8760559 (5009, 5010)			UNCLASSIFIED	264605
2506	87232328 (5011, 5012)	Novel Protein sim. GBank gj2137562[pir]49635 - mouse Dhm1 protein - mouse		nuclease	284488, 52644507, 52645156, 52646365, 65274572, 22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331826, 29331828, 264509, 56182435, 264112, 264593, 60433358, 55812038, 21908754, 265011, 265017, 265018, 265019, 264805, 264762, 18108351, 264448, 264288, 264768, 21908765, 21908766, 21906767, 21906768, 21908769, 35695917, 265020, 265021, 265022, 60170615, 33657023, 27486264, 18108378, 35695855, 264637, 83373044, 18108385, 87168518, 60432113, 22279000, 264563, 264482, 264565
2507	95316233 (5013, 5014)	Novel Protein sim. GBank gj5174489[ref]NP_006035.1[pKIAA - histone deacetylase 6]	Contains protein domain (PF00850) - Histone deacetylase family	histone	284488, 263994, 264592, 264595, 264389, 264686, 264768, 35695917, 35696423, 264563
2508	95315505 (5015, 5016)	Novel Protein sim. GBank gj4826433[emb]CABA2889.1] - (AL031447) dJ126A5.2.1 (novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 60432049, 264259, 29331828, 265006, 265007, 60433438, 33657084, 265010, 265017, 265018, 265019, 18108351, 264448, 18108354, 264369, 18108359, 21906765, 21906769, 55811957, 265020, 265022, 27486261, 33657349, 18108377, 35695855, 60432113, 22279002, 264563, 264565
2509	87813741 (5017, 5018)	Novel Protein sim. GBank gj1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	265007, 265008, 18108357, 264556, 264567

2510	95421379 (5018, 5020)	Novel Protein sim. GBank gjl3293537(gbj)AAC25762.1] - (AF071059) zinc finger RNA binding protein [Mus musculus]				65274572, 22278994, 22278996, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331828, 33656970, 264908, 66712502, 265007, 264910, 60170831, 60432229, 60433356, 60433438, 21906754, 87168474, 265017, 265018, 264448, 264288, 21906767, 21906768, 21906769, 59811957, 35695917, 265020, 265022, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486282, 33657349, 18108370, 35695855, 264555, 56182323, 83373044, 60432113, 22279002, 265017, 21906764, 265020, 264692
2511	87384281 (5021, 5022)	Novel Protein sim. GBank gjl4323152(gbj)AAD16228.1] - (AF098863) Els-protein Spi-C [Mus musculus]				
2512	88084771 (5023, 5024)	Novel Protein sim. GBank gjl4502075(refINP_001135.1)pAMFR - autocrine molality factor receptor	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transport		22278998, 264259, 29331825, 29331826, 29146499, 264907, 264909, 265008, 264591, 60432229, 21906754, 264763, 264883, 264766, 18108357, 264689, 21906769, 264693, 18108370, 263972, 18108374, 264558, 22279000
2513	95357843 (5025, 5026)	Novel Protein sim. GBank gjl3004657 (AF017777) - bobby sox [Drosophila melanogaster]		UNCLASSIFIED		60424179, 52845156, 18108394, 22278994, 35696286, 56994075, 22278996, 29331822, 29331824, 60424269, 29331825, 29331827, 33656970, 60431735, 33657084, 87168559, 265017, 264448, 264369, 56181562, 21906768, 21906767, 21906768, 21908769, 265020, 265021, 33657023, 18108366, 33657109, 27486261, 27486282, 33657349, 18108374, 55810764, 35696423, 56182323, 264558, 18108385
2514	88094578 (5027, 5028)	Novel Protein sim. GBank gjl2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED		264510
2515	87894509 (5029, 5030)	Novel Protein sim. GBank gjl3757727(jemb)CAA18783] - (AL022727) dJ8019.7 (olfactory receptor-like protein (hs6M1-3)) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7		
2516	87786908 (5031, 5032)			UNCLASSIFIED		264259, 29146498, 264905, 264288, 29148629, 35695917, 27486261, 264634
2517	87784966 (5033, 5034)	Novel Protein sim. GBank gjl4220527(jemb)CAA23000] - (AL035356) putative protein [Arabidopsis thaliana]		UNCLASSIFIED		264091, 29331824, 29331825, 29331826, 29331828, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264511, 264910, 33657402, 264757, 33109954, 265017, 265018, 264605, 264760, 264762, 264763, 264766, 264768, 264769, 33657109, 33657182, 264628, 55811576, 35696423, 264631, 264634, 264637, 264638, 264639, 87168518, 22279002, 264564

2518	94147410 (5035, 5038)	Novel Protein sim. GBank gi 4928591 gb AAD34056.1 AF15181 - (AF151818) CGI-61 protein [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	35696286, 264258, 28331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 284907, 284909, 264511, 265007, 60432228, 60433356, 60433438, 55812038, 265010, 265017, 264448, 264288, 264889, 21906768, 21906769, 265022, 52844150, 284693, 18108370, 263972, 284555, 56182323, 83373044, 18108385, 60432113, 264088
2519	94328180 (5037, 5038)	Novel Protein sim. GBank gi 4826722 ref NP_005085.1 pFATP - fatty acid transport protein 4 (AC004883) similar to KIAA0766, similar to PID:g3882253 [Homo sapiens]	kinase		264259, 66714117, 29331826, 29331827, 29331828, 264907, 66712502, 285008, 265008, 264594, 265010, 265011, 265018, 264288, 21906769, 265020, 60431528, 55811576, 65274791, 284632, 284555, 264636, 22279002, 284584
2520	87413235 (5039, 5040)	Novel Protein sim. GBank gi 4826722 ref NP_005085.1 pFATP - fatty acid transport protein 4	transport		284259, 264908, 284910, 284682, 21906769, 265020, 264563
2521	95316244 (5041, 5042)	Novel Protein sim. GBank gi 5174489 ref NP_006035.1 pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - histone Histone deacetylase family		264488, 264489, 263984, 65274572, 22278995, 22278998, 264259, 29331822, 29331826, 264508, 284905, 264509, 264906, 264907, 66712502, 284511, 265008, 264007, 264591, 284592, 264593, 264594, 284595, 264596, 284681, 264448, 284763, 284682, 264764, 264684, 264369, 264288, 264685, 264686, 21906768, 55811857, 284692, 264693, 27486281, 18108370, 284628, 264629, 18108374, 55811576, 35696423, 35695855, 284632, 284558, 18108385, 65274727, 60432113, 264563, 264564, 264565, 264566, 284567
2522	87754032 (5043, 5044)	Novel Protein sim. GBank gi 4580011 gb AAD24201.1 U81002 - (U81002) TRAF4 associated factor 1 [Homo sapiens]	transport		264489, 22278997, 20281171, 21908754, 35695917, 263967, 263976, 263981, 20281169
2523	95340467 (5045, 5046)				263969
2524	95340469 (5047, 5048)	Novel Protein sim. GBank gi 1809327 (U76374) - skm-BOP2 [Mus musculus]	Contains protein domain (PF01753) - MYND finger		56984075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 29331830, 56182435, 284512, 265008, 60170831, 33657402, 265010, 87168559, 285019, 264288, 21906765, 21906769, 35695917, 265020, 265021, 265022, 52844150, 284691, 33657023, 33657109, 27488281, 35698423, 65274791, 264559, 83373044, 56526486, 87168518, 284567

2525	94126928 (5049, 5050)	Novel Protein sim. GBank gij2073584 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]		kinase	264468, 22278997, 22278999, 60432049, 60432289, 29331828, 264905, 265008, 55812038, 21906754, 265019, 264369, 21908785, 21908788, 21908787, 21908769, 35695917, 265020, 265021, 33657109, 60431528, 83373044, 60432113, 22279000, 22279002, 264565
2528	35289404 (5051, 5052)	Novel Protein sim. GBank gij4589628(dj)BAA76836.1) - (AB023209) KIAA0992 protein [Homo sapiens]	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomal prot	60424179, 264768, 264687, 264769, 264689, 65274572, 21906767, 56182575, 21908788, 21908769, 55811957, 22278994, 22278995, 35698286, 35695917, 22278996, 22278997, 265020, 22278998, 265021, 22278999, 265022, 264690, 264691, 60432049, 264259, 264097, 33657023, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 27486262, 264508, 264509, 264905, 264907, 18108370, 66712502, 60431528, 264828, 264909, 18108372, 18108374, 56182435, 18108376, 55810764, 55811576, 35698423, 35695855, 265006, 265007, 264512, 265008, 265009, 264634, 264635, 60431850, 264636, 264555, 264592, 60431735, 264638, 33657402, 56182323, 60433356, 60433438, 264595, 55812038, 264596, 264758, 83373044, 52646317, 18108385, 33657084, 18108387, 55811386, 65274727, 56526486, 87168518, 60432113, 265017, 22279000, 265018, 265019, 264564, 18108351, 264448, 264568, 264288, 264488, 264567, 264768, 264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354, 55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002
2527	88094580 (5053, 5054)	Novel Protein sim. GBank gij2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354, 55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002
2528	88078380 (5055, 5056)	Novel Protein sim. GBank gij2085786 (AC002086) - similar to zinc finger 5 protein from Gallus gallus, U51640 (P1D;g1399185) [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	UNCLASSIFIED	264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354, 55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002
2529	36670828 (5057, 5058)	Novel Protein sim. GBank gij3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:008891) [Caenorhabditis elegans]		synthase	264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354, 55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002
2530	80259978 (5059, 5060)				264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354, 55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002
2531	87768831 (5061, 5062)			UNCLASSIFIED	264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354, 55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002
2532	87419778 (5063, 5064)	Novel Protein sim. GBank gij2864625(embj)CAA16972] - (AL021811) putative protein [Arabidopsis thaliana]			264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354, 55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002
2533	87000255 (5065, 5066)	Novel Protein sim. GBank gij437181 (U02289) - GTPase-activating protein [Caenorhabditis elegans]		UNCLASSIFIED	264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354, 55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002

2534	87332322 (5087, 5088)	Novel Protein sim. GBank glj3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]		UNCLASSIFIED	264259, 35696052, 264905, 265017, 21908769, 265020, 265022, 33657109, 22279000
2535	91225056 (5089, 5070)	Novel Protein sim. GBank glj4468311[emb]CAB37992(- (ALD031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			65274572, 35696266, 60432289, 29331828, 66712502, 265006, 60432228, 265017, 265018, 265019, 264288, 264369, 264689, 21906768, 265020, 265021, 264636, 60170394, 22279002
2536	94218540 (5071, 5072)	Novel Protein sim. GBank glj728836[sp]P39193[ALU8_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII	Kinase		18108398, 56182575, 35696266, 22278997, 22278999, 60432049, 264259, 29331824, 29331826, 29331827, 29331828, 264905, 264511, 265009, 264910, 264596, 52646317, 18108351, 264681, 264683, 18108354, 264288, 264687, 264769, 264689, 21906765, 21906768, 21906767, 265021, 52645129, 33657109, 18108374, 18108380, 56182323, 18108381, 18108388, 87168518, 60432113, 22279000, 22279002, 264587, 18108391
2537	95422283 (5073, 5074)	Novel Protein sim. GBank glj4557026[ref]NP_003913.1 pHERC - guanine nucleotide exchange factor p532	ubiquitin		65274572, 35696266, 29331822, 29331825, 29331827, 29331828, 35696052, 264906, 66712502, 264909, 265008, 265011, 264760, 264288, 264685, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 18108374, 35696423, 35695855, 264636, 264558, 60170394, 56182323, 83373044
2538	36853454 (5075, 5076)			UNCLASSIFIED	
2539	94144816 (5077, 5078)			UNCLASSIFIED	22278996, 22278999, 29331822, 29331825, 29331828, 29146499, 264908, 264112, 60170831, 87168559, 264604, 265019, 264685, 264766, 87168518, 22279000, 264565, 264566
2540	94218545 (5079, 5080)	Novel Protein sim. GBank glj1362647[pir]IS53876 - sex-regulated protein janus A - fruit fly (Drosophila pseudoobscura)		UNCLASSIFIED	22278997, 29331828, 265008, 265009, 264758, 265010, 18108351, 264683, 264288, 21906765, 35695917, 265020, 18108374, 264567
2541	95308238 (5081, 5082)	Novel Protein sim. GBank glj1711658[sp]P54797IT10_MOUSE - SER/THR-RICH PROTEIN T10 IN DCCR REGION		UNCLASSIFIED	264488, 264768, 264689, 264511, 20281171, 264634, 264635, 264691, 264639, 29331824, 264603, 264604, 264905, 264907, 264908, 264766

2542	95288162 (5083, 5084)	Novel Protein sim. GBank gi 5225320 gb AADX0850.1 AF08310 - (AF083107) sirtuin type 2 [Homo sapiens]	Contains protein domain (PF00220) - Neurohypophyseal hormones, N- terminal Domain	UNCLASSIFIED	264488, 18108394, 52646355, 52646842, 65274572, 22278994, 35698286, 22278996, 264259, 52645080, 29331822, 29331824, 29331827, 35698052, 33658970, 264907, 264909, 52644045, 264510, 265006, 264512, 265007, 265008, 265009, 264910, 60431735, 52646317, 52644296, 265010, 265011, 265018, 265019, 18108351, 264883, 264288, 264885, 264887, 52644229, 264769, 21906766, 21906767, 21906789, 52644150, 33657023, 33657109, 52645129, 33657182, 27486261, 27486264, 33657349, 35695763, 18108374, 35696423, 35695855, 264831, 264634, 264635, 264558, 83373044, 18108385, 18108387, 87168518, 264563, 264564
2543	94139088 (5085, 5086)	Novel Protein sim. GBank gi 5419857 emb CAB46374.1  - (AL096723) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)		65274572, 56182575, 22278999, 264259, 29331826, 264907, 264510, 264511, 264592, 264595, 264764, 264369, 264288, 264684, 264766, 264689, 21906765, 21906767, 21906769, 60170815, 264692, 264693, 55811576, 85274791, 264636, 264556, 18108381, 60170394, 264639, 18108385, 60432113, 22279000
2544	94218549 (5087, 5088)	Novel Protein sim. GBank gi 2498110 sp Q63191 AEGP_RAT - APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR	Contains protein domain (PF00629) - MAM domain.	glycoprotein	18108397, 52646385, 22278997, 264259, 60432049, 29331822, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 265006, 265007, 265008, 87168559, 265017, 265018, 265019, 18108351, 264448, 264688, 264687, 264689, 21906765, 265020, 265021, 18108370, 18108374, 18108376, 18108381, 18108385, 18108387, 56526466, 22279000, 264482, 264563, 264567
2545	87742645 (5089, 5090)	Novel Protein sim. GBank gi 3327046 dbj BAA31591  - (AB014516) KIAA0616 protein [Homo sapiens]			29331825, 264906, 265009, 60170831, 265017, 264369, 21906767, 60170615, 264692, 33657109
2546	86033861 (5091, 5092)	Novel Protein sim. GBank gi 2996032 (AF054586) - brain finger protein [Rattus norvegicus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	29331824, 265007, 22279002

2547	84143888 (5093, 5094)	Novel Protein sim. GBank gi 4929607 gb AAD34064.1 AF15182 - (AF151827) CGI-69 protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264488, 18108394, 52646842, 18108397, 56182575, 22278995, 58994075, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 35696052, 29331828, 264104, 264508, 264805, 264906, 264908, 66712502, 264909, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432228, 60431735, 264594, 60433438, 21906754, 52646317, 265010, 265011, 264600, 264601, 265018, 265019, 264760, 18108351, 264682, 264448, 264288, 264369, 264684, 264686, 264687, 56181562, 264688, 264689, 21908785, 21906766, 21908767, 21906768, 29148627, 21906789, 55811957, 265020, 265021, 265022, 264690, 264691, 18108362, 264692, 264693, 27488261, 18108370, 18108374, 55810764, 55811576, 35696423, 35696555, 264635, 264636, 264555, 264637, 263981, 264557, 18108380, 264638, 56182323, 264558, 264559, 83373044, 18108385, 87168518, 22278002, 264564, 264566, 264486
2548	86179079 (5095, 5096)			UNCLASSIFIED	264488, 18108394, 52646365, 22278994, 35696286, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 56182435, 264511, 265007, 264512, 60433356, 87168559, 264684, 264369, 52644229, 265021, 33657023, 264692, 18108374, 52644332, 264557, 18108380, 18108381, 18108382, 18108384, 18108385, 60432113, 22278000, 22278002, 264563, 264567
2549	94196893 (5097, 5098)	Novel Protein sim. GBank gi 728837 sp P39194 ALUT_HUMAN - !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!	Contains protein domain (PF00412) - LIM domain containing proteins	struct	56182575, 22278996, 22278997, 22278998, 22278999, 264259, 264508, 264908, 29331830, 265009, 265010, 265018, 264688, 21906784, 21906785, 21906786, 21908787, 21908789, 265020, 265021, 52644150, 264691, 18108388, 60431602, 18108376, 35696423, 56182323, 18108387, 264567
2550	87778594 (5099, 5100)	Novel Protein sim. GBank gi 2143886 pir j 52523 - nucleoporin p82 homolog - rat (fragment)		UNCLASSIFIED	56182575, 29331822, 264105, 264512, 18108351, 35695917, 264637, 264638



2551	95308400 (5101, 5102)	Novel Protein sim. GBank gi 4337103 gb AAD18079  - (AF129756) NG26 [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	UNCLASSIFIED	18108396, 65274572, 22278995, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 264905, 56182435, 265007, 60433438, 55812038, 21906754, 65274444, 265017, 265018, 264605, 265019, 264288, 21906766, 21906768, 21906769, 265020, 60170615, 284893, 33657109, 35696423, 264638, 56182323, 83373044, 22279000
2552	95332620 (5103, 5104)			UNCLASSIFIED	56182575, 35696286, 29331824, 29331826, 35696052, 29331828, 264508, 264907, 56182435, 265008, 264591, 33109954, 264760, 55811957, 35695917, 33657023, 33657109, 18108374, 55811576, 35696423, 35695855, 56182323, 264558
2553	95308243 (5105, 5106)	Novel Protein sim. GBank gi 171658 sp P54797 T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264686, 264488, 263976, 264768, 29331826, 35696052, 35696423, 264601, 264511, 264602, 264910, 264634, 264760, 264555, 264762, 264906, 264592, 264691, 264566, 264908, 264684, 264567, 264909, 264766
2554	87761520 (5107, 5108)	Novel Protein sim. GBank gi 728835 sp P39192 ALU5_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY IIII		cadherin	22278997, 29331822, 264508, 21906769, 33657023, 33657109, 56182323
2555	87627551 (5109, 5110)	Novel Protein sim. GBank gi 4884319 emb CAB43260.1  - (AL050984) hypothetical protein [Homo sapiens]		nuclease	29331824, 263972
2556	87645533 (5111, 5112)	Novel Protein sim. GBank gi 4106984 (AC003038) - R30923_1 [Homo sapiens]	Contains protein domain (PF00514) - Armadillo/beta-catenin-like repeats	UNCLASSIFIED	22278998, 264509, 33657402, 264683, 264684, 264766, 264689, 33657023, 33657109, 35695855, 264558, 264567, 264595
2557	79437803 (5113, 5114)	Novel Protein sim. GBank gi 19110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	22278997, 29331824, 66714117, 29331825, 264906, 264511, 265018, 264448
2558	87617597 (5115, 5116)	Novel Protein sim. GBank gi 4538998 emb CAB39619.1  - (AL049481) ALG1-like protein [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 29331822, 29331828, 60433356, 265011, 264288, 264765, 264766, 264769, 21906765, 21906766, 60432113, 264482
2559	88096382 (5117, 5118)	Novel Protein sim. GBank gi 5051399 emb CAB44995.1  - (AL078630) 573K1.3 (mm17M1-4 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor LIKE) protein)) [Mus musculus]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)		
2560	87994530 (5119, 5120)	Novel Protein sim. GBank gi 5326825 gb AAD42056.1 AF044953 - (AF044953) NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens]		UNCLASSIFIED	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 265007, 60432229, 87168559, 265017, 265018, 265019, 264688, 21906768, 21906769, 35695917, 265020, 33657023, 33657109, 18108374, 264634, 264559, 18108385, 87168518, 22279002

2562	87845539 (5123, 5124)	Novel Protein sim. GBank gi 4106984 (AC003038) - R30923_1 [Homo sapiens]		UNCLASSIFIED	56994075, 22278998, 22278997, 22278999, 264259, 29331822, 60432289, 33657402, 60433356, 21908765, 55811957, 60170815, 33657023, 284693, 35695855, 87188518, 264488, 35696286, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 284907, 264908, 264909, 52644045, 284510, 284511, 285009, 284910, 264591, 284593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21908787, 21908788, 55811957, 35695917, 285020, 264691, 264693, 27488262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264568, 284488
2563	88095497 (5125, 5126)	Novel Protein sim. GBank gi 4886447 (emb CAB43371.1) - (AL050270) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264488, 35696286, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 284907, 264908, 264909, 52644045, 284510, 284511, 285009, 284910, 264591, 284593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21908787, 21908788, 55811957, 35695917, 285020, 264691, 264693, 27488262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264568, 284488
2564	80502783 (5127, 5128)	Novel Protein sim. GBank gi 1352944 (sp P47178 Y19P_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR		sulfoltransferase	29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2565	85530808 (5129, 5130)			UNCLASSIFIED	66714117, 264909, 263978, 264632
2566	80224956 (5131, 5132)	Novel Protein sim. GBank gi 628012 (pir J53933 - myosin I myr 4 - ral	Contains protein domain (PF00063) - struct	UNCLASSIFIED	18108370, 35695855, 264556, 264558, 18108383
2567	88143580 (5133, 5134)	Novel Protein sim. GBank gi 466009 (sp P34548 YJN4_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III		synthase	265020, 60170615
2568	91233099 (5135, 5136)				60424179, 18108394, 56181686, 56994075, 22278999, 264490, 264259, 26331822, 56182181, 29331824, 60424289, 29331825, 29331826, 29331828, 264509, 29331830, 265007, 265008, 265009, 33657402, 265010, 265011, 265019, 264448, 264683, 264288, 18108354, 264769, 21908766, 21908767, 35695917, 265021, 33657023, 18108362, 33657109, 33657182, 35695763, 60431528, 55810784, 18108379, 83373044, 18108365, 60432113, 264482

2569	95313764 (5137, 5138)	Novel Protein sim. GBank gij2595560igb AAB84166.1  - (AF029674) basic leucine zipper protein LZP [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	18108394, 56182575, 56181686, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 56182181, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 264906, 56182435, 265008, 265009, 264910, 60432229, 264592, 60433356, 60433438, 21906754, 87168559, 265017, 265018, 265019, 264682, 264448, 264288, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 35695917, 265021, 265022, 52644150, 264690, 264691, 264692, 264693, 65274620, 263967, 35695763, 20281069, 263974, 18108374, 55810764, 35696423, 35695855, 264558, 18108381, 56182323, 18108382, 83373044, 18108385, 56526486, 87168518, 22279000, 22279002, 264566
2570	94136754 (5139, 5140)	Novel Protein sim. GBank gij4758954 ref NP_004567.1 pPPP2 - protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	Contains protein domain (PF01240) - Protein phosphatase 2A regulatory subunit PR55	phosphatase	22278996, 29331822, 29331824, 66714117, 29331825, 60432289, 29331827, 35696052, 264907, 264510, 265007, 265009, 264758, 33109954, 265019, 264686, 264689, 265020, 265021, 264691, 264692, 264693, 18108374, 35695855, 264634, 56182323, 264639, 60170394, 83373044, 22279002, 264482
2571	87733750 (5141, 5142)	Novel Protein sim. GBank gij732218 sp P34609 YO60_CAEEL - HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME III		struct	264508, 264905, 264907, 264828, 18108351, 264555, 264556, 264557, 264558, 264559
2572	87627660 (5143, 5144)	Novel Protein sim. GBank gij4884319 emb CAB43260.1  - (AL050084) hypothetical protein [Homo sapiens]		UNCLASSIFIED	35696286, 29331827, 35696052, 264100, 264104, 264110, 264592, 21906754, 29148627, 29148629, 263972, 263974, 18108374, 263976, 35695855, 60170394, 264559, 18108385

2573	95313929 (5145, 5146)	Novel Protein sim. GBank gi 359138 sp P02745 C1QA_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	- complement	264488, 60424179, 65274572, 56182575, 56181686, 22278995, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432288, 29331826, 29331827, 29331828, 264104, 264107, 264508, 264906, 29331830, 264909, 264510, 265006, 264512, 265008, 265009, 264910, 264591, 264592, 60432229, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264759, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264761, 264762, 264763, 264764, 264369, 264288, 264685, 264766, 264686, 264687, 264688, 264769, 56181562, 264689, 21908765, 21906766, 21908767, 29148627, 21906768, 21906769, 265020, 265021, 265022, 60170615, 264690, 52644150, 264691, 264692, 33657023, 65274620, 18108365, 18108368, 27486265, 60431602, 264829, 60431528, 263976, 65274791, 35695855, 20281071, 60431850, 264637, 264638, 264558, 264639, 58182323, 60170394, 83373044, 18108384, 87168518, 60432113, 264482, 264564, 264565, 264566, 264567
2574	94746814 (5147, 5148)	Novel Protein sim. GBank gi 3334982 (AC005306) - R27216_1 [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	UNCLASSIFIED	22278995, 264259, 60432289, 29331827, 29331828, 33656970, 264908, 285008, 264910, 264591, 33657402, 265018, 285019, 264448, 264764, 264369, 264288, 18108357, 21906765, 21906766, 21908768, 55811957, 60170615, 264691, 33657023, 264693, 33657109, 33657182, 27486281, 27486284, 33657349, 264636, 264555, 83373044, 18108385, 264482
2575	87754408 (5149, 5150)	Novel Protein sim. GBank gi 4929729 gb AAD34125.1 AF151888 (AF151888) CGI-130 protein [Homo sapiens]		UNCLASSIFIED	284810, 284601, 264683, 264689, 264080
2576	95357881 (5151, 5152)	Novel Protein sim. GBank gi 4680681 gb AAD27730.1 AF132955 (AF132955) CGI-21 protein [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264259, 35696052, 264908, 60433438, 264681, 18108351, 264288, 52644150, 264628, 35696423
2577	86996621 (5153, 5154)	Novel Protein sim. GBank gi 4337103 gb AAD180791 - (AF129756) NG26 [Homo sapiens]		UNCLASSIFIED	29331825, 265018, 265019, 264685
2578	87786941 (5155, 5156)			UNCLASSIFIED	264488, 264906, 264908, 264910, 264596, 264603, 264604, 264605, 264768, 21908769, 264628, 264630, 264634, 264639, 264583
2579	87292879 (5157, 5158)			UNCLASSIFIED	29331822, 29331824, 264767

2580	80166788 (5159, 5160)	Novel Protein sim. GBank gij2588628 (AC003080) - Similar to KIAA0289; 60% similarity to AB002297 (PID:g2224539) [Homo sapiens]			265007, 265018, 264762
2581	8789048 (5161, 5182)	Novel Protein sim. GBank gij4406642 [gb]AAD20049] - (AF131809) Unknown [Homo sapiens]	Contains protein domain (PF00395) - PDZ domain (Also known as DHR or GLGF).	collagen	56994075, 29331824, 29331826, 29331828, 264905, 60433356, 60433438, 264758, 87168559, 21906769, 265022, 35695855, 263981
2582	87786789 (5163, 5164)	Novel Protein sim. GBank gij2738367 (AC002505) - putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]		eph	264488, 264907, 264908, 264910, 264764, 264684, 264766, 264636, 264555, 264565
2583	91220850 (5165, 5166)	Novel Protein sim. GBank gij4378112 [emb]CAA16521.1] - (AL021578) dJ453C12.2 (similar to transcription factor RBP-L) [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	transcript factor	56181886, 264259, 264510, 264512, 264591, 264592, 264593, 264594, 264595, 264596, 264603, 264629, 55810764, 264630, 264637, 264565
2584	80430941 (5167, 5168)			UNCLASSIFIED	264908, 264910, 264768, 264693, 18108374, 55811576, 56182323
2585	80436126 (5169, 5170)	Novel Protein sim. GBank gij2736151 (AF021935) - myotonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]		kinase	264768
2586	91226136 (5171, 5172)				22278998, 264259, 29331822, 29331824, 29331827, 29331828, 264906, 265007, 265009, 264591, 60433356, 33657402, 265018, 264762, 264288, 21906766, 21906767, 21906769, 265022, 264691, 83373044, 56526488, 22279002
2587	80430943 (5173, 5174)				264908, 265019, 264768, 264693, 55811576, 56182323
2588	80074385 (5175, 5176)			UNCLASSIFIED	264554
2589	85515607 (5177, 5178)	Novel Protein sim. GBank gij3021598 [emb]CAA71415] - (Y10389) nuclear protein [Xenopus laevis]		UNCLASSIFIED	35696052, 264905, 264906, 264907, 264908, 264909, 265009, 265018, 264769, 35696423, 264636
2590	87054526 (5179, 5180)	Novel Protein sim. GBank gij2104689 (U92793) - alpha glucosidase II, alpha subunit [Mus musculus]	Contains protein domain (PF01055) - Glycosyl hydrolases family 31	glucoamylase	22278995, 29331830, 265008, 265010, 265017, 264639
2591	94192167 (5181, 5182)	Novel Protein sim. GBank gij570202 [gb]AAD47199.1 [AF129166] long-chain acyl-CoA synthetase 5 [Homo sapiens]		eph	264259, 29331822, 264106, 264906, 56182435, 265007, 265008, 33109954, 264448, 55811957, 265020, 18108370, 55811576, 22279002

2592	95332648 (5183, 5184)	Novel Protein sim. GBank gi 3024998 sp Q60936 YAB1_MOUSE - HYPOTHETICAL HEART PROTEIN		transport	18108397, 58182575, 35696286, 56994075, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 264806, 264909, 265007, 285008, 264910, 60432228, 264594, 60433358, 60433438, 55812038, 18108348, 21908754, 265011, 87168559, 265017, 265018, 264764, 264369, 264288, 264786, 265021, 60170615, 33837023, 33657109, 264629, 35698423, 35695855, 264557, 264638, 60170394, 56182323, 83373044, 56526486, 87168518, 264563, 264482, 264585
2593	87754416 (5185, 5186)	Novel Protein sim. GBank gi 4929729 gb AA034125.1 AF15188 - (AF15188) CGI-130 protein [Homo sapiens]	im7		22278999, 29331825, 264758, 21906754, 52646317, 265010, 18108351, 264288, 264369, 21906768, 264693, 18108370, 264637, 264638, 264482
2594	95305758 (5187, 5188)	Novel Protein sim. GBank gi 4928587 gb AA034054.1 AF15181 - (AF15181) CGI-59 protein [Homo sapiens]	UNCLASSIFIED		264488, 18108398, 58182575, 35696288, 22278997, 264093, 264259, 29331822, 29331825, 66714117, 29331826, 264805, 264909, 52644045, 56182435, 264510, 264512, 265007, 264757, 21906754, 87168474, 265017, 264760, 264448, 264764, 264288, 264766, 264689, 21906768, 33657109, 263975, 263977, 264634, 264556, 60170394, 56182323, 56526486, 264482, 264583, 264584, 264586, 264587, 264692
2595	79561676 (5189, 5190)	Novel Protein sim. GBank gi 4309681 gb AA015478  - (AC006930) R33423_1 [Homo sapiens]	UNCLASSIFIED		22278999, 264259, 265018, 264448, 265021, 60431528
2596	87538637 (5191, 5192)		UNCLASSIFIED		264905, 264509, 264908, 264762, 264786, 35695917, 35695855, 264835, 264638, 83373044, 264488
2597	94784089 (5193, 5194)		UNCLASSIFIED		22278998, 264259, 29331824, 87168474, 264683, 21906768, 35695917, 264691, 33657023, 33857109, 18108370, 18108374, 264564, 264565
2598	88094948 (5195, 5196)	Novel Protein sim. GBank gi 1001351 db BAA10838  - (D64008) hypothetical protein [Synechocystis sp.]	UNCLASSIFIED		264766, 264769, 21906768, 33657182, 35695763, 18108370, 18108374, 264635, 264636, 56526488, 22279000, 264566, 35696286, 264093, 264288, 21906769, 35696423, 35695855
2598	87642889 (5197, 5198)	Novel Protein sim. GBank gi 3941737 (AF103719) - BAT2 [Mus musculus]	MHC		
2600	87787846 (5199, 5200)	Novel Protein sim. GBank gi 4263521 gb AA015347  - (AC004044) putative WD-repeat protein [Arabidopsis thaliana]	kinasereceptor	Contains protein domain (PF00400) - WD domain, G-beta repeat	

2601	91243070 (5201, 5202)	Novel Protein sim. GBank gij728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	56182575, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 264906, 265007, 265008, 264591, 60433356, 33857402, 60433438, 21906754, 265011, 265018, 265019, 18108351, 264448, 264369, 21906769, 265020, 60170615, 264693, 33857109, 18108370, 18108376, 56182323, 18108381, 18108385, 22279002, 264563, 60433438, 21906754, 87168559, 264601, 264369, 264288, 21906767
2602	88180022 (5203, 5204)	Novel Protein sim. GBank gj 4406632 gb AAD200471 - (AF131801) Unknown [Homo sapiens]			264488, 65274572, 22278995, 22278996, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35896052, 56182435, 264113, 265008, 265009, 60433356, 264757, 60433438, 264759, 33657084, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264683, 18108354, 264288, 264767, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27486262, 18108374, 35696423, 65274791, 35695855, 264555, 264636, 264637, 56182323, 83373044, 56526486, 87168518, 60432113, 22279000
2603	94325821 (5205, 5206)	Novel Protein sim. GBank gj 3122367 sp Q61211 LIGA_MOUSE - LIGATIN		UNCLASSIFIED	264259, 35696052, 264508, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 264910, 33657402, 264604, 264605, 264762, 264763, 264682, 264764, 264683, 264768, 264769, 264689, 33657023, 264693, 18108365, 264628, 35696423, 264631, 264632, 264634, 264635, 264637, 18108381, 264639, 83373044, 264565
2604	94676601 (5207, 5208)	Novel Protein sim. GBank gj 545403 ref NP_006468.1 pRRP2 - RAS-related on chromosome 22		oncogene	22278998, 264490, 60432049, 264259, 60432289, 264909, 265008, 60433356, 60433438, 264758, 21906754, 265010, 265011, 265018, 264681, 18108351, 264288, 264766, 264685, 21906765, 21906766, 21906768, 21906769, 264691, 264692, 264693, 65274791, 264634, 264555, 264636, 22278996, 264510, 264512, 265009, 264766, 22279002, 264566
2605	94316756 (5209, 5210)	Novel Protein sim. GBank gj 3628745 dbj BAA33366) - (AB013721) mltugumin 23 [Oryctolagus cuniculus]		UNCLASSIFIED	
2606	87746406 (5211, 5212)				

2607	87627742 (5213, 5214)	Novel Protein sim. GBank gij4826626[gb AAD30202.1] - (AF135022) mediator [Homo sapiens]			29331822, 29331825, 29331826, 29331827, 29331828, 264908, 264907, 264908, 66712502, 264828, 58182435, 55812038, 265010, 265017, 265018, 265019, 264768, 264688, 21908765, 55811957, 265020, 265022, 264692, 33857023, 264693, 33657109, 18108370, 264639, 58182323, 264509, 264907, 264908, 264592, 264758, 264631
2608	81734786 (5215, 5216)	Novel Protein sim. GBank gij2226005 (U49973) - ORF2: function unknown [Homo sapiens]			
2609	94843791 (5217, 5218)	Novel Protein sim. GBank gij3024889[sp P56524 Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)]	Contains protein domain (PF00850) - histone Histone deacetylase family		264488, 65274572, 35696286, 22278997, 22278999, 60432049, 264259, 56182181, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264907, 60433356, 60433438, 55812038, 265011, 87168559, 265017, 265018, 264448, 264765, 264288, 264766, 264689, 21908765, 21908787, 21906769, 265020, 265021, 264691, 264692, 33857109, 27488261, 18108370, 65274791, 264638, 264556, 56182323, 18108385, 56528486
2610	88177654 (5219, 5220)	Novel Protein sim. GBank gij4336855[gb AAD17989] - (AF106473) leucine-rich-domain inter-acting protein 1; LeR inter-acting protein 1; LEAP1 [Mus musculus]	transcript factor		18108394, 22278994, 56994075, 60432049, 284259, 29331822, 29331825, 60432289, 29331827, 264107, 264109, 264905, 56182435, 264112, 265006, 265007, 265008, 265009, 60433356, 60433438, 265011, 87168559, 265017, 264448, 264682, 264764, 264288, 265021, 33857023, 263967, 33657182, 27486261, 18108374, 263976, 55811576, 264638, 87168518, 60432113, 22278999, 265017, 264684, 21908768, 22278000
2611	87428890 (5221, 5222)	Novel Protein sim. GBank gij387676[emb CAA92994] - (Z68760) predicted using GeneFINDER; Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	
2612	87771188 (5223, 5224)	Novel Protein sim. GBank gij5679136[gb AAD46874.1 AF16093] - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	265009, 264910, 264759, 265017, 21906767, 18108365, 18108388, 60432113
2613	79481496 (5225, 5226)			UNCLASSIFIED	264685
2614	87643948 (5227, 5228)	Novel Protein sim. GBank gij5533081[gb AAD45009.1 AF16118] - (AF161181) P55T protein [Mus musculus]	Contains protein domain (PF00625) - Guanylate kinase		22278998, 22278999, 29331825, 264508, 264906, 21908754, 264602, 264766, 264769, 52644229, 21908765, 33857109, 27488264, 18108370, 263972, 264555, 60432113, 264768, 18108394, 264692, 264693, 264508, 264509, 264907, 264628, 264908, 264909, 18108377, 264511, 264512, 264910, 264635, 264595, 265010, 264404, 264563, 264764, 264685, 264766
2615	87381986 (5229, 5230)			UNCLASSIFIED	



2616	87428895 (5231, 5232)	Novel Protein sim. GBank gij3876761[emb CAA92994] - (Z68760) predicted using GeneFinder; Similarity to Mouse FKBP-type peptidyl-prolyl cis-trans isomerases [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	22278995, 22278997, 22278998, 60432049, 60432289, 264828, 60433356, 264594, 60433438, 33109954, 87168474, 265011, 265017, 265019, 264288, 264766, 21906765, 21906767, 265020, 265021, 18108376, 18108377, 18108387, 87168518, 264482, 264587
2617	36978888 (5233, 5234)	Novel Protein sim. GBank gij728831[sp P39188]ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		kinase	265010, 265019, 264368, 264693, 55811576, 22279002
2618	91231662 (5235, 5236)	Novel Protein sim. GBank gij3319282 (AF049103) - Huntingtin interacting protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	UNCLASSIFIED	264489, 22278996, 264490, 264259, 29331822, 264102, 264509, 264908, 264907, 68712502, 29331830, 265008, 264910, 265009, 60433356, 60433438, 264758, 21906754, 265011, 87168559, 265017, 265018, 264369, 264288, 264768, 264768, 264689, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 33657023, 264692, 33657109, 264628, 18108374, 35695855, 18108381, 83373044, 18108385, 18108388, 56528488, 264563
2619	87694000 (5237, 5238)	Novel Protein sim. GBank gij2431772 (U66411) - putative type III alcohol dehydrogenase [Drosophila melanogaster]	Contains protein domain (PF00465) - iron-containing alcohol dehydrogenases	dehydrogenase	264259, 60432289, 60433438, 21906754, 264369, 60432113, 264566
2620	95314841 (5239, 5240)	Novel Protein sim. GBank gij4322567[gb AAD16097] - (AF090436) dachshund variant 1 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	52644507, 52645156, 52646842, 65274572, 22278995, 56994075, 35696286, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 35696052, 264907, 66712502, 265008, 60433356, 33657402, 52646317, 21906754, 87168474, 265010, 265017, 265018, 264448, 264369, 264288, 264687, 264768, 52644229, 264688, 264689, 21906765, 21906768, 35695917, 52644150, 264692, 33657109, 35695763, 35696423, 264556, 52644332, 18108382, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 22279002, 264594, 264636
2621	80253495 (5241, 5242)	Novel Protein sim. GBank gij4557341[ref NP_001174.1]pATP6 - ATPase, H+ transporting, lysosomal subunit 1; vacuolar proton pump; H-ATPase subunit			264488, 264908, 264907, 264908, 264512, 265007, 264758, 35695917, 264634, 264636, 264563, 264482
2623	91639306 (5245, 5246)	Novel Protein sim. GBank gij3880355[emb CA805289] - (Z82285) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	29331824, 35696052, 265007, 265010, 264288, 29148629

2624	91639308 (5247, 5248)	Novel Protein sim. GBank gi 3860355 emb CA05299  - (Z62285) predicted using GeneFinder [Caenorhabditis elegans]	UNCLASSIFIED	56181688, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331828, 35698052, 29146499, 66712502, 52644045, 285007, 265008, 60433356, 33109954, 21908754, 265010, 265011, 265019, 284448, 264288, 21908765, 21908766, 21908767, 29148629, 35695917, 265021, 285022, 27486285, 18108370, 60431528, 55811576, 35695855, 56182323, 18108385, 87168518, 22279002, 18108391
2625	86452068 (5249, 5250)	Novel Protein sim. GBank gi 2887429 dbj BAA24857  - (AB007887) KIAA0427 [Homo sapiens]	UNCLASSIFIED	264091, 264511, 283981
2626	16533797 (5251, 5252)	Novel Protein sim. GBank gi 487416 L20302  - actin filament protein [Gallus gallus]	struct	265008
2627	87636823 (5253, 5254)	Novel Protein sim. GBank gi 86462 pir A27307 - proline-rich phosphoprotein (gene PRH1, Db allele) - human	UNCLASSIFIED	22278996, 265007, 265009, 264448, 21908767, 265021, 264558, 87168518
2628	94848254 (5255, 5256)	Novel Protein sim. GBank gi 3123552 emb CAA18609  - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) [Homo sapiens]	UNCLASSIFIED	22278997, 22278999, 264259, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264907, 264909, 265008, 264591, 60433356, 60433438, 265010, 265017, 265018, 264389, 264288, 18108357, 21908765, 21908768, 265022, 65274791, 264638, 18108387, 87168518, 22279002
2629	87376490 (5257, 5258)	Novel Protein sim. GBank gi 4929595 gb AAD34058.1 AF15182 - (AF151821) CGI-63 protein [Homo sapiens]	synthase	29331825, 29331826, 264102, 265006, 264786, 35695917, 264891, 33657023, 283972, 18108374, 22279000
2630	79188364 (5259, 5260)	Novel Protein sim. GBank gi 321605 pir JQ1181 - Gag protein - Vsrna virus (strain EV1)	UNCLASSIFIED	264636, 18108385
2631	94845908 (5261, 5262)	Novel Protein sim. GBank gi 321605 pir JQ1181 - Gag protein - Vsrna virus (strain EV1)	Contains protein domain (PF00009) - Zinc finger, CCHC class	52644507, 52645156, 52846365, 52646842, 22278994, 22278995, 35698288, 56994075, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264905, 264509, 264907, 264908, 264511, 264512, 285007, 265008, 264910, 52646317, 33657084, 52644286, 265010, 87168559, 265017, 265018, 265019, 264780, 264762, 264448, 264288, 264368, 264768, 264768, 52644229, 21908764, 21908765, 21908766, 21908767, 21908768, 35695917, 265020, 52644150, 33657023, 52645128, 33657109, 33657182, 27486261, 27486262, 27486285, 33657349, 35695763, 35696423, 65274791, 35695855, 264634, 264637, 52644332, 56182323, 60432113, 284586, 284486, 264685
2632	38730414 (5263, 5264)			

2633	85011617 (5265, 5266)	Novel Protein sim. GBank gij139548[dj]BAA10889] - (D64009) seizure-related gene product 6 type 2 precursor [Mus musculus]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	22278995, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331827, 284508, 264908, 265008, 265007, 265008, 265009, 55812038, 33657084, 55811388, 265010, 265011, 87168559, 265018, 265019, 264683, 264288, 264686, 29148629, 33657023, 264693, 33657182, 35695763, 55811578, 264638, 56182323, 83373044, 18108385, 56526486, 87168518, 22279000, 22279002, 264565
2634	87330921 (5267, 5268)	Novel Protein sim. GBank gij544161[emb]CAB46854.1] - (AJ388555) hypothetical protein [Canis familiaris]	UNCLASSIFIED	29331826, 263972, 264089
2635	86623144 (5269, 5270)	Novel Protein sim. GBank gij4680663[gb]AAD27721.1[AF132946] CGI-12 protein [Homo sapiens]		22278997, 264259, 29331824, 66714117, 29331827, 29331828, 264907, 33657084, 265017, 265018, 264448, 264288, 21906766, 21906767, 21906768, 29148629, 18108376, 55811576, 35695855, 87168518, 22279000, 264569, 29331822, 29331828, 265005, 60170831, 264681, 264765, 264885, 29148627, 21906769, 29148784, 265022, 60170815, 264635, 18108385, 56526486, 22279002, 264567
2636	87260534 (5271, 5272)	Novel Protein sim. GBank gij3879146[emb]CAB07646] - (Z93386) Similarly to Yeast hypothetical 52.9 KD protein (SW:P43616); cDNA EST EMBL:M89432 comes from this gene; cDNA EST EMBL:D71008 comes from this gene; cDNA EST EMBL:D73578 comes from this gene; cDNA EST EMBL:D69025 comes ...	Contains protein domain (PF01546) - Peptidase family M20/M25/M40	264488, 264489, 52644507, 264887, 52646365, 52646842, 22278994, 22278996, 22278999, 20281171, 264259, 29331822, 52645080, 66714117, 29331825, 29331826, 29331827, 35696052, 29331828, 29146498, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264591, 264592, 60432229, 264593, 264594, 33657402, 60433356, 264757, 60433438, 264596, 264758, 52646317, 21906754, 52644296, 265010, 264600, 264602, 264603, 264605, 264761, 264762, 264681, 264448, 264764, 264765, 264288, 264766, 264686, 264768, 264887, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 60170815, 264691, 33657023, 264692, 264693, 65274620, 27486284, 18108370, 264628, 264629, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264637, 264638, 52644332, 264639, 264558, 83373044, 60432113, 264564, 264565, 264566, 264486, 264567
2637	95011299 (5273, 5274)	Novel Protein sim. GBank gij4758208[ref]NP_004081.1[pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	

2638	94326733 (5275, 5276)	Novel Protein sim. GBank gij4925689igb/AAD34105.1(AF15188 - (AF15188) CGI-110 protein [Homo sapiens])	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	60424179, 52644507, 52646842, 18108398, 58182575, 22278995, 22278996, 35696286, 22278997, 22278999, 264259, 60432049, 29331822, 60424269, 29331826, 35696052, 29146498, 264805, 52644045, 58182435, 60433356, 33657402, 55812038, 55811386, 265018, 264288, 264769, 52644229, 56181562, 29148627, 29148629, 55811957, 29148784, 35695917, 265021, 52644150, 33657023, 65274620, 33657109, 35695763, 18108374, 55810784, 35696423, 55811576, 35695855, 60431850, 56182323, 60432113, 264404
2639	95361348 (5277, 5278)	Novel Protein sim. GBank gij2190007idbj/BA20355] - (AB004109) phosphatidylserine synthase II [Cricetulus griseus]	synthase		284488, 29331825, 35696052, 264508, 264509, 264909, 264512, 33657402, 60433438, 264758, 35695842, 264600, 265020, 265021, 33657109, 264628, 35696423, 264555, 264639, 264563, 264564, 264565, 264566, 264488
2640	87781330 (5279, 5280)	Novel Protein sim. GBank gij3158516 (AF067617) - contains similarity to chromo (chromatin organization modifier) domains (Pfam: chromo.hmm, score: 17.76 and 27.94) and to helicases conserved C-terminal domain (Pfam: helicase_C.hmm, score: 87.00) [Caenorhabditis elegans]	helicase		29331822, 29331826, 264906, 33108954, 265017, 265019, 21906768, 35695763, 264636, 264637, 18108387
2641	11669834 (5281, 5282)			UNCLASSIFIED	264828
2642	87412575 (5283, 5284)	Novel Protein sim. GBank gij2564955 (AF030001) - unknown [Mus musculus]		UNCLASSIFIED	264259, 29331822, 33657402, 265019, 264369, 264691, 264634, 56526486, 22279002
2643	87643981 (5285, 5286)	Novel Protein sim. GBank gij4490304jemb/CAB38795.1] - (AL035678) putative protein [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278997, 284259, 29148499, 56182435, 264910, 265010, 18108351, 264682, 264683, 264369, 264684, 264685, 264686, 29148627, 264690, 33657109, 18108370, 263973, 18108374, 264634, 264557, 264558, 18108385, 264482
2644	88177671 (5287, 5288)	Novel Protein sim. GBank gij3789797igb/AAC67502.1] - (AF059568) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	nuc1_rept	284107, 264687
2645	11727228 (5289, 5290)			UNCLASSIFIED	265007
2646	84148542 (5291, 5292)	Novel Protein sim. GBank gij1706722isp/p49749/EVX2_MOUSE - HOMEBOX EVEN SKIPPED HOMOLOG PROTEIN 2 [EVX-2]		UNCLASSIFIED	264909, 264687, 264632, 63373044

2647	91212978 (5293, 5294)			UNCLASSIFIED	56182575, 22278998, 35696286, 22278988, 264259, 29331822, 56182181, 29331825, 60424289, 60432289, 35696052, 66712502, 264908, 265007, 55812038, 33109954, 21906754, 33657084, 265019, 264448, 264288, 56181562, 21906768, 21906768, 21906769, 35695917, 265020, 265021, 52644150, 264693, 33657109, 33657349, 60431528, 18108374, 55810764, 35696423, 56182323, 60432113, 22279002, 264564
2648	87600587 (5295, 5296)				29146498, 56182435, 33109954, 265011, 264682, 55811957, 35695917, 264690, 263976, 18108377, 35696423, 60432113
2649	94128783 (5297, 5298)	Novel Protein sim. GBank gij3041852 (AC004539) - unknown function; similar to Y09105 (PF000054) [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 22278998, 29331824, 29331828, 60432289, 66712502, 56182435, 60170831, 60432229, 33657402, 33109954, 21906754, 265017, 264688, 264693, 21906765, 21906768, 60170815, 264693, 263987, 18108370, 263976, 60170394, 60432113, 22279002, 264563
2650	87297533 (5299, 5300)	Novel Protein sim. GBank gij5360271dbj[BAA81908.1] - (AB029335) HrPET-3 [Halocynthia roretzi]			264685
2651	88088745 (5301, 5302)	Novel Protein sim. GBank gij424025jdbj[BAA74891.1] - (AB020675) KIAA0868 protein [Homo sapiens]	Contains protein domain (PF00054) - Synthase Laminin G domain		29331824, 29331826, 29331827, 265007, 55812038, 21906754, 18108366, 18108384, 22279002, 264567
2652	10343125 (5303, 5304)			UNCLASSIFIED	264692
2653	87798735 (5305, 5306)	Novel Protein sim. GBank gij4493956jemb[CAB11123.2] - (Z98551) predicted using hexExon; MAL3P6.28 (PFC0845c), Hypothetical protein, len: 167 aa. Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR....		UNCLASSIFIED	265018, 18108370, 18108387, 264566
2654	95103240 (5307, 5308)				60424179, 65274572, 56182575, 264259, 56182181, 264908, 56182435, 55811957, 35695917, 265021, 263976, 55810764, 65274791, 56182323, 83373044, 65274727
2655	91228018 (5309, 5310)	Novel Protein sim. GBank gij3875272jemb[CAB02861] - (Z81051) predicted using Genefinder; similar to Zinc finger, C3HC4 type (RING finger); cDNA EST yk443h5.3 comes from this gene; cDNA EST yk443h5.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transcript factor	56182575, 56181686, 264092, 264259, 56182181, 60432289, 264907, 33657402, 55812038, 21906754, 87168559, 265017, 264448, 264369, 264288, 21906765, 21906766, 21906767, 21906768, 33657109, 18108370, 264628, 55811576, 264556, 264639, 83373044, 56526486, 264404, 60432113
2656	84562601 (5311, 5312)	Novel Protein sim. GBank gij3043718jdbj[BAA25523] - (AB011169) KIAA0597 protein [Homo sapiens]			264693

2657	52561728 (5313, 5314)	Novel Protein sim. GBank glj5689509[dbj BAA83036.1] - (AB029009) KIAA1086 protein [Homo sapiens]		dna_rna_bind	264693
2658	88062454 (5315, 5316)	Novel Protein sim. GBank glj3688088 (AC005757) - R32811_1 [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nucleaseinhib	35696286, 264259, 29331822, 29331824, 29331828, 29331828, 265019, 264683, 21908788, 35695917, 264693, 35695855, 264637, 87168518, 264486, 264567
2659	87600755 (5317, 5318)	Novel Protein sim. GBank glj5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01426) - BAH domain	UNCLASSIFIED	264909, 264910, 265018, 264368, 264769, 21908789, 264693, 263972, 18108388
2660	91718472 (5319, 5320)	Novel Protein sim. GBank glj728837[sp P39194/ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III]	Contains protein domain (PF00036) - EF hand	kinase	264488, 65274572, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 60432288, 29331826, 35696052, 264908, 58182435, 265008, 265009, 60433358, 264594, 265010, 265018, 55811150, 18108351, 264682, 264684, 264368, 264288, 264687, 21906765, 29148784, 35695917, 60170615, 52644150, 33657023, 33657109, 35696423, 35695855, 264556, 60170394, 18108385, 22279000, 22279002
2661	95342817 (5321, 5322)	Novel Protein sim. GBank glj4758048[tr NP_004739.1 pCPR8 - cell cycle progression 8 protein]		glycoprotein	60432049, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264908, 264909, 264593, 33108954, 265010, 265017, 285018, 285019, 284760, 264448, 264369, 264288, 21906765, 21906768, 265022, 264691, 33657023, 27486282, 60431528, 18108374, 35695855, 18108388, 264482
2662	80228739 (5323, 5324)	Novel Protein sim. GBank glj3874714[emb CAA91263] - (Z68494) similar to choline dehydrogenase; cDNA EST yk346d5.5 comes from this gene; cDNA EST yk346d5.3 comes from this gene [Caenorhabditis elegans]		dehydrogenase	264555, 264556, 264558, 264486
2663	87780623 (5325, 5326)	Novel Protein sim. GBank glj1389670 (U58977) - Notch homolog Scalloped wings [Lucilia cuprina]	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696286, 264508, 264595, 264288, 264685, 264686
2664	85518329 (5327, 5328)	Novel Protein sim. GBank glj4884406[emb CAB43311.1] - (AL050190) hypothetical protein [Homo sapiens]		UNCLASSIFIED	35696286, 22278999, 29331822, 35696052, 264906, 264907, 264909, 264510, 264511, 264512, 264593, 60433438, 265019, 264681, 21906765, 21908788, 21908787, 21908768, 265020, 265022, 35696423, 35695855, 22279002, 264482, 264488
2665	8770662 (5329, 5330)	Novel Protein sim. GBank glj5106958[gb AAD39906.1 AF11361] - (AF113615) FH1/FH2 domain-containing protein FHO5 [Homo sapiens]		UNCLASSIFIED	29331825, 265007, 264910, 60432229, 265019, 264288, 21906767, 264558, 22279002
2666	87826472 (5331, 5332)	Novel Protein sim. GBank glj2500570[sp Q17533 RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0564.1]	Contains protein domain (PF01138) - 3' exoribonuclease family	nuclease	264907, 29331830, 264681, 264683, 264288, 35695855, 264682, 264556, 264557, 264558, 264559, 264563, 264565, 264567
2667	87422720 (5333, 5334)	Novel Protein sim. GBank glj2500570[sp Q17533 RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0564.1]			

2668	91216716 (5335, 5336)	Novel Protein sim. GBank gi 5454186 ref NP_006327.1 pZYG  - ZYG homolog	UNCLASSIFIED	56181688, 35696286, 22278998, 22278999, 56182181, 29331824, 60424269, 29331825, 35696052, 29331828, 66712502, 56182435, 60433356, 264758, 21906754, 55811386, 265011, 87168559, 265017, 265019, 55811150, 264448, 264369, 264288, 21906765, 21906766, 21906768, 55811957, 35695917, 265020, 265021, 33657023, 264692, 33657109, 35695763, 60431528, 18108374, 35696423, 55811576, 264634, 60431850, 83373044, 18108385, 87168518, 22278000, 264583, 264584
2669	95415721 (5337, 5338)	Novel Protein sim. GBank gi 2147012 pr JC4899 - proline rich protein - rat		264489, 264689, 21906767, 65274572, 56182575, 21906768, 29148627, 21906769, 29148629, 35696286, 35695917, 22278998, 22278998, 285021, 265022, 60170615, 52644150, 60432049, 264259, 264691, 33657023, 264692, 29331822, 29331824, 29331825, 60432289, 33657109, 29331826, 29331827, 35696052, 29331828, 29146498, 29146499, 264905, 264908, 52644045, 264909, 56182435, 35696423, 65274791, 35695855, 265006, 264910, 264635, 60432229, 264592, 264638, 56182323, 60433356, 60170394, 60433438, 264559, 264595, 55812038, 33109954, 87168559, 60432113, 265019, 264448, 264369, 264684, 264288
2670	87613234 (5339, 5340)	Novel Protein sim. GBank gi 1723523 sp Q10382 YD8B_SCHPO - HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger	18108370, 263974
2671	91214936 (5341, 5342)	Novel Protein sim. GBank gi 4768277 gb AAD29444.1 AF06425 - (AF06425) very long-chain acyl-CoA synthetase homolog 2; VLCS-H2 [Homo sapiens]	transport	52646842, 56994075, 264259, 29331822, 29331824, 29331825, 29331827, 33658970, 264509, 265006, 33109954, 21906754, 264682, 264288, 265021, 33657023, 33657109, 33657102, 27486261, 27486262, 27486265, 18108376, 18108385
2672	87399123 (5343, 5344)	Novel Protein sim. GBank gi 4966346 gb AAD34677.1 AC00634 - (AC00634) Contains two PF01344 Ketch motif domains. [Arabidopsis thaliana]	Contains protein domain (PF01344) - Ketch motif	264767

2673	67430749 (5345, 5346)	Novel Protein sim. GBank gij5457337[emb]CAB41505.21 - (AJ236876) poly(ADP-ribose) polymerase-2 [Homo sapiens]	Contains protein domain (PF00644) - polymerase Poly(ADP-ribose) polymerase catalytic region.	22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331828, 35696052, 60433438, 87168474, 87168559, 265017, 265018, 265019, 264448, 21906768, 21906769, 265020, 265021, 33657109, 27486262, 35695763, 60431850, 60170394, 87168518, 264563
2674	94847721 (5347, 5348)	Novel Protein sim. GBank gij4758824[ref]NP_004280.1pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) bZIP transcription factor	264488, 22278996, 35686286, 264091, 264259, 29331824, 29331826, 35696052, 264511, 55812038, 8565842, 264766, 21906765, 35695917, 264629, 35696423, 18108383, 87168518
2675	79563835 (5349, 5350)		UNCLASSIFIED	264691
2676	79628393 (5351, 5352)		UNCLASSIFIED	264906, 285008
2677	94325600 (5353, 5354)	Novel Protein sim. GBank gij1079042[pir]IS2154 - acetyl-CoA synthetase - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00501) - synthase AMP-binding enzyme	18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278999, 264480, 264259, 52645080, 29331824, 29331825, 60432269, 29331827, 29331828, 35696052, 29148499, 29331830, 264908, 52644045, 265008, 265007, 265008, 265009, 60432229, 60433356, 60433438, 55812038, 265010, 265011, 87168559, 265017, 265019, 18108351, 264682, 264448, 264683, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 60170615, 52644150, 264691, 33657023, 263987, 33657109, 27486264, 27486265, 33657348, 35695763, 18108370, 18108374, 18108377, 55811576, 35696423, 35695855, 83373044, 18108387, 22279000, 22279002, 264584



2678	95001694 (5355, 5356)	Novel Protein sim. GBank gij186760 pij140465 - alanine transaminase (EC 2.6.1.2), cytosolic - human	UNCLASSIFIED	264488, 263994, 264489, 18108394, 52648842, 35696286, 22278999, 264259, 29331825, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 264593, 264594, 264596, 264758, 33109854, 52646317, 21906754, 265010, 265011, 87168559, 264600, 264601, 264602, 264603, 265017, 265019, 264805, 264760, 264762, 18108351, 264763, 264682, 264683, 264764, 264288, 264766, 264687, 264768, 264769, 264689, 21906765, 21906767, 35695917, 265020, 265021, 52644150, 264691, 33657023, 264693, 18108364, 18108365, 33657109, 33657349, 264628, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264565, 264566, 264486, 264567
2679	95361544 (5357, 5358)	Novel Protein sim. GBank gi1709233 spjP07514 NC5R_BOVIN - NADH-CYTOCHROME B5 REDUCTASE	Contains protein domain (PF00970) - FAD/NAD-binding Cytochrome reductase	264488, 22278996, 35696286, 264259, 29331826, 29331827, 29331828, 264909, 56182435, 264113, 264511, 265008, 60433438, 264758, 85658542, 87168474, 265011, 265017, 265019, 264288, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 264690, 33657023, 55810784, 35696423, 55811576, 264631, 18108381, 60170394, 83373044, 87168518, 264566, 264259, 264102, 264905, 264908, 285007, 265008, 33109854, 265011, 18108351, 264768, 33657023, 20281149, 263972, 264630, 264635, 264638
2680	87800356 (5359, 5360)	Novel Protein sim. GBank gi14595604 dbjBAA76824.1  - (ABD23197) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	264259, 264102, 264905, 264908, 285007, 265008, 33109854, 265011, 18108351, 264768, 33657023, 20281149, 263972, 264630, 264635, 264638
2681	90933844 (5361, 5362)	Novel Protein sim. GBank gi1728837 spjP39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	kinase	264488, 22278995, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264512, 264910, 264594, 60433438, 264758, 264603, 264604, 265019, 264605, 264760, 264764, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264486
2682	94138934 (5363, 5364)	Novel Protein sim. GBank gi1423468 pirj1JQ1974 - HTF9-C protein - mouse	Contains protein domain (PF00076) - RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain)	35696286, 264908, 55811386, 265017, 55811150, 55811957, 35695917, 60431528, 55810764, 55811576, 35696423, 65274791, 56528486
2683	87774405 (5365, 5366)	Novel Protein sim. GBank gi15114351 gb AAD40286.1  - (AF158271) RING finger protein 107 [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	264909, 264769, 264635, 264636

2684	85787151 (5387, 5388)	Novel Protein sim. GBank gij486469jembjCAB43385.1] - (AL050284) hypothetical protein [Homo sapiens]			264593
2685	88054289 (5369, 5370)	Novel Protein sim. GBank gij3342729 (AC005331) - R31341.2 [Homo sapiens]	UNCLASSIFIED		
2686	87628690 (5371, 5372)	Novel Protein sim. GBank gij4650844[dj]BAA77027.1] - (AB026190) Keich motif containing protein [Homo sapiens]	Contains protein domain (PF01344) - struct Keich motif		264259, 29331822, 60432289, 29331827, 29331830, 264908, 284512, 284596, 264769, 284534, 264555, 264556, 264557, 264558, 60170394, 264559, 264486
2687	87898183 (5373, 5374)	Novel Protein sim. GBank gij5281314[jb]AAD41475.1[AF133123] transcription factor IIIC102 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	transcriptfactor	18108394, 18108396, 22278996, 35696286, 22278997, 29331826, 29331828, 66712502, 21906754, 265011, 264780, 264761, 284763, 264689, 21906765, 35696423, 264559, 18108385, 264563
2688	79959584 (5375, 5376)				264908, 264760
2689	84122440 (5377, 5378)	Novel Protein sim. GBank gij3880023jembjCAA07339] - (Z73098) Similarly to yeast hypothetical protein (Swiss Prot accession number Q09695); cDNA EST EMBL:D72982 comes from this gene; cDNA EST EMBL:D75947 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00560) - Leucine Rich Repeat		22278997, 22278998, 22278999, 29331824, 35696052, 264908, 264908, 56182435, 264512, 264910, 265009, 60433438, 21906754, 18108351, 264682, 264683, 264767, 21906765, 21906768, 21906768, 33657023, 33657182, 27486282, 27486284, 33657349, 18108370, 18108372, 18108374, 35696423, 35695855, 18108385, 22279002
2690	88003055 (5378, 5380)	Novel Protein sim. GBank gij2477513 (AC002398) - F25965.3 [Homo sapiens]	Contains protein domain (PF00620) - RhoGAP domain	struct	
2691	91218241 (5381, 5382)	Novel Protein sim. GBank gij4107276jembjCAA67130] - (X98506) acetyl-CoA synthetase [Solanum tuberosum]		synthase	65274572, 56182575, 264259, 29331822, 29331824, 29331826, 29331828, 264112, 285009, 55812038, 264596, 33109954, 265017, 264448, 264288, 264389, 264684, 21906768, 60170615, 60431528, 55810764, 264634, 264636, 264556, 264637, 22279002, 264564, 264566
2692	84111914 (5383, 5384)	Novel Protein sim. GBank gij3513303 (AC005594) - R26984.1 [Homo sapiens]	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	
2693	20436807 (5385, 5386)			UNCLASSIFIED	264592
2694	84111918 (5387, 5388)	Novel Protein sim. GBank gij3122400[sp]O35682IMUG_MOUSE - MYELOID UPREGULATED PROTEIN			264559
2695	95345513 (5389, 5390)	Novel Protein sim. GBank gij4972740[jb]AAD34765.1] - (AF132177) unknown [Drosophila melanogaster]		collagen	35696286, 56994075, 22278998, 264259, 35696052, 29331830, 265011, 264286, 56181562, 264690, 264692, 33657023, 27486282, 263978, 18108376, 35696423, 35695855, 60170394, 83373044, 56528486, 22279000, 22279002, 264566
2696	87874040 (5391, 5392)	Novel Protein sim. GBank gij728631[sp]P39188[ALU1_HUMAN - IIII] ALU SUBFAMILY J WARNING ENTRY IIII		synthase	264594, 21906768, 18108370, 18108372

2697	91638472 (5393, 5394)	Novel Protein sim. GBank glj5689473[gbjBAA83020.1] - (AB028991) KIAA1088 protein [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 265006, 265007, 264512, 265009, 60170831, 60433358, 264595, 264758, 87168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 264761, 18108351, 264448, 264288, 264766, 264688, 264689, 21906765, 21906768, 265020, 265021, 60170815, 33657109, 18108376, 35696423, 35695855, 264555, 264558, 60170394, 264559, 18108387, 56526486, 87168518, 22279002, 264563, 264482
2698	94325891 (5395, 5396)	Novel Protein sim. GBank glj841318 (U22818) - mutant sterol regulatory element binding protein-2 [Cricetus griseus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcriptfactor	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 33656970, 264906, 29331830, 264909, 52644045, 264910, 60433356, 33657402, 33109954, 265017, 265018, 265019, 264288, 21906785, 21906786, 21906767, 21906769, 29148629, 35695917, 265021, 265022, 52644150, 33657023, 33657182, 27486261, 35696423, 65274791, 264538, 60432113, 22279000
2699	87780650 (5397, 5398)	Novel Protein sim. GBank		UNCLASSIFIED	264768, 18108357, 264690, 264691
2700	94139836 (5399, 5400)	Novel Protein sim. GBank glj5174395[ncp_006006.1]pB120 - Brain protein 120		UNCLASSIFIED	60424269, 56182435, 60432229, 60433438, 55811386, 265017, 55811150, 264448, 56181562, 55811957, 264693, 33657109, 60431528, 264629, 55810764, 55811576, 65274791, 60431850, 60432113
2701	94146584 (5401, 5402)	Novel Protein sim. GBank glj1572801 (U70854) - F38A5.1 gene product [Caenorhabditis elegans]			18108394, 52645156, 35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29146499, 265006, 60433356, 33657402, 60433438, 264595, 33657084, 18108351, 264288, 264769, 18108359, 21906768, 35695917, 33657023, 27486261, 18108374, 18108379, 35696423, 18108382, 83373044, 18108384, 18108388, 60432113, 22279000
2702	57295386 (5403, 5404)	Novel Protein sim. GBank glj2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	29331828, 264512, 264555, 264556, 264557, 264558, 264559
2703	87649514 (5405, 5406)	Novel Protein sim. GBank glj5689399[gbjBAA82983.1] - (AB028954) KIAA1031 protein [Homo sapiens]	Contains protein domain (PF00642) - Zinc finger C-x8-C-x5-C-x3-H type (and similar).		60432289, 265007, 21906765, 21906768, 265021, 264563

2704	87849515 (5407, 5408)	Novel Protein sim. GBank gij4335694[gijAA83294] - (AF008554) Implantation-associated protein [Rattus norvegicus]			264488, 22278995, 22278998, 29331828, 29146499, 264905, 264908, 264907, 52844045, 264511, 33657402, 264600, 264602, 265017, 264605, 264761, 18108351, 264764, 264887, 264769, 265021, 264691, 264692, 18108362, 264693, 18108370, 18108374, 264634, 264635
2705	87771745 (5408, 5410)				264489, 264509, 264511, 264512, 264910, 264593, 87188474, 264804, 264288, 264687, 264769, 264638, 264566, 264486
2706	94326789 (5411, 5412)	Novel Protein sim. GBank gij3255952[emb CAA16821.1] - (AL021728) /prediction=(method); /match=(desc: [Drosophila melanogaster])	UNCLASSIFIED		264488, 52646842, 65274572, 22278994, 56994075, 22278997, 264259, 29331824, 29331825, 29331826, 29331828, 33856970, 264907, 264908, 264909, 52844045, 56182435, 265006, 265007, 60433438, 55812038, 21906754, 52644296, 265010, 264601, 265017, 265019, 264681, 264448, 264682, 264286, 264686, 264687, 264888, 21906766, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 264690, 264691, 33657023, 264692, 264693, 65274620, 27486284, 263972, 18108374, 18108377, 264635, 264636, 264556, 60170394, 83373044, 65274727, 87168518, 22278000, 22278596, 22278998, 56182435, 21906754, 87168559, 265017, 264448, 52645129
2707	88089839 (5413, 5414)	Novel Protein sim. GBank gij3417294 (AC004381) - Unknown gene product [Homo sapiens]			65274572, 264259, 29331822, 29331825, 60432289, 29331826, 29331827, 29331828, 264909, 264510, 265007, 264910, 60433356, 60433438, 33109954, 265010, 265011, 264369, 264288, 264765, 264693, 264565
2708	91011351 (5415, 5416)	Novel Protein sim. GBank gij545790[bsj147178 - DARPP-32=dopamine and cAMP-regulated phosphoprotein [human, brain, Peptide, 204 aa]	UNCLASSIFIED		29331822, 18108370, 18108374, 83373044
2709	94853988 (5417, 5418)	Novel Protein sim. GBank gij3169705 (AC004780) - FT127-1 [Homo sapiens]	UNCLASSIFIED		
2710	87627879 (5419, 5420)	Novel Protein sim. GBank gij4468311[emb CAB37892] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) [isoform 1] [Homo sapiens]			29331824, 264759, 264693, 18108362, 18108368

2711	94111820 (5421, 5422)	Novel Protein sim. GBank gi 3122400 sp O35682 MUG_MOUSE - MYELOID UPREGULATED PROTEIN		UNCLASSIFIED	264488, 264687, 52645156, 264769, 21906764, 21906765, 21906767, 21906768, 21908788, 55811957, 56994075, 22278997, 22278998, 265020, 265021, 264690, 264259, 264691, 264692, 33657023, 29331822, 29331824, 60424269, 29331826, 33657182, 29331827, 27486262, 33657349, 264508, 264905, 264907, 60431528, 264908, 264909, 55810784, 35696423, 65274791, 35695855, 265007, 264910, 60431850, 60432229, 264557, 264558, 55812038, 33108954, 18108385, 21906754, 33657084, 87168518, 87168474, 87168559, 60432113, 265017, 22279000, 265018, 265019, 22279002, 264760, 55811150, 264681, 18108351, 264585, 264764, 264566, 264288, 264766 264488, 35696286, 22278998, 264259, 29331824, 60432228, 35696052, 264508, 264908, 66712502, 52644045, 265006, 60432229, 33657402, 60433356, 265010, 265019, 18108351, 264681, 264288, 264685, 21908785, 21906766, 21906768, 21908789, 55811957, 35695917, 265020, 265021, 60170615, 264691, 264692, 33657023, 33657109, 33657182, 33657349, 18108370, 18108374, 35696423, 35695855, 264555, 52644332, 56182323, 87168518, 60432113 66714117, 264906, 264563
2712	94312071 (5423, 5424)	Novel Protein sim. GBank gi 5081315 gb AAD39343.1 AF07660 - (AF076607) prediabetic NOD sera-reactive autoantigen [Mus musculus]	Contains protein domain (PF00515) - TPR Domain	transferase	
2713	88003064 (5425, 5426)	Novel Protein sim. GBank gi 2477513 (AC002398) - F25965_3 [Homo sapiens]		UNCLASSIFIED	
2714	13528218 (5427, 5428)			UNCLASSIFIED	264636
2715	94122454 (5429, 5430)	Novel Protein sim. GBank gi 4321968 gb AAD158971 - (AF067430) Smarce1-related protein [Mus musculus]		UNCLASSIFIED	264508, 264905, 264907, 264908, 264909, 264910, 264758, 265011, 264760, 264764, 264288, 264766, 264768, 264636
2716	88003068 (5431, 5432)	Novel Protein sim. GBank gi 2477513 (AC002398) - F25965_3 [Homo sapiens]		glycoprotein	264031, 264259, 29331822, 66714117
2717	80077461 (5433, 5434)	Novel Protein sim. GBank gi 3327046 dbj BAA315911 - (AB014516) KIAA0616 protein [Homo sapiens]			264908, 264389, 264693, 264556, 264563 264593, 264558
2718	78604062 (5435, 5436)				264693
2719	88160423 (5437, 5438)	Novel Protein sim. GBank gi 746495 (U23315) - weakly similar to gastrula zinc finger protein [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 87168559, 265019, 265021, 52644150, 264691

2720	95086242 (5439, 5440)	Novel Protein sim. GBank glij1335873 (U46690) - ATP-dependent RNA helicase [Mus musculus]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	18108374, 60424179, 264489, 56182435, 21906765, 21906768, 35698423, 22278997, 285020, 285022, 285008, 285008, 284092, 284636, 60432228, 284691, 284692, 33657023, 284693, 33657402, 83373044, 28331824, 18108366, 60424269, 28331826, 18108385, 52645129, 21906754, 35696052, 29331828, 87168474, 284100, 285010, 285011, 285019, 22278002, 284905, 264482, 264563, 264906, 18108351, 284681, 18108370, 29331830, 284908, 86712502, 52644045, 284908, 284828, 18108354
2721	95345523 (5441, 5442)	Novel Protein sim. GBank glij4929653gblAAD34092.1 (AF15185) CGI-97 protein [Homo sapiens]	Contains protein domain (PF01172) - Uncharacterized protein family UPF0023		22278995, 35696288, 284259, 29331822, 29331824, 66714117, 29331826, 284906, 60433438, 265017, 18108351, 264448, 264288, 264769, 21906768, 265021, 33657109, 263969, 60431528, 284629, 55811576, 65274781, 35695855, 284631, 284637, 60170394, 56182323, 22278000
2722	91638807 (5443, 5444)	Novel Protein sim. GBank glij3212957gblAAC23434.1 - (AC004997) match to ESTs AA667999 (NID:g2626700), AA165465 (NID:g1741481), Z45871 (NID:g575105), and T84026 (NID:g712314); similar to various tre-like proteins including: AF040654 (PID:g2748883), D13644 (PID:g2104571), AL02114...	Contains protein domain (PF00566) - TBC domain	oncogene	35696288, 22278999, 21906754, 265017, 264762, 264288, 21906765, 21906767, 21906768, 35695917, 18108362, 27486262, 35695855, 284558, 284559
2723	87357732 (5445, 5446)			UNCLASSIFIED	264508, 264509, 264906, 264908, 264910, 55812038, 264766, 264687, 264628, 264636, 264488
2724	87639563 (5447, 5448)	Novel Protein sim. GBank glij4680681gblAAD27730.1 (AF13295) CGI-21 protein [Homo sapiens]		ubiquitin	18108396, 22278999, 20281098, 28331824, 29331826, 60432289, 29331828, 60170831, 60432229, 60433438, 18108351, 284682, 21906766, 21906767, 21906769, 35695917, 33657023, 33657109, 18108372, 18108374, 35695855, 22278000, 22278002
2725	94653991 (5449, 5450)	Novel Protein sim. GBank glij3169705 (AC004780) - F17127_1 [Homo sapiens]		UNCLASSIFIED	264488, 52644507, 264259, 29331827, 21906754, 285011, 18108351, 264448, 264288, 264685, 264689, 35695917, 265020, 33657182, 27486261, 18108370, 18108374, 35696423, 18108385, 22278000
2726	86880599 (5451, 5452)	Novel Protein sim. GBank glij3342738 (AC005328) - R26960_1, partial CDS [Homo sapiens]		MHC	264488, 264828, 264685

2727	91010470 (5453, 5454)	Novel Protein sim. GBank gij17312671spjP39219jRLUA_ECOLI - RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)	Contains protein domain (PF00849) - RNA pseudouridylylate synthase	synthase	65274572, 56182575, 22278994, 56994075, 22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 33656970, 264509, 66712502, 264910, 33657402, 60433438, 264758, 55812038, 21906754, 33657084, 55811386, 265018, 265019, 264767, 21906765, 21906767, 21906769, 55811957, 35695917, 52644150, 33657023, 33657109, 33657182, 27486281, 27486282, 27486285, 33657349, 55811576, 35696423, 35695855, 264630, 60431850, 264636, 56182323, 87168518, 60432113, 22279000, 264564, 264565
2728	94126022 (5455, 5456)	Novel Protein sim. GBank gj13880433jemb CAA91399  - (Z66521) similar to mitochondrial RNA splicing MSRA like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	18108394, 56182435, 21906767, 55811857, 35695855, 265021, 264690, 264556, 264259, 264557, 29331822, 264559, 264448, 264288
2729	94126024 (5457, 5458)	Novel Protein sim. GBank gj12408095jemb CAB16300  - (Z99168) putative RNA splicing protein [Schizosaccharomyces pombe]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	65274572, 264259, 60432289, 56712502, 56182435, 264448, 264288, 264369, 55811957, 265021, 264557, 60432113
2730	94126026 (5459, 5460)	Novel Protein sim. GBank gj13880433jemb CAA91399  - (Z66521) similar to mitochondrial RNA splicing MSRA like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264887, 29331824, 29331826, 35696052, 264107, 56182435, 265008, 265009, 264592, 60431735, 265011, 264601, 265017, 18108351, 264288, 29148627, 55811957, 265021, 264690, 18108368, 18108374, 264557, 264558, 264559, 18108387, 56526486, 264566, 264486
2731	87723022 (5461, 5462)	Novel Protein sim. GBank gj11723239jspjQ10166jYAU_SCHPO - HYPOTHETICAL 35.7 KD PROTEIN C28A3.11 IN CHROMOSOME 1	Contains protein domain (PF00795) - Carbon-nitrogen hydrolase		264259, 35696052, 265008, 264758, 264762, 264448, 264288, 29148627, 21908769, 87168518, 22279002
2732	94126028 (5463, 5464)	Novel Protein sim. GBank gj13880433jemb CAA91399  - (Z66521) similar to mitochondrial RNA splicing MSRA like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	264687, 264489, 18108358, 56182435, 264689, 35696423, 55811957, 265021, 265006, 265008, 264910, 265009, 264690, 264555, 264259, 264556, 264557, 264558, 264559, 18108383, 33657109, 87168518, 265010, 264601, 60432113, 265017, 264905, 264448, 263972, 264369, 264567
2733	87363060 (5465, 5466)	Novel Protein sim. GBank gj14519621jdbjBAA75670.1  - (AB017614) OASIS protein [Mus musculus]	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	29331825, 264509, 264909
2734	94140286 (5467, 5468)			transcript factor	60424179, 52844507, 56182575, 264259, 29331828, 264907, 264510, 264910, 60433356, 265019, 55811150, 264681, 264763, 264687, 33657182, 18108370, 60431528, 60431850, 56182323, 83373044

2735	87712338 (5469, 5470)	Novel Protein sim. GBank gij3850569 (AC005278) - ESTs gb T21276, gb T45403, and gb AA586113 come from this gene. [Arabidopsis thaliana]		glycoprotein	22278996, 60432289, 29331827, 29148498, 284108, 284909, 264112, 33657402, 87188474, 285017, 284782, 284448, 284764, 284884, 21906765, 264693, 33657109, 263976, 284638, 264638, 264557, 22279000, 22278002, 284567
2736	80247655 (5471, 5472)			UNCLASSIFIED	264905, 284628, 284629, 263978, 264632, 284584
2737	87604526 (5473, 5474)	Novel Protein sim. GBank gij2558501[dbj BA22896] - [DB3850] hepatoma-derived growth factor [Mus musculus]			284890
2738	85731808 (5475, 5476)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			264488, 285009, 264768, 264691
2739	94318834 (5477, 5478)	Novel Protein sim. GBank gij3417386[emb CAA75495] - (Y15197) microtubule-associated protein, MAP-115 [Mus musculus]		UNCLASSIFIED	264684, 83373044, 264568
2740	94148762 (5479, 5480)			UNCLASSIFIED	264488, 56182575, 22278995, 35696288, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 29148498, 29331830, 285006, 265007, 265008, 60432228, 33657402, 55812038, 87188474, 285010, 265011, 265017, 285018, 265019, 284605, 264681, 264288, 264369, 52844228, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 284691, 264692, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 60431850, 264639, 56182323, 18108382, 18108385, 65274727, 22278002, 284584
2741	98047518 (5481, 5482)	Novel Protein sim. GBank gij3242764 (AC005154) - similar to protein U28928 (PID:9881308) [Homo sapiens]		UNCLASSIFIED	22278996, 52844045, 52644229, 21906768, 21906769, 285020, 60170815, 264691
2742	87648644 (5483, 5484)	Novel Protein sim. GBank gij4758412[ref NP_004472.1]pGALN - UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 2 (GalNAc-T2)	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	264259, 284805, 284758, 55812038, 264369, 29148627
2743	87627891 (5485, 5486)	Novel Protein sim. GBank gij4466311[emb CAB37992] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 284806, 284908, 285008, 60433438, 265017, 18108351, 264448, 264764, 284288, 21906765, 21906767, 264690, 284691, 284693, 263969, 263971, 35695855, 264637, 264558, 18108382, 60432113
2744	94126030 (5487, 5488)	Novel Protein sim. GBank gij3880433[emb CAA91399] - (Z68521) similar to mitochondrial RNA splicing MSRA like protein; cDNA EST EMBL:CO9217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	kinase	18108374, 264488, 56182435, 21906765, 35696423, 35695917, 35695855, 265020, 285021, 264511, 285009, 284490, 284556, 284259, 284557, 56182323, 264558, 264559, 18108383, 29331824, 18108385, 33657109, 29331826, 21906754, 29331827, 29331828, 33657349, 87168518, 265018, 264905, 284482, 264448, 264488, 264369, 264288



2745	87740125 (5489, 5490)	Novel Protein sim. GBank gij4403795[jb]AAD19826] - (AF038963) RNA helicase [Homo sapiens]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	35696286, 264509, 264905, 264907, 264908, 264909, 264510, 264512, 265008, 264758, 264601, 265017, 264604, 264763, 264288, 264886, 264769, 264893, 35696423, 35695855, 264634, 264636, 264563, 264564, 264565
2746	95418601 (5491, 5492)	Novel Protein sim. GBank gij458738[ref]NP_004680.1[pMTA1 - metastasis associated 1	Contains protein domain (PF00320) - GATA zinc finger	UNCLASSIFIED	22278996, 22278998, 22278999, 29331822, 29331826, 29331827, 35696052, 29331828, 264905, 264906, 264907, 264908, 264909, 52644045, 265006, 60170831, 264598, 55812038, 265018, 264683, 264288, 21906765, 21906767, 21906768, 21906769, 265020, 264690, 33657023, 264693, 33657109, 18108368, 18108374, 264558, 18108385, 22279000, 264563
2747	94112677 (5493, 5494)	Novel Protein sim. GBank gij4557803[ref]NP_000262.1[pNPC1 - Niemann-Pick disease, type C1		glycoprotein	264559, 52644507, 18108394, 22278995, 35696286, 22278997, 22278999, 52645080, 29331824, 56182181, 29331826, 29331827, 35696052, 264907, 264908, 264909, 265009, 33109954, 55811386, 87168474, 265010, 87168559, 264603, 265019, 264760, 264688, 264768, 21906769, 35695917, 60170615, 264692, 33657023, 52645129, 27486264, 60431328, 18108374, 35696423, 35695855, 264556, 56182323, 18108395, 264482
2748	91214983 (5485, 5496)	Novel Protein sim. GBank gij4191272[emb]CAA09984] - (AJ012295) apaG protein [Rhizobium etli]	Contains protein domain (PF00646) - F-box domain.		65274572, 29331828, 264112, 264511, 265019, 264760, 264767, 264768, 264769, 21906768, 21906769, 265020, 27486262, 56526488, 87188518, 22279000
2749	87346307 (5497, 5498)				264259, 264908, 264510, 265008, 265009, 264760, 264369, 264768, 264563
2750	87336344 (5499, 5500)	Novel Protein sim. GBank gij1872498 (U74297) - Pilus [Oryctolagus cuniculus]		UNCLASSIFIED	264488, 52644507, 18108396, 56994075, 264259, 29331825, 29331826, 29331827, 29331828, 264508, 265009, 264910, 264591, 264595, 33657084, 265011, 265019, 18108351, 264288, 264686, 264769, 264689, 55811957, 264693, 27486264, 18108370, 18108374, 264558, 18108385, 264482, 264563
2751	87057465 (5501, 5502)			UNCLASSIFIED	29331822, 29331824, 265017, 33657023
2752	88082875 (5503, 5504)	Novel Protein sim. GBank gij3041859 (AC004634) - OG-2 homeodomain protein-like; similar to U65067 [PID:g1575526] [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2753	84138972 (5505, 5506)	Novel Protein sim. GBank glij3851648 (AF088301) - neural F box protein NFB42 [Rattus norvegicus]	Contains protein domain (PF00046) - F-box domain.	UNCLASSIFIED	56182575, 56994075, 22278988, 29331822, 29331824, 29331825, 29331826, 265007, 264593, 55812038, 33109954, 18108351, 284288, 56181562, 21908787, 21908788, 285021, 264693, 18108374, 85274791, 264632, 56182323, 22279002, 264563, 264587
2754	84115513 (5507, 5508)	Novel Protein sim. GBank glij535428 (U13736) - calmodulin-like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	struct	22278999, 66714117, 29331827, 35696032, 29331828, 264908, 264908, 264909, 265011, 265017, 265018, 265019, 264288, 21908785, 21908787, 265022, 33657023, 264693, 56182323, 18108382, 22279000
2755	88001472 (5508, 5510)	Novel Protein sim. GBank glij2996653 (AC004510) - R30385_2 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	
2756	11465908 (5511, 5512)	Novel Protein sim. GBank glij173539 (U30473) - putative src-like adapter protein; non-catalytic src-like adapter protein containing SH3 and SH2 domains; homolog of mouse SLAP; Method: conceptual translation supplied by author [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	UNCLASSIFIED	264594
2757	95361590 (5513, 5514)	Novel Protein sim. GBank glij3608372 (AF053768) - brain specific cortactin-binding protein CBP90 [Rattus norvegicus]	Contains protein domain (PF00017) - Src homology domain 2	eph	85658542, 264693
2758	79637846 (5515, 5516)	Novel Protein sim. GBank glij2072200 (U94863) - p40 [Borna disease virus]		struct	264693
2759	81005312 (5517, 5518)	Novel Protein sim. GBank glij4914573 (lemb)(CAB43685.1) - (AL050390) hypothetical protein [Homo sapiens]	Contains protein domain (PF00023) - Anky repeat	UNCLASSIFIED	65274572, 35698286, 66714117, 29331828, 284508, 56182435, 21908754, 55811957, 264629, 264636, 56182323, 22279002
2760	78824798 (5519, 5520)	Novel Protein sim. GBank glij3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00098) - PAS domain	struct	22278998, 29331822, 29331830, 265010, 265019, 264288, 21908785, 21908786, 21908769, 265020, 56182323, 22279002, 264563
2761	87639597 (5521, 5522)	Novel Protein sim. GBank glij2905643 (AF045244) - ribitol kinase [Klebsiella pneumoniae]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases	transcriptfactor	18108394, 22278988, 264908, 264909, 265006, 265007, 284757, 265010, 265011, 265017, 265019, 18108351, 264448, 264683, 264686, 264768, 265020, 265021, 265022, 264691, 18108362, 264693, 18108385, 33657109, 18108368, 18108370, 18108381, 18108382, 18108384, 18108388, 87168518
2762	87582698 (5523, 5524)	Novel Protein sim. GBank glij3511122 (AF060503) - zinc finger protein [Homo sapiens]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases	transcriptfactor	264368, 35698423
2763	87539968 (5525, 5526)	Novel Protein sim. GBank glij2905643 (AF045244) - ribitol kinase [Klebsiella pneumoniae]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases	transcriptfactor	52946842, 264256, 29331822, 29331825, 29331826, 29331828, 33656970, 264905, 264907, 29331830, 265006, 265009, 21906754, 265019, 264448, 21908788, 27488282, 56182323, 56528486, 87168518, 264487

2765	94315105 (5528, 5530)	Novel Protein sim. GBank gij4688672[emb CAA17688.2] - (AL022018) /prediction=(method:; /match=(desc: [Drosophila melanogaster])		264488, 65274572, 22278995, 35896286, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264512, 264910, 265009, 264592, 264595, 264758, 55812038, 33109954, 265010, 87168558, 264600, 265018, 264760, 264761, 264762, 264763, 264448, 264764, 264288, 264766, 264767, 264768, 56181562, 21906764, 21906765, 21906768, 35695917, 265021, 264691, 264692, 33657023, 33657109, 264628, 18108370, 264629, 18108374, 55811578, 35696423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 264558, 264639, 83373044, 87168518, 22279000, 22279002, 264553, 264482
2766	94315109 (5531, 5532)	Novel Protein sim. GBank gij5441611[emb CAB46854.1] - (AJ388555) hypothetical protein [Canis familiaris]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	264488, 65274572, 60432289, 264907, 264909, 264511, 264512, 60433356, 264288, 264685, 264689, 35695917, 265022, 264693, 264628, 65274791, 264635, 264555, 264556, 264557, 264638, 264558, 264559, 83373044, 80432113
2767	80204297 (5533, 5534)	Novel Protein sim. GBank gij1079451[pir A55463] - tropomodulin, skeletal muscle - chicken	struct	264112, 263974, 264558
2768	94322238 (5535, 5536)	Novel Protein sim. GBank gij5441322[emb CAB46721.1] - (AL031427) dJ167A19.1 (novel protein) [Homo sapiens]	UNCLASSIFIED	264488, 263994, 264489, 35696286, 22278998, 22278999, 264259, 29331822, 60432289, 29331826, 35698052, 264508, 264509, 264905, 264908, 264907, 29331830, 264908, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264757, 264596, 265011, 264604, 265019, 264760, 264681, 18108351, 264764, 264288, 264766, 264686, 264768, 18108357, 264769, 264689, 21906766, 21906768, 21906769, 35695917, 265021, 265022, 33657023, 33657109, 264628, 264629, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 264639, 83373044, 264563, 264564, 264565, 264566, 264486, 264587

2769	95311088 (5537, 5538)	Novel Protein sim. GBank gij5419859[embjCAB46375.1] - (AL098725) hypothetical protein [Homo sapiens]		tubulin	254488, 56182575, 264259, 29331822, 29331824, 68714117, 29331825, 60432289, 29331828, 284908, 29331830, 56182435, 264592, 33657402, 264448, 264389, 284288, 60170815, 264691, 33657023, 264692, 33657109, 18108374, 55811576, 264634, 264636, 56182323, 83373044, 60432113, 18108398, 22278995, 22278996, 22278999, 264105, 265006, 265019, 18108351, 284687, 21906765, 18108364, 284629, 18108374, 264631, 18108385, 18108388, 264259, 29331822, 29331824, 29331825, 264369
2770	87730182 (5539, 5540)	Novel Protein sim. GBank gij5701965[embjCAB52157.1] - (AL109736) WD repeat protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	
2771	86084071 (5541, 5542)	Novel Protein sim. GBank gij3093433 (AC004125) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	
2772	95357308 (5543, 5544)	Novel Protein sim. GBank gij488551[re]NP_005465.1[prNY C - histone deacetylase 5	Contains protein domain (PF00850) - Histone deacetylase family	histone	264259, 29331822, 29331824, 68714117, 60432289, 29331827, 264905, 265009, 264592, 55812038, 63274444, 264766, 21908769, 33657109, 263978, 264555, 264638, 264557, 83373044, 264563, 264564, 264488
2773	94138994 (5545, 5546)	Novel Protein sim. GBank gij3288888 (AC005253) - R26445_1 [Homo sapiens]		UNCLASSIFIED	18108374, 264686, 264687, 263978, 56182435, 264689, 56810764, 21908766, 35896423, 55811576, 65274791, 56181886, 55811957, 35695855, 264110, 265021, 264112, 265022, 265006, 265008, 264092, 264094, 60431850, 264637, 264691, 264259, 264692, 263981, 264594, 60433356, 56182323, 264693, 264757, 56182181, 55812038, 29331825, 60424269, 18108385, 29331828, 29331827, 27486281, 29331828, 35696052, 55811386, 264107, 60432113, 265017, 55811150, 18108351, 264681, 264906, 18108370, 264484, 264682, 20281069, 264448, 68712502, 264683, 264764, 264288, 264684, 264766, 263974, 22278955, 35696288, 22278996, 22278999, 264259, 29331826, 60432289, 35696052, 264112, 33657402, 21908754, 87168559, 265017, 265018, 264288, 21908766, 21906767, 21908768, 35695917, 285020, 265021, 33657023, 33657109, 18108370, 263976, 35696423, 35696855, 87168510, 22278900, 264482
2774	87819908 (5547, 5548)	Novel Protein sim. GBank gij465852[spP34388]YLS3_CAEEL - HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III	Contains protein domain (PF00380) - Ribosomal protein S9/S16	ribosomal protein	

2775	95307987 (5548, 5550)	Novel Protein sim. GBank gi4689132 gb AAD27775.1 AF07704 - (AF077042) 30S ribosomal protein S7 homolog [Homo sapiens]	Contains protein domain (PF00177) - Ribosomal protein S7p/S5e	- ribosomal prot	264488, 22278995, 56994075, 22278998, 35695288, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 265007, 21906754, 265017, 265019, 264448, 264682, 264389, 264288, 18108354, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 60170815, 264691, 18108370, 35696423, 65274791, 35695855, 264634, 60431850, 60170394, 56182323, 264558, 18108388, 22279000, 264563, 264565, 264486, 264567
2778	87781557 (5551, 5552)				56182575, 22278998, 22278999, 264259, 29331822, 29331824, 264908, 29331830, 264510, 33657402, 21906754, 55811386, 265017, 265019, 264448, 264288, 21906765, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 265022, 60170615, 55810784, 55811578, 264555, 56526486, 22279000
2777	78818729 (5553, 5554)			UNCLASSIFIED	264907, 264766
2778	82112411 (5555, 5556)			UNCLASSIFIED	264907, 264593, 264760, 264628
2779	87649729 (5557, 5558)	Novel Protein sim. GBank gi4680711 gb AAD27745.1 AF13297 - (AF132970) CGI-36 protein [Homo sapiens]		UNCLASSIFIED	22278997, 264259, 29331824, 66714117, 35696052, 265006, 264512, 264448, 264288, 29148627, 18108364, 20281149, 18108370, 264629
2780	94679397 (5559, 5560)	Novel Protein sim. GBank gi4758524 ref NP_004823.1 PHGK] - HPK/GCK-like kinase	Contains protein domain (PF00780) - CNH domain	kinase	29146499, 65274791, 264634, 264639
2781	91220037 (5561, 5562)	Novel Protein sim. GBank gi4469352 gb AAD21222] - (AF069502) ubiquitin specific protease UBP43 [Mus musculus]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	60424179, 29331824, 60424269, 66714117, 29331826, 56182435, 87168474, 265017, 264764, 56181562, 21906765, 21906766, 21906768, 35695917, 265020, 33657023, 35695855, 56182323, 87168518
2782	94233146 (5563, 5564)	Novel Protein sim. GBank gi4505013 ref NP_002310.1 pLRN] - leucine-rich neuronal protein	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	55274572, 22278998, 22278998, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331828, 264905, 264907, 264908, 264909, 52644045, 265009, 265017, 265018, 264604, 265019, 264760, 264683, 264288, 264766, 264685, 264688, 264788, 52644228, 264689, 21906768, 265020, 265021, 264691, 18108362, 264692, 33657023, 264693, 33657109, 33657349, 18108370, 264628, 263978, 35695855, 264557, 56182323, 83373044, 18108385

2783	80016828 (5565, 5566)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		Im7	264908, 264628, 263878, 263981
2784	87614360 (5567, 5568)				264259, 26331822, 26331824, 29331825, 284482
2785	88071930 (5569, 5570)	Novel Protein sim. GBank gi 2134933 pr S58890 - collapsin response mediator protein - human		UNCLASSIFIED	22278999, 264908, 264758, 265018, 264769, 21906765, 21808768, 21806768, 265020, 284584
2786	87408542 (5571, 5572)	Novel Protein sim. GBank gi 2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase, DGCN2 [Drosophila melanogaster]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264905, 265017
2787	87801268 (5573, 5574)	Novel Protein sim. GBank gi 5174507 ref NP_006020.1 pMA1 - paraneoplastic neuronal antigen		UNCLASSIFIED	264768, 21906765, 21806768, 55811957, 22278999, 264093, 60170815, 284259, 29331822, 18108365, 29331824, 33857109, 29331827, 35696052, 264100, 264105, 264908, 263977, 55811576, 264835, 264637, 60433438, 60432113, 285017, 285019, 22279002, 55811150, 284369, 264288
2788	88090844 (5575, 5576)	Novel Protein sim. GBank gi 3252826 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	
2789	85491275 (5577, 5578)	Novel Protein sim. GBank gi 2485729 sp Q92558 Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA8725)		UNCLASSIFIED	264103, 21808769, 284693
2790	87602784 (5579, 5580)	Novel Protein sim. GBank gi 5101772 emb CAB45135.1  - (AJ242978) p621 [Homo sapiens]		struct	264488, 264769, 284810, 264631, 284636, 264690, 264691, 284259, 284638, 29331824, 264508, 284509, 284905, 284905, 264563, 264908, 264628, 18108370, 264907, 264764, 264908, 264288, 284908
2791	88083195 (5581, 5582)	Novel Protein sim. GBank gi 2911266 (AC002550) - Unknown gene product [Homo sapiens]			21806764, 18108368
2792	95083783 (5583, 5584)	Novel Protein sim. GBank gi 2854163 gb AAC02581.1  - (AF045642) No definition line found [Caenorhabditis elegans]			22278998, 22278997, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 35696052, 264908, 66712502, 29331830, 264909, 60432229, 60433356, 60433438, 33109954, 265010, 265011, 265017, 285018, 265019, 284682, 264448, 284288, 284369, 284768, 52844229, 21906765, 21906768, 265020, 265021, 33857023, 263974, 18108374, 65274791, 35895855, 284636, 284558, 264558, 56182323, 83373044, 18108385, 56526488, 60432113, 22279000, 264567
2793	87425476 (5585, 5586)			UNCLASSIFIED	264259, 60432289, 66712502, 265008, 284636
2794	85794830 (5587, 5588)			UNCLASSIFIED	284689, 265022, 264691, 18108388, 284567

2795	95334888 (5589, 5590)	Novel Protein sim. GBank gi 5454146 ref NP_008348.1 pUBE2 - ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5)	Contains protein domain (PF001179) - Ubiquitin-conjugating enzyme	ubiquitin	65274572, 56182575, 35988286, 22278998, 22278999, 60432049, 264259, 29331822, 29331825, 68714117, 60432289, 29331826, 29331827, 35698052, 29331828, 264907, 68712502, 56182435, 264511, 265007, 264512, 264910, 60432229, 60433356, 60433438, 33109954, 85658542, 265018, 265019, 264288, 264686, 21906764, 21906765, 21906766, 21906768, 21906769, 55811957, 265020, 265021, 285022, 52644150, 33857023, 264693, 65274620, 33657109, 35696423, 55811576, 65274791, 56182323, 56526486, 60432113, 22279002, 264482, 264563, 264484, 264567
2796	94848657 (5591, 5592)	Novel Protein sim. GBank gi 4680651 gb AAD27715.1 AF13294 - (AF132940) CGI-06 protein [Homo sapiens]		UNCLASSIFIED	18108394, 65274572, 56182575, 56994075, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 264509, 264906, 264907, 264908, 68712502, 56182435, 264510, 265008, 264512, 265007, 265008, 264910, 265009, 264591, 264592, 60433356, 264594, 264595, 55812038, 264596, 21906754, 60174639, 87168474, 265010, 265011, 265017, 285018, 265019, 55811150, 264762, 18108351, 264448, 264682, 264369, 264288, 264685, 264766, 264687, 56181562, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 264692, 33857023, 18108362, 264693, 65274620, 33657109, 33657182, 27486265, 33657349, 18108374, 35696423, 65274791, 35695855, 264556, 264557, 56182323, 264558, 60170394, 83373044, 65274727, 87168518, 22279000, 264563, 264564, 264565, 264566, 264567
2797	95110790 (5593, 5594)	Novel Protein sim. GBank gi 4838557 gb AAD31040.1  - (AF143859) potassium channel modulatory factor DEBT-91 [Mus musculus]	Contains protein domain (PF005689) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	56182575, 22278995, 22278996, 22278997, 29331827, 29148499, 264509, 264906, 56182435, 264757, 21906754, 265010, 265017, 265019, 264681, 264682, 264683, 264686, 21906765, 21906767, 21906768, 21906769, 29148629, 265020, 52644150, 264690, 33657182, 264629, 18108376, 56182323, 22279002, 264563
2798	86188005 (5595, 5596)	Novel Protein sim. GBank gi 2852645 (AF007160) - unknown [Homo sapiens]		UNCLASSIFIED	264486, 264489, 264259, 264448, 20281149, 20281152, 264556, 264557, 264558, 264559, 264483, 264488, 264567

2799	88090651 (5597, 5598)	Novel Protein sim. GBank gi 3252825 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331828, 35698052, 29331828, 264809, 60433356, 33657402, 33109954, 87168474, 264448, 52844229, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 52844150, 35695855, 264634, 60432113, 22279000
2800	88316481 (5598, 5600)	Novel Protein sim. GBank gi 4240301 (dbj BAA74929.1) - (AB020713) KIAA0906 protein [Homo sapiens]		glycoprotein	264488, 56994075, 264259, 20281089, 29331825, 29331827, 264905, 56182435, 265006, 265011, 87168559, 265017, 265019, 264448, 264288, 264766, 264688, 60170815, 264691, 264692, 27486265, 264628, 264629, 264636, 264557, 264558, 264559, 87168518, 264584, 264586, 264567
2801	86068814 (5601, 5602)		Contains protein domain (PF00627) - UBA domain		265007, 264687
2802	88082477 (5603, 5604)	Novel Protein sim. GBank gi 2337865 (AC002464) - organic cation transporter, 50% similarity to JC4884 (P1D'g2143892) [Homo sapiens]	Contains protein domain (PF00083) - Sugar (and other) transporter	transport	264448, 35695855
2803	78577446 (5605, 5606)	Novel Protein sim. GBank gi 4559368 (gb AAD23029.1) (AC006585) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF01565) - G-patch domain	UNCLASSIFIED - peptidase	264639 264566
2804	57111131 (5607, 5608)				
2805	87398466 (5609, 5610)				264032, 264259, 29331822, 29331824, 29331827, 29331828, 264508, 265007, 265009, 21906754, 264369, 264288, 264632, 60170394, 264563, 264482
2806	87898951 (5611, 5612)	Novel Protein sim. GBank gi 1168973 (sp P44403) (CLPB_HAEIN - CLPB PROTEIN		UNCLASSIFIED	22278995, 22278996, 22278998, 264259, 29331822, 29331824, 29331826, 29331827, 29146498, 265008, 265009, 60433438, 265017, 265018, 265019, 264448, 284288, 21906765, 21906767, 21906769, 29148629, 265022, 52644150, 56182323



2807	91720702 (5613, 5614)	Novel Protein sim. GBank gj4468310[emb]CAB379911 - (AL031432) dJ465N24.1 (PUTATIVE novel protein similar to predicted yeast and worm proteins) [Homo sapiens]		UNCLASSIFIED	52844507, 52845156, 52846842, 18108398, 56182575, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 52845080, 29331822, 29331824, 29331825, 29331826, 35698052, 29331828, 33856970, 264100, 264105, 264907, 52644045, 60433356, 264594, 60433438, 52646317, 21908754, 33109954, 33657084, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 264763, 264687, 52644229, 21905765, 21905766, 21905767, 21906768, 21906769, 35695917, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 27486265, 35695783, 18108370, 18108372, 18108374, 18108376, 263977, 18108377, 35696423, 35695855, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113
2808	95359111 (5615, 5616)	Novel Protein sim. GBank gj5541863[emb]CAB51071.1 - (AL096857) hypothetical protein [Homo sapiens]	MHC		60432289, 264510, 265010, 265017, 265018, 264681, 264686, 265021, 264690, 22279000, 264566
2809	88083530 (5617, 5618)	Novel Protein sim. GBank gj2727561 (AC004002) - similar to ciliary dynein beta heavy chain, 78% Similarity to P23098 (PID:g118965) [Homo sapiens]	ATPase-associated		18108351
2810	87259032 (5619, 5620)			UNCLASSIFIED	264569, 22278996, 264091, 264259, 29331828, 29146499, 29146629, 29148784, 264693
2811	91235845 (5621, 5622)			UNCLASSIFIED	264106
2812	88093334 (5623, 5624)	Novel Protein sim. GBank gj3264583 (AC005189) - match to ESTs H97758 (NID:g118843) and AA085546 (NID:g1628773) [Homo sapiens]		UNCLASSIFIED	
2813	91218755 (5625, 5626)	Novel Protein sim. GBank gj4240273[dbj]BAA74915.1 - (AB020699) KIAA0882 protein [Homo sapiens]		UNCLASSIFIED	56182575, 29331828, 264906, 66712502, 55811386, 265017, 265018, 265019, 264683, 265020, 87168518, 80432113
2814	90880906 (5627, 5628)	Novel Protein sim. GBank gj3548791 (AC005620) - R33590.1 [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor		55274572
2815	79774521 (5629, 5630)			UNCLASSIFIED	264907, 264909
2816	95358229 (5631, 5632)	Novel Protein sim. GBank gj5420389[emb]CAB46880.1 - (AJ243480) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 35696286, 29331825, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264760, 264681, 264766, 264769, 264689, 21906765, 264693, 264628, 18108370, 264629, 264631, 264634, 264563, 264564, 264566, 264486

2817	87749542 (5633, 5634)	Novel Protein sim. GBank gll1293846 (U56966) - coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3 [Caenorhabditis elegans]			264259, 29331822, 29331827, 264508, 264509, 264905, 264907, 264908, 264909, 56182435, 264510, 265006, 264511, 264512, 264593, 264758, 265010, 264760, 264781, 264764, 264288, 264687, 264769, 55811957, 35685917, 33657109, 263978, 264634, 264636, 264639, 284564, 264565, 264568, 264488, 264587, 66712502
2818	88073578 (5635, 5636)	Novel Protein sim. GBank gll549986 (U13149) - possible apusporin-associated protein [Pennisetum ciliare]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	
2819	87793527 (5637, 5638)			UNCLASSIFIED	264909, 264511
2820	87765744 (5639, 5640)	Novel Protein sim. GBank gll4929773 [gb AAD34147.1 AF152097] CGI-05 protein [Homo sapiens]	Contains protein domain (PF00919) - Uncharacterized protein family UPF0004	UNCLASSIFIED	18108394, 52646365, 52644045, 264112, 265009, 21906754, 265017, 18108351, 264683, 264369, 264886, 264769, 21906769, 33657023, 33657109, 18108370, 18108374, 18108377, 18108385, 264636
2821	95320511 (5641, 5642)	Novel Protein sim. GBank gll399144 [sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR (AB002363) KIAA0385 [Homo sapiens]	Contains protein domain (PF00386) - C1q domain	complement	
2822	94260221 (5643, 5644)	Novel Protein sim. GBank gll222467 [dbj BAA20820  - (AB002363) KIAA0385 [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 60432289, 264905, 60433356, 33657402, 265011, 264760, 21906765, 60170815, 264838, 264766
2823	95320513 (5645, 5646)	Novel Protein sim. GBank gll399144 [sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	
2824	95320515 (5647, 5648)	Novel Protein sim. GBank gll399144 [sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR		UNCLASSIFIED	264907
2825	19742170 (5649, 5650)				264760
2826	94311905 (5651, 5652)	Novel Protein sim. GBank gll3659683 [emb CAA22020  - (AL033503) conserved hypothetical protein [Candida albicans]			52645156, 22278994, 35696288, 22278997, 22278998, 52645080, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 33658970, 52644045, 52646317, 33657084, 52644296, 265017, 265018, 265019, 264288, 21906764, 21906765, 21906766, 21906767, 21906769, 35685917, 52644150, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 35696423, 35695855, 52644332, 18108385, 87168518, 264484

2827	95320519 (5653, 5654)	Novel Protein sim. GBank gi 398144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - complement C1q domain	264488, 263994, 264489, 65274572, 29331822, 66714117, 29331827, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 264910, 264591, 60432229, 264592, 264593, 264595, 264596, 21906754, 265011, 264600, 264601, 264602, 265017, 264604, 264605, 264288, 264766, 264767, 264689, 55811957, 264534, 264690, 264691, 264692, 264693, 263972, 264829, 35695855, 264631, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264558, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264565, 264566, 264567, 264486, 18108391
2828	91229615 (5655, 5656)	Novel Protein sim. GBank gi 3598974 (AF077000) - protein tyrosine phosphatase TD14 [Rattus norvegicus]	Contains protein domain (PF00102) - phosphatase Protein-tyrosine phosphatase	29331822, 35696052, 264104, 264908, 265007, 264591, 265010, 265011, 265019, 264766, 264688, 55811957, 18108370, 18108374, 55810764, 35696423, 55811576, 56182323, 83373044, 87168518
2829	87651244 (5657, 5658)	Novel Protein sim. GBank gi 4680689 gb AAD27734.1 AF13295 - (AF13295) CGI-25 protein [Homo sapiens]		22278996, 22278997, 264091, 264093, 60432049, 264259, 29331822, 29331825, 29331827, 29331828, 264905, 264509, 66712502, 264510, 264511, 264593, 60433438, 21906754, 265011, 264603, 18108351, 264288, 21908765, 21906768, 21906769, 29148629, 52644150, 264693, 33657109, 18108374, 264634, 18108385, 60432113, 22279000, 264565, 264488
2830	86087109 (5659, 5660)	Novel Protein sim. GBank gi 2498667 sp Q61200 NPH1_MOUSE - NEUREXOPHILIN 1		265008, 265019, 264639, 22279002
2831	87614717 (5661, 5662)		UNCLASSIFIED	265017
2832	87631809 (5663, 5664)		UNCLASSIFIED	22278997, 22278999, 52646317, 264288, 264688, 21906767, 60431528, 264638, 22279000
2833	87612938 (5665, 5666)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1  - (AL080156) hypothetical protein [Homo sapiens]	UNCLASSIFIED	264555, 264556, 264558
2834	86974703 (5667, 5668)	Novel Protein sim. GBank gi 2224567 dbj BAA20772  - (AB002311) KIAA0313 [Homo sapiens]		263972
2835	87775712 (5669, 5670)	Novel Protein sim. GBank gi 4589532 dbj BAA76788.1  - (AB023161) KIAA0944 protein [Homo sapiens]	ATPase-associated	60432289, 29331828, 265008, 265010, 265017, 264448, 55811957, 265020, 18108370
2836	85724748 (5671, 5672)	Novel Protein sim. GBank gi 2351568 (U76618) - N-RAP [Mus musculus]	Contains protein domain (PF00412) - LIM domain containing proteins	264259, 264112, 265010, 264762, 264764, 293974, 264555, 264558, 264559

2837	87766482 (5673, 5674)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	18108394, 22278997, 22278998, 29331822, 284907, 284909, 285008, 285007, 285018, 285019, 284682, 284288, 21905766, 21906767, 55811957, 35695917, 18108374, 55182323, 22279000, 22279002
2838	87775392 (5675, 5676)	Novel Protein sim. GBank gij973378 (U31263) - core protein [Hepatitis C virus]	UNCLASSIFIED	18108394, 18108397, 264259, 29331826, 285007, 285019, 264448, 18108388, 20281149, 284585, 284587
2839	85799317 (5677, 5678)		UNCLASSIFIED	264555
2840	87774665 (5679, 5680)	Novel Protein sim. GBank gij1575515 (U64899) - (thrombospondin-related anonymous protein [Plasmodium gallinaceum])		264509, 264511, 265011, 264288, 264769, 265020, 284634, 284638, 284556
2841	86982568 (5681, 5682)	Novel Protein sim. GBank gij2224605[dbj]BAA20790] - (AB002330) KIAA0332 [Homo sapiens]	dna_rna_bind	55182575, 35698052, 284907, 284908, 284909, 284910, 284593, 284595, 284768, 285022, 284691, 33657182, 35695763, 18108370, 35695855, 284631, 284559, 284583, 264567
2842	80080088 (5683, 5684)			264600
2843	91012494 (5685, 5686)	Novel Protein sim. GBank gij5578957[emb]CAB51350.1] - (AL050306) dJ47587.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]	UNCLASSIFIED	284906, 284907, 284908, 284909, 284910, 284784, 35695855, 83373044, 18108385
2844	56731154 (5687, 5688)	Novel Protein sim. GBank gij585123[sp]Q08878[FBL_C_MOUSE - FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)]	Contains protein domain (PF00008) - EGF-like domain	264685
2845	94321719 (5689, 5690)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	homeobox	29146498, 87168474, 264686, 35696423, 83373044, 264564
2846	88318613 (5691, 5692)	Novel Protein sim. GBank gij5305263[gb]AAD41995.1[AC00623] - (AC00623) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	29331830, 284909, 285008, 265011, 87168559, 284629, 264558
2847	81811757 (5693, 5694)	Novel Protein sim. GBank gij3399676 (AC005300) - R31180.1 [Homo sapiens]	UNCLASSIFIED	284908, 264766, 284789, 284629, 284637, 284568
2848	87612943 (5695, 5696)	Novel Protein sim. GBank gij5262615[emb]CAB45747.1] - (AL080156) hypothetical protein [Homo sapiens]	UNCLASSIFIED	284490, 284259, 284508, 284905, 284907, 284510, 285007, 285008, 284591, 284592, 284593, 284594, 284595, 55812038, 265010, 265011, 284604, 284763, 284764, 284765, 284766, 284686, 284628, 284629, 284555, 284638, 284556, 284557, 284638, 284558, 284559, 284583, 284566, 284567
2849	88084283 (5697, 5698)	Novel Protein sim. GBank gij3342218 (AC004131) - Unknown gene product [Homo sapiens]		29331822, 35696052, 284509, 264906, 265007, 284594, 265018, 284288, 263972, 35696423, 18108384, 56528488, 18108390
2850	87623636 (5699, 5700)		UNCLASSIFIED	35696288, 265008, 265009, 265018, 284288, 35695917, 284693, 18108374, 35695855, 22279000

2851	87820548 (5701, 5702)	Novel Protein sim. GBank gij4321619jgb/AAD15788.11 - (AF051098) seven transmembrane domain orphan receptor [Mus musculus]		UNCLASSIFIED	264906, 264907, 56182435, 264758, 55811386, 265010, 18108351, 264448, 264369, 21906765, 264691, 264692, 264693, 35695655, 264556, 18108385, 264567, 264591
2852	86987023 (5703, 5704)	Novel Protein sim. GBank gij1825729 (U88308) - similar to drosophila membrane protein PATCHED SP-P18502 (PID:g128645) [Caenorhabditis elegans]		UNCLASSIFIED	
2853	87784630 (5705, 5706)	Novel Protein sim. GBank gij2702347 (AF027503) - putative membrane-associated guanylate kinase 1 [Mus musculus]	Contains protein domain (PF00397) - WW domain	kinase	56182575, 55811150, 264690, 27486282, 27486265, 264632, 56182323, 56526486, 22279002
2854	86083557 (5707, 5708)	Novel Protein sim. GBank gij2795825 (AC004021) - leitch protein; ring canal component involved in cytoplasmic bridges. 77% Similarity to A45773 (PID:g1079096) [Homo sapiens]	Contains protein domain (PF01344) - Keich molif	-dna_ma_bind	35696286, 29331824, 29331826, 29331828, 264908, 264768, 264693, 22279002, 264482
2855	94723856 (5709, 5710)	Novel Protein sim. GBank gij1504040jdbj/BAA13219 - (D86983) similar to D.melanogaster peroxidase(U11052) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278994, 29331822, 29331824, 29331825, 264906, 264908, 265009, 33109954, 265018, 265019, 264448, 21906765, 265020, 264690, 27486265, 83373044, 22279000, 22279002, 264482
2856	88093359 (5711, 5712)	Novel Protein sim. GBank gij3264583 (AC005189) - match to ESTs H97758 (NID:g118643) and AA085546 (NID:g1628773) [Homo sapiens]			21906766, 22278997, 265022, 29331822, 29331826, 27488282, 265007, 265009, 265017, 264482, 264563, 18108351
2857	95348286 (5713, 5714)	Novel Protein sim. GBank gij3041855 (AC004537) - similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	-struct	22278995, 35696286, 29331824, 29331825, 35696052, 264103, 264108, 56182435, 21906765, 21906769, 265020, 18108368, 35695763, 22279002, 264563
2858	87434748 (5715, 5716)	Novel Protein sim. GBank gij462585jdp35227ME18 - HUMAN - DNA-BINDING PROTEIN MEL-18 (ZINC FINGER PROTEIN 144)	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	-dna_ma_bind	264569, 264887, 22278995, 22278996, 22278997, 22278999, 264259, 29331826, 29331827, 29331828, 264509, 264905, 264906, 29331830, 264908, 52644045, 264909, 264511, 264512, 265007, 265008, 264910, 265009, 264593, 60433356, 264595, 264758, 21906754, 265010, 265011, 264604, 265018, 264760, 18108351, 264783, 264682, 264764, 264765, 264288, 264369, 264685, 264766, 264768, 18108357, 264769, 21906766, 21906767, 265021, 264534, 60170615, 264691, 264692, 18108370, 264629, 18108374, 264631, 264636, 263981, 18108381, 264558, 18108385, 22279002, 264584, 264566, 264486, 264587
2859	90937675 (5717, 5718)	Novel Protein sim. GBank gij4325320jgb/AAD17331.11 - (AF124427) claudin-15 [Mus musculus]		UNCLASSIFIED	60424179, 65274572, 29331828, 264905, 264511, 264758, 265011, 21906767, 21906769, 55811957, 265021, 56182323

2860	87532599 (5719, 5720)	Novel Protein sim. GBank gll469186[emb CAB38414.1] - (AL031588) dJ1163J1.2.1 (novel protein similar to C. elegans B0035.16 and bacterial IRNA (5-Methylaminomethyl-2-thiouridylyl)-Methyltransferases) (isoform 1) [Homo sapiens]		UNCLASSIFIED	284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 284510, 284511, 33109954, 18108351, 264683, 284785, 284369, 284886, 21908765, 284691, 284692, 284693, 18108388, 22278002, 264482
2861	86688507 (5721, 5722)	Novel Protein sim. GBank gll3941730 (AF108083) - BS4 [Homo sapiens]			284369, 284692
2862	87569585 (5723, 5724)	Novel Protein sim. GBank gll4505013[ref NP_002310.1 pLRL] - leucine-rich neuronal protein		UNCLASSIFIED	264691, 264638
2863	91220421 (5725, 5726)	Novel Protein sim. GBank gll3249088 (AC004473) - Contains similarity to goliath protein gb M97204 from D. melanogaster. [Arabidopsis thaliana]	Contains protein domain (PF00096) - struct Zinc finger, C2H2 type		56994075, 35686286, 22278998, 29331822, 29331824, 35686052, 29331828, 284108, 284511, 55812038, 33657084, 55811366, 265018, 265019, 21908765, 21908766, 21908769, 35685917, 265020, 265022, 33657023, 33657109, 33657349, 264628, 18108376, 60431850, 56182323, 18108385, 18108387, 87168518, 22278002
2864	87420030 (5727, 5728)	Novel Protein sim. GBank gll1079451[pir JA55463] - tropomodulin, skeletal muscle - chicken	struct		284259, 284910
2865	95312191 (5729, 5730)	Novel Protein sim. GBank gll438840 (L19048) - MSA-2 [Plasmodium falciparum]			22278995, 21906764, 284482
2866	95105480 (5731, 5732)	Novel Protein sim. GBank gll585703[sp Q07086 PMP2_RAT] - 22 KD PEROXISOMAL MEMBRANE PROTEIN		glycoprotein	65274572, 22278998, 22278998, 22278998, 264259, 29331824, 29331827, 29331828, 60433438, 21908754, 265018, 284448, 264784, 52844150, 83373044
2867	86808001 (5733, 5734)	Novel Protein sim. GBank gll4580997[gb AAD24571.1 AF121081] cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	264488, 264768, 21908768, 22278998, 265022, 264259, 284508, 284905, 284907, 284511, 284910, 284635, 284638, 284637, 265011, 265017, 265018, 265019, 264583, 284088, 284566, 264784, 264369, 264587, 264486, 264288, 264768

2868	95303283 (5735, 5736)	Novel Protein sim. GBank gij1292868[emb](CAA63023) - (X94232) t-Cell activation protein [Homo sapiens]		18108392, 264488, 22278994, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 264508, 52844045, 264828, 265006, 265007, 265008, 265009, 264591, 60432229, 264593, 60433358, 264595, 21906754, 265017, 265019, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 264691, 33657182, 18108388, 27486261, 27486262, 27486264, 27486265, 18108370, 18108374, 35696423, 35695855, 264632, 56182323, 87168518, 264404, 22279000, 22279002, 264482, 264563, 264564, 264567, 264487
2869	86094412 (5737, 5738)		UNCLASSIFIED	264369
2870	84404574 (5739, 5740)		UNCLASSIFIED	264905, 264908, 264764, 21906769, 264634
2871	86318621 (5741, 5742)	Novel Protein sim. GBank gij5306263[gb]A041995.1(AC00623) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264907, 265008, 265017, 265018, 264682, 264764, 18108354, 265021, 27486265, 264629, 18108387, 264567
2872	95312197 (5743, 5744)	Novel Protein sim. GBank gij112205[pir]B39066 - proline-rich protein 15 - rat	kinase	263981
2873	86094252 (5745, 5746)		UNCLASSIFIED	264488, 18108374, 264768, 264687, 264688, 264689, 35696423, 35696286, 35695917, 264510, 264511, 265007, 264512, 265008, 264910, 264534, 264634, 264635, 264555, 264592, 264259, 264558, 60433438, 60432289, 35696052, 265011, 264600, 264601, 60432113, 264508, 264563, 264482, 264509, 264905, 264906, 264564, 18108351, 264763, 18108370, 264907, 264566, 264908, 264764, 264288, 264567, 264909, 264486, 264765, 18108391

2874	94313548 (5747, 5748)	Novel Protein sim. GBank gij3212854 (AC004005) - unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	52844507, 52845156, 52846385, 58182575, 22278994, 22278995, 56994075, 35696286, 60432049, 264259, 52645080, 29331822, 56182181, 29331824, 60424269, 29331825, 66714117, 29331826, 29331827, 35696052, 29331828, 33656970, 66712502, 52844045, 285007, 265009, 60433356, 264758, 55812038, 18108348, 52846317, 33109954, 33657084, 265017, 264604, 285018, 285019, 264682, 264369, 264288, 264688, 52644229, 21906766, 21906767, 21906768, 55811957, 265020, 265021, 265022, 52644150, 33657023, 52645129, 18108374, 18108376, 35696423, 56182323, 18108387, 87168518, 60432113, 22279000, 22279002, 264563, 264565
2875	88083726 (5749, 5750)	Novel Protein sim. GBank gij2781386 (AC004010) - similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	22278996, 22278997, 22278998, 29331828, 29331828, 29148489, 66712502, 265008, 265017, 18108351, 264683, 264689, 21906767, 18108378, 18108377, 55811576, 60170394, 22279000, 264487
2876	88080854 (5751, 5752)	Novel Protein sim. GBank gij2979530 (AC004449) - R33683_2 [Homo sapiens]	Contains protein domain (PF00167) - Igi	
2877	94747029 (5753, 5754)	Novel Protein sim. GBank gij4704208 [emb]CAB41646.1] - (AL035419) dJ1100H13.1 (putative novel protein) [Homo sapiens]		52646365, 65274572, 56182575, 22278997, 22278998, 22278999, 60432048, 52645080, 60424269, 60432289, 29331827, 35696052, 29331828, 66712502, 52644045, 56182435, 60433356, 33657402, 33657084, 265018, 55811150, 264448, 264369, 21908766, 21906768, 21906769, 265020, 33657023, 33657109, 33657182, 27486262, 264629, 60431528, 55811576, 52644332, 56182323, 264558, 83373044, 18108385, 56526486, 60432113, 22279000, 22279002, 264563
2878	88085309 (5755, 5756)	Novel Protein sim. GBank gij387677 [emb]CAB03087] - (Z81077) predicted using GeneFinder; Similarity to Yeast protein 8248 (TR:G587531) [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264259, 29331822, 29331826, 264905, 264509, 264907, 264909, 264510, 265006, 264511, 264512, 33657402, 264758, 21906754, 18108351, 264681, 264682, 264288, 264884, 264685, 264768, 264689, 21906769, 264690, 33657023, 264693, 18108384, 33657109, 264629, 18108374, 264630, 264632, 264556, 264637, 264639, 264558, 18108385, 18108387, 264563, 264564, 264565, 264566, 264488, 264567



2878	87868122 (5757, 5768)	Novel Protein sim. GBank gij4895145igbjAAD32752.11 - (AF127374) unknown [Streptomyces lavendulae]	Contains protein domain (PF00315) - UNCLASSIFIED Uracil-DNA glycosylase	18108359, 264259, 264905, 18108370, 264629, 264908, 264909, 18108374, 18108377, 265006, 264910, 264637, 60170394, 264559, 265017, 264564, 264565, 264587, 264684, 264369
2880	94851439 (5759, 5760)	Novel Protein sim. GBank gij4680703igbjAAD2774.11AF13296 - (AF132966) CGI-32 protein [Homo sapiens]		264488, 52646365, 52646842, 22278994, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 52644045, 264510, 265006, 264511, 265007, 264512, 265009, 264910, 264594, 21906754, 52646317, 52644296, 87168559, 264600, 264604, 264605, 264760, 264764, 264288, 264766, 264768, 264687, 264769, 21906766, 21906769, 35695917, 265021, 264690, 264692, 33657023, 52645129, 33657109, 33657182, 27486262, 33657349, 264629, 18108374, 35695855, 264634, 264635, 264636, 264637, 264638, 264557, 52644332, 264558, 264559, 83373044, 264404, 22278000, 264563, 264483, 264567, 264486
2881	87650539 (5761, 5762)	Novel Protein sim. GBank gij733571 (U23452) - No definition line found [Caenorhabditis elegans]	UNCLASSIFIED	22278998, 29331822, 52644045, 21906765, 264639, 60432113
2882	87714367 (5763, 5764)	Novel Protein sim. GBank gij1118112 (U41559) - No definition line found [Caenorhabditis elegans]		264488, 22278996, 22278999, 29331822, 29331826, 264908, 60170831, 60433356, 55812038, 264681, 264682, 264686, 264687, 264688, 21906768, 21906769, 264693, 263967, 18108374, 55811576, 56182323, 22279002, 264566
2883	85362875 (5765, 5766)	Novel Protein sim. GBank gij4868008igbjAAD31087.1AF10693 - (AF106934) vitamin D receptor-interacting protein [Homo sapiens]	Contains protein domain (PF00400) - UNCLASSIFIED WD domain, G-beta repeat	264112, 264682
2884	87784843 (5767, 5768)	Novel Protein sim. GBank gij2224597dbjBAA208321 - (AB002376) KIAA0378 [Homo sapiens]	UNCLASSIFIED	265018, 264634
2885	83006308 (5769, 5770)	Novel Protein sim. GBank gij1255889 (U53344) - T07H6.5 gene product [Caenorhabditis elegans]	Contains protein domain (PF00084) - complementrecept Sushi domain (SCR repeat)	60432049, 264259, 29331828, 264908, 264511, 264595, 60433438, 264596, 265017, 264605, 263969, 263972, 264555, 83373044, 87168518, 264566
2886	91237823 (5771, 5772)			18108351, 264686, 264629, 264631, 264639, 83373044, 264482
2887	91227860 (5773, 5774)	Novel Protein sim. GBank gij3882323dbjBAA34521.11 - (AB018344) KIAA0801 protein [Homo sapiens]	UNCLASSIFIED	264488, 264259, 29331828, 264508, 264906, 264593, 264758, 264766, 264769, 18108374, 83373044, 264486
2888	95105816 (5775, 5776)	Novel Protein sim. GBank gij4508015refjNP_003447.1lpZNF2 - zinc finger protein 205 Zinc finger, C2H2 type	transcriptfactor	

2889	87606562 (5777, 5778)				UNCLASSIFIED	56994075, 29331824, 265009, 264760, 18108354, 264288
2890	78703853 (5779, 5780)	Novel Protein sim. GBank gij854085[emb CAA58337] - (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	264591, 264786
2881	88094428 (5781, 5782)	Novel Protein sim. GBank gij3877750[emb CAB01508] - (Z78064) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65885 comes from this gene; cDNA, EST EMBL:D69451 comes from this gene; cDNA EST EMBL:D68028 comes from this gene; cDNA EST EMBL:D69658 comes from this gene...			UNCLASSIFIED	264591, 264595, 264389, 264685, 284893, 264628, 264583, 264588
2892	95419745 (5783, 5784)	Novel Protein sim. GBank gij4929759[gb AAD34140.1][AF15190] - (AF151903) CGI-145 protein [Homo sapiens]			UNCLASSIFIED	65274572, 35698286, 29331828, 264110, 265009, 60433438, 265018, 265019, 18108351, 264288, 21906765, 21908766, 21906789, 55811937, 264690, 65274820, 263967, 35695855
2893	87798014 (5785, 5786)				UNCLASSIFIED	264259, 265010, 264682, 18108370, 264555, 264556
2894	87755985 (5787, 5788)	Novel Protein sim. GBank gij5689015[gb AA046135.1] - (AF080171) zinc finger protein ZNF232 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type		transcript factor	264259, 265006, 60433438, 52644298, 265011, 264389, 35695917, 18108381, 18108382, 18108388
2895	86938778 (5789, 5790)	Novel Protein sim. GBank gij3924708[emb CAA84646] - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMBL...	Contains protein domain (PF01437) - Plexin repeat			29331824, 265007, 264762, 264636, 264583
2896	87752122 (5791, 5792)	Novel Protein sim. GBank gij4885549[ref NP_005456.1]pPKBG - protein kinase B gamma	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase		18108392, 18108394, 18108398, 22278898, 264259, 29331822, 29331824, 29148499, 264908, 264908, 265007, 265009, 265018, 265019, 264389, 264685, 264689, 21906788, 265021, 264693, 33857182, 264638, 18108384, 18108388, 264567
2897	95413057 (5793, 5794)	Novel Protein sim. GBank gij4502877[ref NP_001296.1]pCLDN - Clostridium perfringens enterotoxin receptor 1			UNCLASSIFIED	60424179, 56182575, 22278896, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331825, 60424289, 60432289, 29331828, 29331828, 35696052, 264908, 56182435, 265009, 264910, 60170831, 60431735, 60433358, 60433438, 65274444, 55811386, 265018, 18108351, 264448, 264288, 264687, 21906765, 21906788, 21906787, 21906769, 55811857, 35695817, 264534, 33657023, 33657109, 35695763, 264628, 264628, 60431528, 18108374, 55810764, 55811578, 35696423, 35695855, 264555, 56182323, 18108385, 264404, 22279000, 22279002, 264586
2898	87750340 (5795, 5796)				UNCLASSIFIED	22278995, 264604, 18108385, 264586

2898	80357670 (5787, 5788)	Novel Protein sim. GBank gii4581470[emb][CAB40137.1] - (Y18483) SLC7A8 protein [Homo sapiens]	UNCLASSIFIED	264764, 21906764, 264692
2900	94233538 (5789, 5800)		glycoprotein	65274572, 56182575, 35696286, 60432048, 264259, 29331824, 66714117, 29331826, 35696052, 29331828, 66712502, 56182435, 285006, 265007, 265008, 265009, 60433356, 264758, 265018, 264764, 264765, 264288, 264768, 21906764, 21906768, 21906769, 265020, 284692, 264693, 32833986, 264631, 83373044, 60432113
2901	87444731 (5801, 5802)	Novel Protein sim. GBank gij4759272[ref][NP_004614.1pTTC4 - tetraicopeptide repeat domain 4	phosphatase	22278995, 22278997, 22278999, 60432048, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 264910, 265009, 21906754, 33657084, 87169474, 265010, 265018, 21906764, 21906765, 21906766, 21906767, 21906769, 33657023, 264693, 33657109, 33657349, 35696423, 35695855, 263981, 56182323, 22279002
2902	85745271 (5803, 5804)	Novel Protein sim. GBank gij2414615[emb][CAB16364] - (Z99259) hypothetical protein [Schizosaccharomyces pombe]		264683, 264691
2903	87606733 (5805, 5806)	Novel Protein sim. GBank gii1079319[pir][S52241 - XLCL2 protein - African clawed frog		264887, 22278994, 264259, 29331826, 29331828, 264905, 52644045, 56182435, 264511, 265017, 265018, 18108351, 264448, 284683, 264769, 264889, 35695917, 52644150, 87168518, 60432113, 22279002
2904	86458072 (5807, 5808)	Novel Protein sim. GBank gij5638823[gb][AAD45885.1][AF14367] - (AF143676) multispinning nuclear envelope membrane protein nurim [Homo sapiens]	UNCLASSIFIED	52646365, 22278999, 264259, 35696052, 265011, 265017, 264683, 264769, 35695917, 265020, 263967, 18108374, 35695855, 284637, 264952, 18108385, 18108387
2905	84449926 (5809, 5810)	Novel Protein sim. GBank gij728837[sp][P39194][ALU7_HUMAN - IIII ALU SUBFAMILY SO WARNING ENTRY IIII]	oncogene	265009, 264681, 264682
2906	95341051 (5811, 5812)	Novel Protein sim. GBank gij4689256[gb][AAD27831.1][AF12185] - (AF12185) sorting nexin 8 [Homo sapiens]	UNCLASSIFIED	22278996, 35696286, 22278998, 264259, 60432289, 29331828, 29331830, 66712502, 265009, 60170831, 33109954, 264448, 264883, 264288, 264689, 21906766, 21906767, 21906768, 55811957, 35695917, 265022, 52644150, 264691, 33657023, 264692, 264693, 35695855, 60432113, 264566

2807	91211383 (5813, 5814)	Novel Protein sim. GBank gi 1707079 (U80451) - contains strong similarity to a DNAJ-like domain (P:PS00636) [Caenorhabditis elegans]	Contains protein domain (PF00226) - DnaJ domain	eph	52844507, 56182575, 56181686, 22278895, 56984075, 35696286, 60432049, 58182181, 35696052, 60431735, 284595, 55812038, 21908754, 55811388, 265019, 284682, 264389, 56181562, 21908766, 55811957, 35695917, 285020, 285021, 33857023, 33657109, 60431528, 55811576, 35696423, 35695855, 264638, 22279000
2808	80414246 (5815, 5816)	Novel Protein sim. GBank gi 2673917 (AC002561) - putative ATP-dependent RNA helicase [Arabidopsis thaliana]		helicase	265009, 33109954, 18108351, 264766, 265021, 264691, 264692, 18108374, 264556, 284638, 284557, 284558
2809	87420225 (5817, 5818)			eph	264259, 87188474, 285018, 18108365, 264828
2910	86601075 (5819, 5820)	Novel Protein sim. GBank gi 4539335 (emb CAB37483.1) - (AL035539) putative protein [Arabidopsis thaliana]			22278995, 284509, 284512, 265007, 33657402, 265017, 264369, 285022, 18108365, 264626
2911	94216615 (5821, 5822)	Novel Protein sim. GBank gi 4469187 (emb CAB38415.1) - (AL031588) dJ1163J1.3 (novel protein similar to mouse B99) [Homo sapiens]		glucoamylase	52546365, 18108397, 22278995, 22278997, 22278998, 22278999, 28331824, 28331825, 52544045, 265006, 265018, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 18108370, 18108372, 18108374, 22279000
2912	87731803 (5823, 5824)	Novel Protein sim. GBank gi 4929637 (gb AAD34079.1) (AF15184 - (AF151842) CGI-84 protein [Homo sapiens])	Contains protein domain (PF00904) - Involucrin repeat		52845156, 264092, 60432049, 264259, 52845080, 29331824, 29331825, 66712502, 33109954, 284760, 264683, 264288, 264686, 265021, 264693, 18108388, 283976, 284604
2913	87713823 (5825, 5826)	Novel Protein sim. GBank gi 854065 (emb CAA58337) - (X83413) U88 [Human herpesvirus 6]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	52844507, 52845156, 52846842, 56182575, 35696286, 22278997, 264259, 52845080, 29331827, 35696052, 29331828, 264628, 52844045, 56182435, 55812038, 52846317, 21908754, 52844296, 87168474, 265017, 265018, 265019, 18108351, 264682, 264686, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 285020, 52844150, 27486261, 27486262, 27486265, 35695763, 55811576, 35695855, 52844332, 22279000, 22279002, 284563
2914	87797300 (5827, 5828)				264557

2915	18081872 (5828, 5830)	Novel Protein sim. GBank gjl5174485[ref]NP_006030.1pKIAA - endocytic receptor (macrophage mannose receptor family)	Contains protein domain Lectin C-type domain	- eph	264569, 264488, 264687, 264768, 21906766, 52846942, 21906767, 21906768, 56182575, 29148629, 35695917, 22278998, 22278997, 22278998, 265021, 22278999, 52644150, 264691, 264259, 60432049, 264692, 52645129, 33657109, 33657182, 29331827, 27486261, 35696052, 29331828, 27486262, 27486264, 27486265, 33657348, 29146498, 29146499, 264906, 264907, 18108370, 264908, 18108372, 52644045, 18108374, 56182435, 35695855, 264112, 264510, 265008, 60432229, 264593, 60433356, 56182323, 18108382, 56812038, 18108385, 33109954, 21906754, 33657084, 87168518, 265010, 265011, 60432113, 265017, 265018, 22278000, 265019, 55811150, 264681, 18108351, 264763, 264448, 264683, 264566, 18108354, 264369, 264288, 264766
2916	95337790 (5831, 5832)	Novel Protein sim. GBank gjl5104851[dbj]BAA80165.1] - (APO00061) 305aa long hypothetical dTDP-4- dehydroharmose reductase (Aeropyrum pernix)		dehydrogenase	52645156, 63274572, 22278994, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33656970, 264509, 264906, 29331830, 52644045, 264909, 56182435, 60170831, 264592, 264593, 33657402, 60433356, 52646317, 21906754, 33109954, 33657084, 52644296, 85658542, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486264, 35695763, 18108376, 55811576, 35696423, 65274791, 35695855, 52644332, 264557, 264638, 56182323, 18108387, 87168518, 22279002, 264482
2917	87454546 (5833, 5834)	Novel Protein sim. GBank gjl3169065[emb]CAA19280.1] - (AL023704) putative translocation elongation factor-Tu fa mily [Schizosaccharomyces pombe]		UNCLASSIFIED	60433438, 264602, 264682, 87168518, 60432113
2918	85690528 (5835, 5836)	Novel Protein sim. GBank gjl539218[pir]S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)			264638
2919	87641497 (5837, 5838)	Novel Protein sim. GBank gjl2564955 (AF030001) - unknown [Mus musculus]			66714117, 66712502, 263981

2920	87769523 (5839, 5840)				35696286, 22278997, 264259, 52645080, 29331824, 29331826, 29331827, 284828, 264909, 56182435, 264511, 264758, 33109954, 21908754, 52644298, 265010, 265011, 264601, 265017, 265019, 284881, 264687, 21906767, 265021, 52644150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486282, 27486284, 27486265, 35696423, 35695855, 264632, 264636, 264637, 264638, 56182323, 60170394, 18108385, 87168518, 60432113
2921	91639982 (5841, 5842)	Novel Protein sim. GBank gii4580013 gb AAD24202.1 U83194 - (U83194) TRAF4-associated factor 2 (Homo sapiens)	Contains protein domain (PF00787) - PX domain		35696286, 22278997, 264091, 264092, 264094, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 29148498, 264104, 264105, 264107, 264508, 264110, 264112, 264512, 60433356, 21906754, 87168474, 265017, 18108351, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 263974, 18108374, 263976, 263977, 18108378, 264555, 263981, 56526488, 87168518, 22279000, 22279002, 264908, 264809, 264511, 285006, 285008, 264593, 33657402, 60174639, 18108351, 264763, 21906765, 29148627, 35695917, 264692, 264628, 263978, 55811576, 35695855, 264555, 264558, 56182323, 60170394, 22279000, 264486
2922	87749762 (5843, 5844)	Novel Protein sim. GBank gii4589514 dbj BAA76779.1  - (AB023152) KIAA0935 protein [Homo sapiens]	Contains protein domain (PF01074) - kinase Glycosyl hydrolases family 38		264488, 18108397, 22278995, 22278996, 22278997, 22278998, 22278999, 29331825, 29331826, 29331827, 29331830, 264511, 265008, 33657402, 265011, 265017, 265018, 264683, 18108354, 21906765, 21906767, 21906768, 21906769, 52644150, 264691, 264692, 33657109, 263974, 18108378, 264631, 264636, 18108385, 18108387, 22279000, 264583, 264586
2923	95337789 (5845, 5846)	Novel Protein sim. GBank gii4835268 emb CAB42888.2  - (Z83844) dJ37E16.4 (similar to mouse p116Rip protein) [Homo sapiens]	Contains protein domain (PF00169) - struct PH domain		265017, 264628, 20281152, 264556
2924	87791967 (5847, 5848)	Novel Protein sim. GBank gii2133095 pir S72254 - ribosomal protein L36, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00444) - ribosomal prot Ribosomal protein L36		
2925	95090120 (5849, 5850)	Novel Protein sim. GBank gii2388986 emb CAB11718  - (Z98980) actin associated protein [Schizosaccharomyces pombe]	UNCLASSIFIED		58182575, 35698286, 264259, 60432289, 29331827, 264508, 52644045, 264910, 264591, 60432228, 55812038, 21906754, 264681, 264448, 264683, 264288, 264685, 52644229, 264688, 21906765, 21906768, 21906769, 265021, 265022, 60170615, 264692, 33657023, 264693, 33657109, 35698423, 65274791, 56182323

2926	95343003 (5851, 5852)	Novel Protein sim. GBank gi 283032 pir S22456 - hydroxyproline-rich glycoprotein - perennial teasinte			29331828, 265011, 264768, 264689, 264764, 264788, 264630, 264637
2927	80408018 (5853, 5854)				
2928	20452179 (5855, 5856)			UNCLASSIFIED	264559
2929	91622820 (5857, 5858)	Novel Protein sim. GBank gi 3413320 emb CAA06915  - (AJ006215) CMP-N-acetylneuraminic acid synthetase [Mus musculus]		UNCLASSIFIED	264569, 264489, 22278994, 35696286, 22278996, 22278998, 22278999, 264094, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 33656970, 264109, 29331830, 52644045, 285009, 33109954, 52644296, 87168559, 264760, 264762, 264448, 264764, 264288, 264766, 264768, 21906765, 21906766, 21906768, 21906769, 35695917, 264691, 33657023, 264693, 33657109, 18108374, 263976, 35696423, 35695855, 263981, 22279000, 22279002, 264567, 264486
2930	95302755 (5859, 5860)			UNCLASSIFIED	56182575, 56181686, 35696286, 22278996, 22278998, 22278999, 264259, 29331825, 60432289, 29331828, 264905, 52644045, 56182435, 285009, 60170831, 264592, 60432229, 60433356, 87168474, 265010, 265011, 265017, 265018, 265019, 264762, 264448, 264683, 264288, 264766, 21906765, 21906769, 35695917, 60170615, 33657023, 33657109, 264628, 18108370, 18108372, 35696423, 35695855, 264556, 56182323, 60432113, 264567
2931	94312693 (5861, 5862)	Novel Protein sim. GBank gi 3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]	Contains protein domain (PF00471) - Ribosomal protein L33	UNCLASSIFIED	52645156, 22278997, 22278998, 29331822, 52645080, 29331824, 60432289, 33656970, 60433356, 60433438, 33109954, 21906765, 21906768, 21906767, 21906768, 265020, 52644150, 33657023, 33657109, 33657182, 27486265, 35696423, 35695855, 264555, 87168518, 60432113, 264566
2932	78632623 (5863, 5864)				264506, 264507
2933	91720776 (5865, 5866)	Novel Protein sim. GBank gi 3378056 (AF017777) - helicase [Drosophila melanogaster]	helicase		264488, 18108392, 56182575, 22278999, 264091, 264259, 29331825, 60432289, 29331827, 264508, 52644045, 56182435, 265007, 265009, 264592, 60433356, 60433438, 21906754, 265017, 264682, 264288, 52644229, 21906765, 21906768, 21906769, 265022, 52644150, 33657023, 33657109, 27486265, 264635, 264636, 60170394, 56182323, 18108385, 60432113, 264565, 264566, 264567

2834	86576025 (5867, 5868)				22278997, 22278999, 29331824, 33657402, 264691, 27486262, 264628, 87168518, 22279000
2835	86410579 (5869, 5870)				UNCLASSIFIED
2836	87603863 (5871, 5872)	Novel Protein sim. GBank gi4153862 (AC005065) - determined by GENSCAN prediction and spliced EST; match to EST RB4329 (NID:942735) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	nuclease	56182575, 22278995, 60433356, 33657402, 264758, 33109854, 21908754, 265018, 265018, 264448, 264789, 21908784, 21908765, 265021, 264692, 33657023, 33657109, 33657349, 55810784, 22279000, 22278997, 29331827, 29331828, 265009, 265017, 264605, 265020, 55811576, 18108387, 60432113, 264563
2837	94653096 (5873, 5874)	Novel Protein sim. GBank gi15174409 (ref NP_006101.1 pCD28 - CD2 antigen (cytoplasmic tail)-binding protein 2		UNCLASSIFIED	56994075, 22278999, 264759, 60432049, 29331822, 56182181, 29331827, 29331828, 264906, 264908, 264909, 56182435, 265008, 264512, 264910, 60170831, 60433356, 265011, 265018, 18108351, 264448, 264288, 264766, 52644229, 21908765, 29148784, 65274791, 264556, 56182323, 60170394, 264558, 60432113, 264565, 264486, 264567
2838	95419773 (5875, 5876)	Novel Protein sim. GBank gi3319990 (emb CAA76720  - (Y17267) ubiquitin-conjugating enzyme [Mus musculus])	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	264488, 56182575, 22278998, 35688286, 22278997, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 29331827, 35690552, 264107, 264905, 66712502, 52544045, 56182435, 264511, 265008, 265009, 60432228, 33657402, 60433438, 55812038, 21908754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264681, 264288, 264689, 21908765, 21906767, 21908788, 55811957, 35695917, 265020, 60170815, 264690, 264691, 264692, 33657023, 264693, 65274620, 33657109, 18108370, 18108374, 263978, 35696423, 35695855, 264555, 264556, 18108381, 56182323, 60170394, 83373044, 18108385, 56526486, 60432113, 22279002
2839	87786622 (5877, 5878)	Novel Protein sim. GBank gi13978900 (emb CAA99809  - (Z75547) similar to WD domain, G-beta repeat; cDNA EST yk371b7.5 comes from this gene; cDNA EST yk312h1.5 comes from this gene; cDNA EST yk465d5.5 comes from this gene; cDNA EST yk472c4.5 comes from this gene; cDNA EST yk2921b.....	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase-associated	264907, 265018, 264681, 264685, 264686



2940	95011103 (5879, 5880)			UNCLASSIFIED	22278996, 29331822, 29331824, 66714117, 29331826, 29331828, 264905, 264908, 66712502, 29331830, 265011, 265017, 264764, 264369, 21906766, 21906767, 33657023, 33657109, 32833986, 18108374, 18108377, 264634, 83373044, 18108385, 18108387, 264586
2941	21423370 (5881, 5882)	Novel Protein sim. GBank gi 3413872 dbj BAA32300  - (AB007924) KIAA0455 protein [Homo sapiens]		UNCLASSIFIED	264557
2942	87430203 (5883, 5884)	Novel Protein sim. GBank gi 172845 sp P46629 RB25_RABIT - RAS-RELATED PROTEIN RAB-25		glycoprotein	264910, 265010, 264768
2943	95314504 (5885, 5886)	Novel Protein sim. GBank gi 4929653 gb AAD34087.1 AF15185 - (AF151850) CGI-92 protein [Homo sapiens]		collagen	60432048, 264259, 60432289, 29331827, 29146498, 265008, 264593, 60433356, 60433436, 265010, 265011, 265017, 265018, 264683, 264766, 18108381, 65274727, 60432113, 264567
2944	95081063 (5887, 5888)	Novel Protein sim. GBank gi 4678282 emb CAB41190.1  - (AL049660) 1-acylcerol-3-phosphate acyltransferase-like protein [Arabidopsis thaliana]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	- ATPase_associated	56994075, 22278998, 60432049, 264259, 29331822, 29331824, 60424269, 60432289, 29331826, 29331828, 264905, 264907, 52644045, 264909, 264511, 265006, 265009, 264594, 21906754, 87168559, 264603, 265017, 265018, 18108351, 264682, 264766, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170615, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 33657182, 33657349, 18108370, 18108374, 18108377, 55811576, 35695423, 35695855, 264635, 264555, 264556, 56182323, 60170394, 264558, 264559, 83373044, 56526486, 87168518, 60432113, 22279002, 264482, 264563, 264484, 264567
2945	94233560 (5889, 5890)	Novel Protein sim. GBank gi 728831 sp P39189 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!!	Contains protein domain (PF00086) - Zinc finger, C2H2 type	UNCLASSIFIED	60424179, 22278995, 22278996, 22278998, 22278999, 264259, 56182181, 29331824, 60424269, 60432289, 35695052, 264908, 265006, 60433356, 55812038, 264759, 55811386, 265018, 264681, 18108351, 264448, 264683, 264389, 264288, 264687, 56181562, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264693, 60431528, 55810764, 35696423, 35695855, 264630, 60170394, 83373044, 22279000, 264586, 264567

2846	94317315 (5891, 5892)	Novel Protein sim. GBank gi 5441952 gb AA043195.1 AF072864 peroxisomal membrane protein PMP 24 [Homo sapiens]	UNCLASSIFIED	264488, 264259, 264508, 264509, 264906, 284907, 284908, 264510, 264511, 265007, 264512, 264910, 264591, 264593, 18108351, 264764, 264288, 264684, 264769, 265021, 264692, 33657108, 264628, 264629, 18108374, 264631, 264634, 264636, 264637, 18108390, 264638, 264639, 83373044, 264585, 264586, 264486, 264587
2947	87362952 (5893, 5894)	Novel Protein sim. GBank gi 3540281 gb AAC34383.1  - (AF056116) All-1 related protein [Fugu rubripes]	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 29146498, 264508, 29331830, 265007, 265008, 265009, 60432228, 21906754, 265010, 265017, 265019, 264766, 264685, 21908785, 21908786, 21908787, 21908788, 21906789, 265020, 264628, 18108370, 264629, 264630, 18108387, 60432113, 52646842, 22278995, 264259, 29331824, 29331825, 29331827, 29331830, 264909, 265007, 265009, 265019, 264763, 264684, 264288, 264685, 264686, 21908787, 264691, 264692, 264693, 18108374, 55811576, 18108395, 22279002, 264583, 264587
2948	87626527 (5895, 5896)	Novel Protein sim. GBank gi 5566614 gb AA05654.2  - (AF001533) mitogen-induced [Mus musculus]	UNCLASSIFIED	22278995, 22278997, 60432228, 29331826, 29331827, 29331828, 35698052, 29146499, 284104, 264107, 264905, 66712502, 264908, 60433356, 60433438, 87168559, 264764, 52644229, 56181582, 21906767, 21908768, 21906769, 265022, 60170615, 33657023, 35696423, 263981, 264558, 60432113, 22279002
2949	88175545 (5897, 5898)	Novel Protein sim. GBank gi 2132923 pr J567133 - probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae)	UNCLASSIFIED	264488, 35698286, 264259, 35698052, 264907, 265007, 264910, 265017, 265018, 264288, 264768, 35695917, 265020, 18108362, 18108370, 18108379, 35698423, 65274791, 35695855, 264556, 56526466, 264486
2950	95066870 (5899, 5900)	Novel Protein sim. GBank gi 466102 sp P34629 YOJ8_CAEEL - PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III	peptidase Contains protein domain (PF00863) - Cytosol aminopeptidase family	264488, 35698286, 264259, 35698052, 264907, 265007, 264910, 265017, 265018, 264288, 264768, 35695917, 265020, 18108362, 18108370, 18108379, 35698423, 65274791, 35695855, 264556, 56526466, 264486
2851	87392357 (5901, 5902)	Novel Protein sim. GBank gi 4688902 emb CAB41450.1  - (AJ238248) centaurin beta2 [Homo sapiens]		264488, 35698286, 264259, 35698052, 264907, 265007, 264910, 265017, 265018, 264288, 264768, 35695917, 265020, 18108362, 18108370, 18108379, 35698423, 65274791, 35695855, 264556, 56526466, 264486

2952	95329952 (5903, 5904)	Novel Protein sim. GBank gij5596693[emb/CAB51405.1] - (AL098881) hypothetical protein [Homo sapiens]	Contains protein domain (PF00650) - CRAL/TRIO domain.	transcript factor	264687, 52645156, 21906766, 21906769, 22278996, 265020, 264690, 60432049, 264259, 264693, 29331822, 18108365, 29331825, 60432289, 33657109, 18108368, 29331827, 35696032, 27486262, 264508, 264905, 20281149, 264905, 264907, 29331830, 264908, 264909, 35695855, 264511, 265008, 285009, 264910, 264635, 264636, 60432229, 264638, 60433356, 264639, 284758, 87188518, 285017, 22279000, 22279002, 264760, 264563, 264482, 18108351, 264448, 264288
2953	88093575 (5905, 5906)	Novel Protein sim. GBank gij118522[sp P10658]ISRC_RABIT - PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP)	Contains protein domain (PF00266) - Aminotransferases class-V	UNCLASSIFIED	18108396, 58994075, 22278996, 29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264908, 264907, 264510, 264591, 264594, 33657402, 264595, 264596, 264758, 52646317, 21906754, 33657084, 52644298, 87188539, 264600, 264760, 264681, 18108351, 264764, 264369, 264288, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 18108364, 52645129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87188518, 284482, 264563, 264565, 29331822
2954	88086288 (5907, 5908)	Novel Protein sim. GBank gij4885261[ref NP_005251.1 pGDF9 - growth differentiation factor 9	Contains protein domain (PF00019) - Transforming growth factor beta like domain	Igf	
2955	87698426 (5909, 5910)	Novel Protein sim. GBank gij3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331822, 29331824, 29331825, 29331826, 35696032, 264908, 52644045, 264512, 60432229, 265018, 265019, 5581150, 264769, 21906767, 21906768, 21906769, 265021, 60170615, 55810764, 264567
2956	83789745 (5911, 5912)	Novel Protein sim. GBank gij4885254[gb AAD27830.1 AF121857] sorting nexin 7 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		22278996, 264259, 29331827, 264908, 21906768
2957	90933301 (5913, 5914)	Novel Protein sim. GBank gij4503023[ref NP_000089.1 pCPT2 - carnitine palmitoyltransferase II precursor		cadherin	22278999, 264259, 29331824, 29331827, 265008, 264595, 264758, 265010, 265011, 264448, 264763, 264683, 264288, 264685, 18108357, 29148629, 264690, 18108392, 264693, 18108370, 60431528, 18108374, 264634, 18108381, 56182323, 18108382, 18108385, 18108388, 56526486, 87168518, 264482, 264487
2958	87440014 (5915, 5916)	Novel Protein sim. GBank gij4240257[dbj BAA74907.1] - (AB020691) KIAA0884 protein [Homo sapiens]			264595, 264596, 264681, 264369, 264629, 264631, 264567

2859	95109420 (5917, 5918)	Novel Protein sim. GBank gij988221 (U33005) - Tbc1 [Mus musculus]	Contains protein domain (PF00566) - oncogene TBC domain	263994, 22278997, 264259, 60432048, 29331826, 29331828, 35696052, 29331830, 66712502, 56182435, 265006, 264512, 265008, 265009, 60433358, 60433438, 264596, 265017, 265018, 264883, 264288, 264766, 264769, 21906766, 21906767, 21906769, 265020, 60170615, 264692, 27466265, 18108374, 65274791, 35695855, 83373044, 56528486, 60432113
2860	87420091 (5918, 5920)		UNCLASSIFIED	35696266, 56182435, 87168474, 265010, 60170615, 35696423, 56182323, 18108383, 87168518, 264483
2861	95413418 (5921, 5922)	Novel Protein sim. GBank gij5596648[emb] (CAB05177.2) - (Z82286) predicted using GeneFinder: similar to WD domain, G-beta repeats [Caenorhabditis elegans]	Contains protein domain (PF00400) - transcript factor WD domain, G-beta repeat	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 264907, 264908, 52844045, 265008, 33857402, 21906754, 87168474, 265011, 87168559, 265017, 21906769, 265020, 60170615, 264692, 33657023, 35695763, 18108370, 18108374, 35696423, 264632, 264636, 18108385, 87168518, 22279002, 264564, 264567
2862	87912700 (5923, 5924)		UNCLASSIFIED	35696286, 22278997, 264092, 264094, 264259, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264509, 264907, 264908, 264909, 264510, 264512, 264593, 264594, 60433438, 264758, 52846317, 264602, 264603, 264605, 264780, 264782, 264784, 264288, 264766, 264686, 264768, 264769, 35695917, 265020, 264691, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264565, 264566, 264567, 264486
2863	85313464 (5925, 5926)	Novel Protein sim. GBank gij4240223[dbj] (BAA74890.1) - (AB020674) KIAA0867 protein [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	18108392, 56994075, 22278998, 22278999, 29331822, 29331825, 29331826, 29331827, 29331828, 265007, 265008, 264592, 264594, 21906754, 265018, 264760, 264687, 264693, 65274620, 33657182, 27486281, 264629, 55810764, 35696423, 264555, 264636, 264637, 264557, 264558, 264563
2864	84324617 (5927, 5928)		UNCLASSIFIED	264259, 29331828, 33657402, 265017, 265018, 264692, 18108368, 35696423, 83373044, 18108388

2965	80384762 (5929, 5930)	Novel Protein sim. GBank gi 485447 ref NP_005452.1 pKRML - Kreiser (mouse) mal- related leucine zipper homolog			transcriptfactor	284259, 29331826, 284508, 284509, 284509, 284905, 284907, 284908, 284909, 284511, 285008, 284910, 284591, 284593, 284594, 33657402, 265011, 284760, 284762, 284764, 284288, 284685, 284766, 284692, 33657109, 284628, 284629, 35895855, 284630, 284631, 284632, 284634, 284635, 284636, 284637, 284638, 284639, 284563, 284567, 18108391 60432289, 284682, 284448
2966	91725248 (5931, 5932)	Novel Protein sim. GBank gi 5262751 emb CAB45690.1  - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]				
2967	94656303 (5933, 5934)	Novel Protein sim. GBank gi 624225 (U19181) - Rabin3 [Rattus norvegicus]			UNCLASSIFIED	264488, 284508, 284509, 284908, 284909, 284511, 284910, 284594, 284758, 85658542, 284762, 284764, 285021, 284556, 18108381, 284584, 284486
2968	95302776 (5935, 5936)	Novel Protein sim. GBank gi 4929715 gb AAD34118.1 AF15188 - (AF151881) CGI-123 protein [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)			284687, 52845156, 21906765, 52846365, 21906767, 18108398, 35696423, 22278996, 35896286, 22278997, 265020, 22278999, 265021, 265022, 284093, 284638, 284690, 52644150, 284259, 33657023, 52645080, 284693, 29331822, 56182181, 29331824, 68714117, 29331825, 33109954, 52845129, 29331826, 21906754, 33657182, 29331827, 29331828, 35696052, 27486262, 87168518, 87168474, 265010, 87168559, 265018, 22279000, 265019, 22279002, 264563, 18108351, 284906, 284907, 284448, 68712502, 284566, 284369, 284288
2969	95310957 (5937, 5938)	Novel Protein sim. GBank gi 3024743 sp O24734 THSA_SULS7 - THERMOSOME, ALPHA SUBUNIT (CHAPERONIN ALPHA SUBUNIT)			eph	52846842, 22278996, 22278998, 22278999, 60432049, 284259, 29331824, 29331825, 29331826, 29331828, 284509, 284909, 52844045, 56182435, 265009, 60433438, 55812038, 21906754, 265011, 87168559, 265018, 265019, 284448, 284288, 284369, 52844229, 21906768, 21906769, 29148784, 265020, 265021, 52644150, 284691, 33657109, 18108374, 56182323, 60170394, 87168518, 60432113, 22279000
2970	88088071 (5939, 5940)	Novel Protein sim. GBank gi 3165407 (AC004755) - fos37502_1 [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain		homeobox	

2971	94196930 (5941, 5942)	Novel Protein sim. GBank gii728837spP39194JALU6 SQ WARNING ENTRY IIII		im7	264488, 56182575, 35696286, 56984075, 29331824, 29331826, 29146498, 284508, 264905, 264907, 264112, 264910, 21908754, 87168559, 265018, 265019, 18108351, 264689, 21908765, 21908767, 21806788, 265020, 265021, 60170615, 18108364, 264828, 264829, 18108374, 264636, 264556, 264558, 83373044, 18108384, 18108385, 87168518, 264584, 264587 265017, 35695917, 265021, 33657109, 22278002, 264563
2972	86625943 (5943, 5944)	Novel Protein sim. GBank gii728836spP39193JALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		kinase	29331822, 264692, 33657349, 55811576, 264583 18108392, 52644507, 56182575, 56181688, 22278985, 22278986, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331824, 29331825, 86714117, 60424289, 29331826, 29331827, 29331828, 35696052, 68712502, 264908, 52644045, 265007, 264910, 265009, 60433438, 33108954, 21906754, 55811386, 52644286, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264448, 264369, 264288, 52644229, 18108359, 21906765, 21906767, 21906768, 35695917, 265020, 265021, 52644150, 264691, 264692, 33657023, 27486282, 27486284, 35695763, 18108370, 18108376, 55810764, 55811576, 35696423, 35695855, 264630, 264635, 264557, 52644332, 264558, 83373044, 18108387, 87168518, 60432113, 22278000, 264482, 264487
2975	95325213 (5949, 5950)	Novel Protein sim. GBank gii3880812[emb]CAA19508] - (AL023839) similar to HECT-domain (ubiquitin-transferase); cDNA EST yk480d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00632) - ubiquitin HECT-domain (ubiquitin-transferase).	ubiquitin	29331824, 29331827, 29331828, 264910, 85858542, 265011, 265018, 264448, 264288, 264769, 21908767, 265020, 264691, 264559, 83373044
2976	87771202 (5951, 5952)	Novel Protein sim. GBank gii5679136[gb]AAD46874.1[AF16093] - (AF160934) BCDNA.LD14188 [Drosophila melanogaster]		transport	22278996, 264906, 265007, 265010, 265011, 265017, 265019, 18108351, 264685, 264689, 18108370, 264639, 18108385
2977	91725254 (5953, 5954)	Novel Protein sim. GBank gii5262751[emb]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		UNCLASSIFIED	264509, 264288

2978	87332059 (5955, 5956)	Novel Protein sim. GBank gij746549 (U23522) - No definition line found [Caenorhabditis elegans]	Contains protein domain (PF00480) - UNCLASSIFIED ROK family	22278995, 22278996, 22278997, 22278999, 264259, 60432289, 29331827, 29146499, 56182435, 265006, 265007, 265009, 60433356, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 264288, 264685, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 35696423, 264639, 60432113, 22279000, 22279002
2979	91725256 (5957, 5958)	Novel Protein sim. GBank gij526275 [emb]CAB45680.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]	complement	264488, 65274572, 56994075, 22278999, 264093, 29331822, 29331824, 264288, 55811957, 33657023, 33657109, 18108370, 55811576, 58182323, 60432113, 264482, 265009, 21906767, 263981, 22279000
2980	86296600 (5959, 5960)		UNCLASSIFIED	264629, 264564
2981	87376330 (5961, 5962)	Novel Protein sim. GBank gij4929767 [gb]AAD34144.1 [AF151907] CGI-149 protein [Homo sapiens]		22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264092, 29331824, 29331827, 29331828, 264905, 264591, 264592, 264594, 264595, 264596, 33657084, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 18108365, 33657182, 33657349, 35696423, 83373044, 22279000, 22279002
2982	86303675 (5963, 5964)			60424178, 52646842, 18108398, 22278997, 264093, 60432049, 264259, 29331822, 60432289, 33656970, 264905, 52644045, 265006, 60431735, 87168474, 265018, 265019, 18108351, 264448, 21906765, 21906768, 35695917, 33657023, 52645129, 18108370, 35696423, 83373044, 56526486, 60432113, 264404, 22279002
2983	91725258 (5965, 5966)	Novel Protein sim. GBank gij526275 [emb]CAB45680.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]	ATPase associated	
2984	94136467 (5967, 5968)	Novel Protein sim. GBank gij2983734 (AC002542) - similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID.g1130619) [Homo sapiens]		
2985	87099072 (5969, 5970)	Novel Protein sim. GBank gij103160 [pir] [S22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)]	UNCLASSIFIED	264910, 55812038, 56181562, 55811957, 264628, 55810764, 264632, 264635, 60432113
2986	86284861 (5971, 5972)			55811957, 264566
2987	86455934 (5973, 5974)		UNCLASSIFIED	264369

2888	95357753 (5975, 5976)	Novel Protein sim. GBank gi 4678028 gb AAD27002.1  - (AF07207) HSPC021 (Homo sapiens)	UNCLASSIFIED	264488, 65274572, 22278995, 22278998, 22278997, 22278998, 264092, 264094, 264259, 60432049, 29331824, 29331828, 60432289, 35696052, 29331828, 264107, 264905, 264907, 264908, 66712502, 264828, 264909, 56182435, 265008, 265007, 265008, 60170831, 60432229, 264593, 60433358, 264757, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264682, 264448, 264389, 264288, 264685, 52844229, 21906765, 21906767, 21906769, 35695917, 265021, 265022, 52644150, 264690, 33657023, 65274820, 263967, 33657109, 27486262, 18108370, 18108372, 18108374, 55810764, 65274791, 35695855, 264635, 264636, 264637, 263981, 264638, 56182323, 83373044, 60432113, 22279000, 264563, 264564, 264565, 264566, 264567
2889	91225118 (5977, 5978)	Novel Protein sim. GBank gi 113671 sp P23964 ALUF_HUMAN - IIII ALU CLASS F WARNING ENTRY IIII	kinase	22278996, 22278997, 264905, 264511, 60170831, 264593, 265018, 21906765, 21906767, 21906768, 18108374
2890	87330444 (5979, 5980)	Novel Protein sim. GBank gi 2829838 sp P97348 RHOD_MOUSE - RHO-RELATED GTP-BINDING PROTEIN RHOD	Contains protein domain (PF00071) - oncogene Ras family	265007, 264512, 18108351, 264288, 264689, 265020, 264691, 33657023, 33657109
2891	94325361 (5981, 5982)		UNCLASSIFIED	264563
2892	85425164 (5983, 5984)		UNCLASSIFIED	264259, 265019, 264689, 18108385
2893	94325363 (5985, 5986)		UNCLASSIFIED	264488, 29331822, 265017, 264761, 21906769, 65274791, 263981, 264585
2894	94136634 (5987, 5988)	Novel Protein sim. GBank gi 2496549 sp Q50658 YU02_MYCTU - HYPOTHETICAL 28.7 KD PROTEIN CY339.02	transport	22278994, 22278995, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 265006, 265009, 264910, 33109954, 87168474, 87168559, 265018, 265019, 264448, 264288, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 33657023, 264693, 35695855, 83373044, 18108385, 22279000, 264565, 264568, 264905, 264907, 265019, 18108351, 264683
2895	87591070 (5989, 5990)	Novel Protein sim. GBank gi 2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		65274572, 35698288, 264259, 29331824, 35698052, 29148499, 264508, 264907, 265007, 265008, 60433438, 18108348, 265017, 264681, 264683, 264288, 264768, 264769, 264689, 35695917, 60170815, 33657023, 264692, 264634, 264555, 18108381, 18108382, 18108388, 264484
2896	91013788 (5991, 5992)	Novel Protein sim. GBank gi 2829912 (AC002291) - Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - helicase DEAD/DEAH box helicase	



2997	87627440 (5993, 5994)	Novel Protein sim. GBank gi 4589652 dbj BA76848.3  - (AB023221) KIAA1004 protein [Homo sapiens]		homeobox	264488, 56182575, 264259, 66714117, 29331828, 35698052, 264508, 264509, 264907, 264908, 265006, 87168474, 265019, 264448, 264682, 264685, 264766, 21906764, 21906766, 21906768, 21906769, 21906770, 18108374, 35698423, 264634, 264635, 264636, 264557, 18108385, 87168518
2998	88095381 (5995, 5996)	Novel Protein sim. GBank gi 3947589 emb CAA22252  - (AL034384) cDNA EST yk25589.3 comes from this gene; cDNA EST yk25589.5 comes from this gene; cDNA EST EMBL M75923 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	52646365, 22278997, 264508, 264908, 18108351, 21908765, 21908767, 18108370, 18108374, 35696423, 264636, 264639
2999	94847055 (5997, 5998)	Novel Protein sim. GBank gi 15408 sp P18835 CC19_CAEEL - CUTICLE COLLAGEN 19		UNCLASSIFIED	56182575, 22278996, 29147620, 29331825, 29146498, 29146499, 264905, 66712502, 265006, 265009, 21906754, 85658542, 18108351, 29148627, 29148629, 60170615, 33657109, 27486262, 18108370, 18108374, 264556, 264557, 264558, 60170394, 18108385, 264563
3000	95099370 (5999, 6000)	Novel Protein sim. GBank gi 1163174 U32575  - similar to yeast Sec6p. Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author [Rattus norvegicus]		UNCLASSIFIED	264887, 22278997, 22278999, 264259, 29331822, 29331824, 35696052, 29146498, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 265008, 265009, 264910, 33657402, 264757, 264595, 264598, 264758, 21906754, 265011, 264600, 265017, 265018, 264605, 265019, 264760, 264761, 264762, 264681, 264682, 264764, 264288, 264685, 264766, 264686, 264768, 264769, 21906765, 21906768, 35695917, 265020, 264691, 264692, 33657023, 264693, 33657109, 33657182, 27486261, 264628, 264629, 18108374, 18108376, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 60170394, 83373044, 20798451, 22279002, 264563, 264486, 264567
3001	88078454 (6001, 6002)	Novel Protein sim. GBank gi 2078470 AC002073  - Putative gene. Genscan predictions confirmed by EST splicing; coded for by human cDNAs AA122029 (NID:g1678048), D31562 (NID:g844442), AA158721 (NID:g1733515), R59640 (NID:g830335) and F13082 (NID:g709111) [Homo sapiens]		calhepsin	18108394, 52646842, 56182575, 29331824, 29331825, 29331827, 264910, 33109954, 52644296, 265017, 265019, 264288, 265020, 265021, 52644150, 264692, 35695763, 55810764, 35696423, 56182323, 18108387, 264563, 264564
3002	87718167 (6003, 6004)	Novel Protein sim. GBank gi 3599478 AF085185  - Myosin-IA [Acanthamoeba castellanii]		UNCLASSIFIED	264488, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 264510, 265009, 21906754, 264682, 264688, 33657023, 264565

3003	86848078 (6005, 6006)	Novel Protein sim. GBank gl 1754869 (U30292) - collagen type XIII alpha-1 chain [Mus musculus]	Contains protein domain (PF01391) - collagen Collagen triple helix repeat (20 copies)	264512, 264593, 264564, 264567, 264486
3004	88066876 (6007, 6008)	Novel Protein sim. GBank gl 2224829[gb BAAZ0802] - (AB002342) KIA0344 [Homo sapiens]		29331830, 21906769, 264681, 33657109, 263972, 18108385
3005	87794843 (6009, 6010)	Novel Protein sim. GBank gl 4680659[gb AAD27719.1 AF13294 - (AF132944) CGI-10 protein [Homo sapiens]	Contains protein domain (PF01360) - oxygenase Monoxygenase	265011, 265019, 21906766, 21906767, 21906768, 265020, 33657023, 33657349, 60170394, 22279002, 264567
3006	87422224 (6011, 6012)	Novel Protein sim. GBank gl 3930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - MHC Ank repeat	264259, 29331822, 264512, 21906754, 265018, 264687, 21906765, 264681, 264555, 264556, 264558, 18108385
3007	90936005 (6013, 6014)	Novel Protein sim. GBank gl 2565052 (U80738) - CAGH1a [Homo sapiens]	Contains protein domain (PF00036) - transcript factor Zinc finger, C2H2 type	52644507, 52645156, 65274572, 264909, 264512, 265018, 264760, 264448, 264765, 264689, 60170815, 18108374, 20261152, 264636, 52644332
3008	80416249 (6015, 6016)			264905, 264593, 264766, 264636
3009	91213387 (6017, 6018)	Novel Protein sim. GBank gl 3127193 (AF062389) - kidney-specific protein [Rattus norvegicus]	Contains protein domain (PF00501) - synthase AMP-binding enzyme	52646842, 56182575, 22278995, 22278998, 264259, 29331823, 29331826, 29331827, 29331828, 35698052, 264508, 264509, 264907, 56182435, 264511, 265007, 264512, 265008, 264757, 264758, 5612038, 264759, 33109954, 21906754, 265010, 265011, 264600, 265017, 265018, 265019, 264760, 18108351, 264288, 264369, 21906764, 21906765, 21906767, 55811957, 265020, 265021, 264691, 18108386, 27486262, 20281149, 18108370, 55811576, 264637, 264556, 264557, 18108381, 264558, 56182323, 264559, 18108385, 18108386, 22279002, 264486
3010	95317217 (6019, 6020)	Novel Protein sim. GBank gl 4927370[gb AAD33084.1 AF06797 - (AF067972) DNA cytosine methyltransferase 3 alpha [Homo sapiens]	Contains protein domain (PF01923) - UNCLASSIFIED Protein of unknown function	264686, 264687, 21906767, 21906769, 55811957, 22278995, 35695917, 22278996, 22278997, 265020, 265021, 60170615, 264692, 33657023, 29331822, 264693, 18108364, 29331824, 33657109, 60432289, 29331827, 27486261, 29331828, 264508, 264509, 55811576, 35695855, 265008, 264556, 60433438, 83373044, 18108387, 65274727, 60432113, 265017, 22279000, 265019, 264564, 264682, 264764
3011	94323597 (6021, 6022)	Novel Protein sim. GBank gl 5052319[gb AAD38501.1 AF11883 - (AF11883) citrin; adult-onset type II citrullinemia protein [Homo sapiens]	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	35696052, 56182435, 264758, 21906754, 265018, 264760, 264762, 18108351, 264682, 264448, 21908766, 65274620, 18108374, 264482, 264564
3012	87753087 (6023, 6024)		UNCLASSIFIED	263972

3013	91238789 (6025, 6026)	Novel Protein sim. GBank gij3702286 (AC005787) - R33374_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcriptfactor	264488, 263994, 35698286, 22278997, 264259, 29331824, 60424269, 66714117, 35696032, 264905, 264906, 264907, 264908, 264909, 56182435, 264511, 264512, 264910, 264591, 264592, 264593, 264594, 33657402, 60433438, 264595, 264596, 55812038, 264758, 33109954, 21906754, 265010, 265018, 264604, 264760, 264682, 264683, 264764, 264369, 264288, 264765, 264768, 264686, 264768, 264687, 21906767, 35695917, 265020, 33657023, 264692, 264693, 33657109, 264628, 264629, 55811578, 35698423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 264563, 264565, 264566, 264567
3014	79877263 (6027, 6028)	Novel Protein sim. GBank gij3878374[emb CAA93081] - (Z68879) Similarity to Yeast Chl12p protein (PIR Acc. No. S54453); cDNA EST EMBL:D27950 comes from this gene; cDNA EST EMBL:D27949 comes from this gene; cDNA EST EMBL:D33447 comes from this gene; cDNA EST EMBL:D33316 comes from...		ATPase_associated	264760
3015	86995466 (6029, 6030)				22278995, 22278996, 22278997, 264259, 29331824, 29331828, 264906, 265007, 265008, 264910, 265011, 265017, 265019, 264691, 33657109, 18108370, 35695855, 264556, 264564
3016	87759945 (6031, 6032)	Novel Protein sim. GBank gij1168819[sp P41733 CC91_YEAST - CELL DIVISION CONTROL PROTEIN 91		UNCLASSIFIED	52644507, 52646842, 56994075, 52645080, 29331822, 29331824, 35696052, 33655970, 52844045, 264596, 33657084, 265017, 265019, 52644229, 21906767, 35695917, 52644150, 33657023, 33657109, 27486281, 27486262, 27486264, 33657349, 27486265, 35695763, 35695855, 87168518
3017	95011154 (6033, 6034)	Novel Protein sim. GBank gij458965[dbj BAA76851.1] - (AB023224) KIAA1007 protein [Homo sapiens]			264488, 18108397, 22278996, 35696286, 22278999, 264259, 29331822, 60432289, 264908, 29331830, 264909, 56182435, 265006, 265007, 265008, 265009, 264591, 60433356, 60433438, 52646317, 21906754, 55811386, 265010, 265011, 87168559, 21906765, 21906766, 21906767, 21906769, 265017, 265018, 265019, 264288, 264687, 265020, 265022, 65274620, 52645129, 33657109, 33657182, 18108370, 263972, 18108374, 264631, 52644332, 83373044, 18108385, 18108388, 56526486, 87168518, 264404, 60432113, 22279000, 264567

3018	11073891 (6035, 6036)	Novel Protein sim. GBank gij3218332 (AC004020) - Unknown gene product [Homo sapiens]		oncogene	264558 264589, 52844507, 18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278998, 22278999, 264259, 29331822, 29331824, 60432228, 29331827, 264808, 56182435, 265007, 265009, 60432229, 264593, 60433356, 55812038, 21906754, 87168474, 265011, 87168559, 265017, 265018, 265019, 264681, 18108351, 264448, 264682, 264683, 18108354, 264685, 264687, 264689, 21906766, 21906768, 21906769, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 52645129, 33657349, 264629, 65274781, 264634, 52644332, 56182323, 18108385, 87188518, 22279000, 22279002, 264563
3020	94318251 (6039, 6040)	Novel Protein sim. GBank gij3414809 (AF061529) - [Mus musculus]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	ATPase-associated	264488, 283994, 35696286, 264259, 264508, 264905, 264509, 264906, 264907, 264808, 264909, 264510, 264910, 60174538, 264600, 264603, 264760, 264762, 264682, 264783, 264784, 264288, 264369, 264768, 264687, 264688, 264769, 55811957, 35695917, 33657023, 264628, 35696423, 35695855, 264630, 264632, 264634, 264635, 264636, 264637, 264556, 264557, 264638, 264639, 83373044, 18108385, 264564, 264567, 264486
3021	80478512 (6041, 6042)	Novel Protein sim. GBank gij3880889[emb] (CAB09005) - (Z95559) cDNA EST yk236d4.5 comes from this gene; cDNA EST EMBL C13455 comes from this gene; cDNA EST yk329g6.5 comes from this gene; cDNA EST CEMSH45R comes from this gene [Caenorhabditis elegans]			264769, 264629, 264482
3022	87718500 (6043, 6044)			UNCLASSIFIED	264259, 29331826, 29331828, 264286, 264586
3023	95305484 (6045, 6046)	Novel Protein sim. GBank gij416592[sp]P32323[AGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR]	Contains protein domain (PF00614) - Phospholipase D. Active site motif	UNCLASSIFIED	264488, 22278995, 35696286, 22278997, 29331826, 35696052, 264807, 29331830, 52644045, 56182435, 60432229, 264592, 60433358, 60433438, 264689, 21906787, 55811957, 35695917, 265021, 18108376, 263978, 264635, 264558, 22279000
3024	86675305 (6047, 6048)			UNCLASSIFIED	60432049, 264760, 21906789, 55811957, 35695917, 264680, 264555, 264559
3025	85706629 (6049, 6050)	Novel Protein sim. GBank gij295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]			264593, 55811578

3026	87543662 (6051, 6052)	Novel Protein sim. GBank gjl3024052[sp]P97924[KARI_RAT] - KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10)		UNCLASSIFIED	22278996, 22278997, 264490, 29331825, 264111, 265007, 60170831, 265010, 87168559, 265019, 21906765, 29148627, 263987, 20281149, 20281089, 263975, 263977, 20281071, 58528486, 22279000
3027	94844563 (6053, 6054)	Novel Protein sim. GBank gjl4929647[gb]AAD3-084.1[AF151847] CGI-89 protein [Homo sapiens]	Contains protein domain (PF01529) - DHC zinc finger domain	UNCLASSIFIED	18108394, 22278995, 22278996, 35696286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 264907, 29331830, 264908, 264909, 264510, 265007, 265008, 265009, 264810, 33657402, 264596, 21906754, 265010, 265011, 87168559, 264600, 265018, 18108351, 264682, 264683, 264764, 264288, 264685, 264687, 264769, 264689, 21906765, 21906768, 21906767, 21906768, 21906769, 29148629, 35695917, 265020, 265021, 265022, 52644150, 264692, 33657023, 264693, 52645129, 33657109, 27486261, 18108374, 55811576, 35696423, 65274791, 264636, 264556, 264557, 264638, 60170394, 264639, 264558, 83373044, 18108385, 58528486, 22279000, 22279002
3028	94231997 (6055, 6056)	Novel Protein sim. GBank gjl3080521[emb]CAA186501 - (AL022599) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 29331824, 29331827, 35696052, 264908, 265007, 265008, 265009, 60170831, 21906754, 265011, 87168559, 265018, 264762, 264683, 264765, 264689, 21906765, 21906768, 21906769, 29148629, 35695917, 265021, 265022, 33657109, 27486265, 264628, 264629, 18108374, 35696423, 35695855, 264638, 60170394, 22279000, 22279002, 264482, 264564
3029	87619284 (6057, 6058)			UNCLASSIFIED	22278997, 22278999, 29331827, 264905, 264509, 264909, 264510, 264511, 264512, 87168474, 265019, 18108351, 21906768, 264534, 264890, 264893, 263969, 18108370, 264558, 22279000, 22279002, 264482
3030	87544928 (6059, 6060)	Novel Protein sim. GBank gjl3757726[emb]CAA187821 - (AL022727) dJ80119.1 (olfactory receptor-like protein (hs6M1-1)) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	Im7	
3031	91677953 (6061, 6062)	Novel Protein sim. GBank gjl4530587[gb]AAD22105.11 - (AF132000) TADA1 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 35696052, 264808, 265018, 21906765, 21906766, 21906767, 21906768, 265021, 263974, 18108374, 264558, 58528486, 22279000, 22279002

3032	84130124 (6063, 6064)	Novel Protein sim. GBank gi1019951 (U37429) - similar to M. musculus MER5 and other AHPC/TSA proteins [Caenorhabditis elegans]	Contains protein domain (PF00534) - Glycosyl transferases group 1	- synthase	22278996, 35696286, 264259, 28331824, 29331828, 264907, 29331830, 264758, 33109954, 87168474, 87168559, 285019, 264288, 21908769, 265021, 264683, 35696423, 35695855, 264636, 56182323, 83373044, 87168518
3033	95308321 (6065, 6066)	Novel Protein sim. GBank gi5031573(reiNP_005712.1)PACTR - ARP3 (actin-related protein 3, yeast) homolog	Contains protein domain (PF00022) - Actin	- struct	35696286, 264259, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265008, 264591, 21906754, 265010, 265019, 264681, 264369, 264768, 21906764, 21908768, 35695917, 33657023, 264628, 35695855, 264632, 264635, 264639, 264482, 264563
3034	80415373 (6067, 6068)			UNCLASSIFIED	264908, 264907, 264510, 264592, 265010, 264762, 264766, 264637, 264638, 264486, 264636
3035	91220692 (6069, 6070)	Novel Protein sim. GBank gi3738207(emb)CAA21262] - (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe]		UNCLASSIFIED	
3036	91718323 (6071, 6072)	Novel Protein sim. GBank gi728837(ispP39194)ALU7 - HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III		kinase	264907, 33657402, 265021
3037	95307434 (6073, 6074)	Novel Protein sim. GBank gi4406590(gb)AAD20040] - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]			265017
3038	95421807 (6075, 6076)	Novel Protein sim. GBank gi5360093(gb)AAD2865.1(AF155099) NY-REN 18 antigen [Homo sapiens]	Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	22278998, 22278997, 264259, 284905, 265007, 265009, 60433356, 21906754, 265018, 265019, 18108351, 264687, 21906765, 265020, 265021, 65274620, 27486262, 264636, 56182323, 18108365, 22278000
3039	87332257 (6077, 6078)	Novel Protein sim. GBank gi4757128(emb)CAB42094.1] - (AJ238717) ZRP protein [Rattus norvegicus]		UNCLASSIFIED	35696286, 29331828, 264109, 264110, 264511, 265007, 21906754, 265011, 264681, 264683, 264687, 21906768, 264691, 18108370, 263972, 264629, 18108374, 263977, 35696423, 264564, 18108391, 264692, 264558, 18108382, 18108385, 264587
3040	90933517 (6079, 6080)	Novel Protein sim. GBank gi4884278(emb)CAB43247.1] - (AL050037) hypothetical protein [Homo sapiens]			
3041	88312357 (6081, 6082)	Novel Protein sim. GBank gi3876073(emb)CAB04122.1] - (Z81505) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28025 comes from this gene; cDNA EST EMBL:D28024 comes from this gene; cDNA EST EMBL:D33210 comes from this gene; cDNA EST EMBL:D33441 comes from this gene		UNCLASSIFIED	56994075, 22278997, 22278998, 29331827, 33656970, 33109954, 21906754, 87168559, 264600, 264683, 21906765, 21906768, 22279002
3042	85748402 (6083, 6084)	Novel Protein sim. GBank gi790236 (U21156) - sarcolemmal associated protein-2 [Oryzias latipes]		glycoprotein	264636

3043	87773026 (6085, 6086)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	35686286, 60424289, 35686052, 264508, 264905, 66712502, 56182435, 55811386, 52644296, 55811150, 35695917, 60170615, 33657109, 18108374, 264634, 60431850
3044	87646182 (6087, 6088)	Novel Protein sim. GBank gi 4104922 (AF042276) - 0251 homolog [Pseudomonas putida]	Contains protein domain (PF01209) - ubiE/COQ5 methyltransferase family	glycoprotein		22278996, 22278998, 22278999, 29331824, 56182435, 264511, 265007, 60170831, 60432229, 60433356, 33109954, 18108351, 264288, 35695917, 18108368, 18108370, 60170394
3045	94127598 (6089, 6090)	Novel Protein sim. GBank gi 4589680 dbj BAA76859.1  - (AB023232) KIAA1015 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind		264488, 264259, 35686052, 264508, 264905, 264509, 264906, 264907, 264909, 264511, 265006, 264591, 264593, 33109954, 264604, 264764, 264683, 264288, 264766, 264768, 21906765, 21906768, 55811957, 35695917, 27486262, 18108370, 264628, 18108374, 35695855, 264630, 264632, 264635, 264563, 264564, 264566
3046	88088247 (6091, 6092)			UNCLASSIFIED		22278999, 26331822, 29331824, 29331825, 28331826, 60432289, 29331827, 28331828, 264906, 52646317, 55811957, 60432113, 22279000, 22279002, 264482, 264564
3047	95089924 (6093, 6094)			UNCLASSIFIED		264488, 22278996, 22278997, 22278999, 29331824, 29331825, 56182435, 264511, 265008, 265009, 265011, 265017, 264766, 21906768, 21906769, 35695917, 52644150, 33657349, 65274791, 35695855, 264555, 60432113, 22279000, 264566
3048	87629419 (6095, 6096)	Novel Protein sim. GBank gi 4588034 gb AAD25962.1 AF092878 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED		264102, 29148784
3049	88229955 (6097, 6098)	Novel Protein sim. GBank gi 5454158 ref NP_006286.1 pVARS - valyi-IRNA synthetase 1	Contains protein domain (PF01406) - IRNA synthetases class I (C)	UNCLASSIFIED		22278997, 28331826, 264907, 264758, 87168559, 265018, 264448, 21906766, 265020, 33657109, 35695855, 60432113, 22279000
3050	87643679 (6098, 6100)	Novel Protein sim. GBank gi 4589642 dbj BAA76843.1  - (AB023216) KIAA0999 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase		264259, 29331825, 264909, 265007, 264512, 265019, 264288, 21906766, 265020, 264693, 18108365, 56526486, 87168518, 22279002, 264566
3051	87750599 (6101, 6102)					22278997, 264595, 265019, 284288, 264693, 87168518
3052	57108030 (6103, 6104)	Novel Protein sim. GBank gi 117528 sp P14755 CRYL_RABIT - LAMBDA-CRYSTALLIN		dehydrogenase		264534

3053	95350373 (6105, 6106)	Novel Protein sim. GBank gll3947613[emb]CAA19465.1] - (AL023828) cDNA EST EMBL:M89008 comes from this gene; cDNA EST YK282d3.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56181686, 22278995, 35696286, 22278998, 264259, 60432289, 265008, 265009, 60433438, 21906754, 265010, 87168559, 264603, 265018, 265019, 264763, 264764, 264288, 21906765, 21906766, 21906768, 21906769, 35695917, 18108374, 35696423, 264636, 56182323, 22279000, 264563
3054	86943510 (6107, 6108)	Novel Protein sim. GBank gll1076211[prj]S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	35696286, 35696052, 28331830, 264908, 264909, 264512, 264910, 265017, 264604, 264766, 265020, 33657109, 264628, 35695855, 264638, 264564, 264566, 264486, 60424178, 65274572, 56182375, 35696286, 60424269, 60432289, 60432049, 264259, 22278998, 22278999, 60432049, 264259, 265008, 265009, 60170831, 60432229, 60431735, 60433356, 264584, 60433438, 21906754, 55811386, 265011, 87168559, 265019, 18108351, 264683, 264288, 264369, 264689, 21906768, 55811957, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 60431528, 18108374, 55810784, 55811576, 35696423, 65274791, 264636, 60431850, 18108381, 56182323, 60170394, 18108385, 60432113, 264564, 264565, 264566
3055	95350537 (6109, 6110)	Novel Protein sim. GBank gll4680855[gb]AAD27717.1[AF13294] CGI-08 protein [Homo sapiens]		transport	284488, 264569, 18108394, 52646842, 22278997, 22278998, 22278999, 264259, 66714117, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 264512, 265007, 265008, 265009, 264910, 33657402, 55812038, 264596, 264758, 265010, 265011, 265017, 265019, 264760, 18108351, 264762, 264763, 264764, 264288, 264766, 264687, 18108357, 264768, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264691, 264693, 33657109, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 18108381, 83373044, 18108385, 22278900, 22279002, 264583, 264584, 264565, 264566, 264488, 264567
3056	91661636 (6111, 6112)	Novel Protein sim. GBank gll728837[sp]P39184[ALU7_SQ WARNING ENTRY IIII]		glycoprotein	284488, 264569, 18108394, 52646842, 22278997, 22278998, 22278999, 264259, 66714117, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 264512, 265007, 265008, 265009, 264910, 33657402, 55812038, 264596, 264758, 265010, 265011, 265017, 265019, 264760, 18108351, 264762, 264763, 264764, 264288, 264766, 264687, 18108357, 264768, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264691, 264693, 33657109, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 18108381, 83373044, 18108385, 22278900, 22279002, 264583, 264584, 264565, 264566, 264488, 264567



3057	95412746 (6113, 6114)	Novel Protein sim. GBank gi 3878119 emb CAA88860  - (Z49068) similar to GTP-binding protein; cDNA EST EMBL: M89111 comes from this gene; cDNA EST EMBL: D27709 comes from this gene; cDNA EST EMBL: D27708 comes from this gene; cDNA EST EMBL: D73788 comes from this gene; cDNA EST yk353....		sinucl	264508, 264905, 264907, 264908, 264909, 264510, 264512, 264910, 264592, 264594, 264767, 18108374, 264635, 264555, 264637, 264639, 264563, 264564, 264565, 264486
3058	78646226 (6115, 6116)			UNCLASSIFIED	264683
3059	87629425 (6117, 6118)	Novel Protein sim. GBank gi 4588034 gb AAD25982.1 AF092878  zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264490, 264259, 29331824, 29331825, 29331827, 35896052, 29331828, 265007, 60433438, 265017, 265018, 265019, 264681, 264448, 264288, 264768, 21906765, 21906766, 21906787, 21906789, 29148629, 29148784, 265022, 52644150, 18108370, 264636, 18108385, 264563, 264567
3060	79346691 (6119, 6120)			UNCLASSIFIED	264567
3061	87740964 (6121, 6122)			UNCLASSIFIED	264112, 52644296, 21906768, 33657023, 263974, 18108385
3062	87619465 (6123, 6124)	Novel Protein sim. GBank gi 4454690 gb AAD20963  - (AF070857) glutathione S-transferase subunit 13 homolog [Homo sapiens]		transferase	264908, 265008, 18108351, 264566
3063	80078023 (6125, 6126)	Novel Protein sim. GBank gi 2246532 U03872  - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	18108359, 264558
3064	91241526 (6127, 6128)	Novel Protein sim. GBank gi 4240315 db JBAAT4936.1  - (AB020720) KIAA0813 protein [Homo sapiens]	Contains protein domain (PF00403) - Heavy-metal-associated domain	UNCLASSIFIED	52646365, 52646842, 65274572, 56182575, 58181886, 22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 66714117, 264508, 264907, 264908, 56182435, 265009, 60432229, 60433438, 55812038, 52644296, 265018, 264682, 264288, 264686, 264768, 264687, 52644229, 264689, 21906768, 264691, 264692, 264693, 18108370, 18108377, 55811576, 264636, 56182323, 264558, 264639, 18108385, 22279000, 22279002
3065	91639201 (6129, 6130)	Novel Protein sim. GBank gi 5656743 gb AAD45960.1 AC00506 - (AC005067) Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and gensecan [Homo sapiens]		UNCLASSIFIED	22278996, 22278998, 264093, 264094, 264095, 29331824, 60424269, 66714117, 264100, 264907, 265007, 264591, 60432229, 264593, 265011, 265019, 18108351, 264766, 264767, 21906765, 21906768, 264693, 20281069, 22279000, 22279002, 264482, 264568, 264567

3066	91224437 (6131, 6132)	Novel Protein sim. GBank gl 488426 emb CA43245.1  - (AL050028) hypothetical protein [Homo sapiens]	UNCLASSIFIED	18108397, 22278995, 56994075, 22278998, 284905, 68712502, 285008, 284512, 284910, 284758, 60174639, 284760, 18108351, 284784, 284683, 18108359, 284692, 18108384, 18108368, 18108370, 18108377, 18108379, 60170394, 284567
3067	95422551 (6133, 6134)	Novel Protein sim. GBank gl 4689258 gb AAD27832.1 AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]	Contains protein domain (PF00787) - struct PX domain	284488, 284489, 35686286, 22278998, 56994075, 284259, 28331822, 29331825, 3569052, 29331828, 284508, 284905, 284509, 284908, 284807, 284908, 284909, 284112, 284510, 284511, 284512, 285008, 285009, 284910, 284591, 284592, 284593, 284594, 284757, 284595, 284598, 284758, 285010, 285011, 87168559, 284601, 284602, 284603, 284604, 284605, 285019, 284780, 284762, 284448, 284763, 284764, 284288, 284369, 284766, 284768, 284687, 284769, 284689, 21908765, 21908767, 21908768, 35695917, 265020, 265021, 264534, 52644150, 284691, 33657023, 284693, 284628, 60431528, 283977, 35695855, 284630, 284631, 284634, 284635, 284636, 284637, 284638, 284639, 83373044, 56526486, 87168518, 22278900, 22279002, 284563, 284483, 284564, 284565, 284566, 284587, 284488
3068	85360851 (6135, 6136)	Novel Protein sim. GBank gl 3878119 emb CAA88860  - (Z49068) similar to GTP-binding protein; cDNA EST	Contains protein domain (PF01926) - struct GTPase of unknown function	22278996, 56994075, 22278998, 22278999, 284258, 284107, 284905, 29331830, 52644045, 284110, 60170831, 284592, 284594, 33657402, 21908754, 33109954, 87168474, 87168559, 285017, 284448, 284784, 284683, 284768, 52644229, 21908765, 21908768, 21908769, 60170615, 33657023, 18108370, 18108376, 284634, 284557, 60170394, 56182323, 18108385, 87168518, 22278900, 284482
3069	95412763 (6137, 6138)	Novel Protein sim. GBank gl 3878119 emb CAA88860  - (Z49068) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...		

3070	94318173 (6139, 6140)	Novel Protein sim. GBank gij387778[emb]CAB055271 - (283110) cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST yk472b5.5 comes from this gene; cDNA EST yk468c10.3 comes from this gene; cDNA EST yk468c10.5 comes from this gene; cDNA EST EM...		synthase	264488, 22278994, 22278995, 22278996, 36994075, 22278997, 22278999, 264239, 29331822, 29147620, 29331824, 66714117, 29331826, 29146498, 29146499, 66712502, 29331830, 52644045, 56182435, 264511, 265007, 264512, 264910, 60170831, 264592, 264758, 33109954, 21906754, 87168474, 265018, 18108351, 264448, 264683, 264288, 52644229, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 264691, 33657023, 27486261, 27486264, 264628, 18108370, 18108377, 55811576, 35695955, 264634, 264635, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 18108387, 56526486, 264404, 264563, 264566
3071	94325573 (6141, 6142)	Novel Protein sim. GBank gij4502425[ref]NP_001709.1[pBMP6 - bone morphogenetic protein 6 precursor	Contains protein domain (PF00085) - lgr Thioedoxin		264488, 65274572, 18108398, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 66714117, 29331826, 35696052, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 52644045, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432229, 264592, 60433356, 33657402, 60433438, 33109954, 52644296, 87168474, 265010, 265017, 264681, 264288, 264685, 264766, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 263971, 18108374, 18108377, 35696423, 55811576, 65274791, 35695955, 264630, 264635, 264636, 264557, 60170394, 83373044, 60432113, 22279000, 22279002, 264563, 264564, 264565, 264566, 264567
3072	95115892 (6143, 6144)	Novel Protein sim. GBank gij1263289 (U47856) - fibroin-4 [Araneus diadematus]		transcriptiactor	56182575, 28331822, 29331824, 29331825, 29146498, 264908, 52644045, 56182435, 265009, 60433438, 55812038, 18108351, 264683, 264369, 52644229, 52644150, 33657023, 264693, 33657109, 18108374, 55811576, 65274791, 284555, 56182323, 60432113, 264564

3073	86147248 (6145, 6146)	Novel Protein sim. GBank gi134640 sp P22528 CORB_HUMAN - CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULLIN)		UNCLASSIFIED	264769	
3074	88089351 (6147, 6148)	Novel Protein sim. GBank gi13419847 (AC004982) - similar to yeast hypothetical protein ybk4; similar to P38164 (P1D:g586463) [Homo sapiens]		UNCLASSIFIED	264488, 265019, 264448, 264288, 21906787, 264693, 18108388, 18108370, 18108374, 264567	
3075	88095752 (6149, 6150)	Novel Protein sim. GBank gi14557349 ref NP_000456.1 pBARD - BRCA1 associated RING domain 1	Contains protein domain (PF00023) - Ank repeat	homeobox	264509, 264907, 264689, 264693, 36526488	
3076	87819219 (6151, 6152)			UNCLASSIFIED	18108398, 29331822, 29331827, 60432228, 285017, 284691, 284693	
3077	88734277 (6153, 6154)	Novel Protein sim. GBank gi13023956 sp Q00808 HET1_PODAN - VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	65274572, 35696052, 264511, 60170831, 87168474, 284389, 35695917, 33657182, 27486284, 33657349, 35695783, 35695855, 264639	
3078	88089355 (6155, 6156)	Novel Protein sim. GBank gi13500850 (AC004994) - similar to KIAA0600; similar to d1026456 (P1D:g3043724) [Homo sapiens]			22279002	
3079	87821893 (6157, 6158)	Novel Protein sim. GBank gi13875410 emb CA802876  - (Z81052) Similarity to Yeast ABC1P protein (SW:ABC1_YEAST); cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5 comes from this gene [Caenorhabditis elegans]		transport	29331824, 29331826, 264758, 55811386, 265017, 55811150, 52644228, 21908788, 265020, 265021, 264693, 18108376, 264631, 52644332, 22279002	
3080	93298274 (6159, 6160)	Novel Protein sim. GBank gi15257221 gb AAD41265.1  - (AF117887) protein arginine methyltransferase [Mus musculus]		interferon	264488, 52644507, 22278998, 22278998, 264490, 264259, 29331824, 66714117, 29331825, 29331828, 29331827, 29331828, 29146499, 264508, 264905, 264828, 52644045, 58182435, 265006, 264591, 264596, 21908754, 60174639, 265010, 264882, 264448, 264763, 264683, 264784, 264288, 264685, 264769, 264688, 264689, 21906765, 21906767, 21908769, 55811957, 35695917, 265020, 60170615, 52644150, 264692, 33657023, 264693, 65274620, 33657109, 27486261, 35695763, 264628, 18108370, 65274791, 264558, 56182323, 60170394, 264482, 264565, 264484	
3081	88094864 (6161, 6162)	Novel Protein sim. GBank gi1728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	18108398, 264509, 284905, 284906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264595, 264758, 265011, 265018, 264760, 264761, 264763, 284764, 18108354, 284685, 264766, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264555, 264638, 18108382, 18108385, 264583, 264565, 264568	
3082	80310121 (6163, 6164)				264764, 55811957, 264555, 264584	

3083	88095756 (6165, 6166)	Novel Protein sim. GBank gi 868241 (U29488) - C56C10.3 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264259, 29331824, 264106, 265008, 264591, 264592, 21906754, 264288, 264787, 21906768, 21906769, 29148784, 264691, 264632, 22279000
3084	87448568 (6167, 6168)	Novel Protein sim. GBank gi 476774 ipr A37475 - probable structural component p38 - borna disease virus			22278995, 60432289, 35696052, 264905, 264906, 264907, 264908, 264909, 265006, 265007, 264910, 264593, 264595, 264758, 264389, 264288, 264766, 35695917, 265020, 18108374, 35696423, 264631, 264556, 264565, 264566, 264567, 264486, 265011, 264681
3085	87795781 (6169, 6170)	Novel Protein sim. GBank gi 2565057 (U80741) - CAGH44 [Homo sapiens]		UNCLASSIFIED	
3086	87769942 (6171, 6172)	Novel Protein sim. GBank gi 3894189 (AC005662) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	22278998, 264092, 264259, 29331822, 29331825, 264108, 264112, 18108351, 264687, 263987, 263974, 55810764, 263981, 18108385, 284487
3087	67462988 (6173, 6174)				52846365, 56994075, 22278997, 22278998, 29331824, 29331825, 35696052, 60433438, 33109954, 21906754, 52846317, 265017, 264682, 264369, 264684, 21906767, 21906768, 265020, 264691, 33657023, 33657109, 52645129, 33657182, 27486262, 35695855, 87168518
3088	91224441 (6175, 6176)	Novel Protein sim. GBank gi 3355304 (AF001549) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264591
3089	95361242 (6177, 6178)	Novel Protein sim. GBank gi 4689146 JAAAD27782.1 AF077049 lambda-crystallin [Homo sapiens]	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	dehydrogenase	18108397, 65274572, 56182575, 56181886, 56994075, 35696288, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 29331828, 264907, 29331830, 264909, 56182435, 264510, 265007, 60170831, 60432228, 21906754, 55811386, 285017, 265018, 265019, 284760, 55811150, 284288, 264766, 56181562, 21906765, 21906766, 21906767, 21906768, 265021, 60170815, 27486262, 18108370, 60431528, 35696423, 264558, 264559, 60432113, 284488

3080	95342371 (6178, 6180)	Novel Protein sim. GBank gi 1354050 (U47024) - MEM3 [Mus musculus]	UNCLASSIFIED	60424170, 52845156, 65274572, 56182575, 56181886, 22278995, 35696286, 56984075, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264908, 264908, 52644045, 264828, 265006, 265007, 265008, 60170831, 60432229, 60433356, 33657402, 55812038, 264756, 21908754, 33109954, 52646317, 55811386, 52644296, 87188474, 265011, 87168558, 265017, 265018, 265019, 55811150, 18108351, 284681, 264448, 264288, 264369, 18108357, 264768, 52644228, 56181562, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265022, 60170815, 264680, 52644150, 264691, 33657023, 18108365, 65274620, 33657109, 18108368, 33657182, 27486261, 27486265, 35695763, 18108374, 18108376, 55810764, 35696423, 55811576, 65274791, 35695855, 264557, 56182323, 83373044, 18108387, 18108388, 87168516, 22278000, 22278002, 264563, 264482
3091	95317424 (6181, 6182)	Novel Protein sim. GBank gi 3873932 emb CAB01859  - (Z79596) Similarity to Bovine aspartyl beta hydroxylase (Tr:G162694); cDNA EST EMBL:D27916 comes from this gene; cDNA EST EMBL:D27915 comes from this gene; cDNA EST EMBL:D64881 comes from this gene; cDNA EST EMBL:D68139 comes f...	UNCLASSIFIED	35696286, 29331822, 35696052, 264508, 264509, 264805, 264908, 264808, 264809, 264510, 264758, 265010, 265011, 264683, 264685, 264766, 264768, 264769, 264693, 264628, 35698423, 35695855, 264632, 264635, 264639, 264482, 264583, 264486

3092	95314592 (6183, 6184)	Novel Protein sim. GBank gii1710756 sp P15880 RS2_HUMAN - 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	264488, 60424179, 18108396, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 29148498, 29148499, 264508, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264113, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170831, 264591, 264592, 60431735, 264593, 264594, 60433438, 264595, 264758, 21906754, 265010, 265011, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 265019, 264760, 264762, 264681, 18108351, 264763, 264682, 264448, 264764, 264683, 264288, 264369, 264765, 264766, 264686, 264767, 264687, 264768, 264769, 264688, 21906764, 264689, 21906765, 21906766, 21905787, 21906788, 21906769, 29148629, 29148784, 35695917, 265020, 265021, 264534, 60170615, 264690, 264691, 264692, 65274620, 33657109, 27486262, 264628, 264629, 18108374, 263978, 18108377, 35696423, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264557, 264558, 264639, 60170394, 18108385, 264259, 29331824, 35696052, 264905, 265006, 60432229, 60431735, 264684, 264369, 264288, 264766, 21906767, 35696423, 83373044, 18108385
3093	94316457 (6185, 6186)	Novel Protein sim. GBank gii5002587 emb CAB44347.1 - (Y17454) LSR1 protein [Homo sapiens]		UNCLASSIFIED	
3094	94316675 (6187, 6188)	Novel Protein sim. GBank gii400734 sp P31044 PBP_RAT - PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (23 KD MORPHINE-BINDING PROTEIN) (P23K)	Contains protein domain (PF01161) - Phosphatidylethanolamine-binding protein	collagen	18108398, 264259, 60432289, 29331827, 264511, 264763, 264288, 264767, 265022, 264691, 264693, 65274791, 56182323, 264584, 264565

3095	94848182 (6189, 6190)	Novel Protein sim. GBank gij487759gbjAAD31421.1 AF12444 - (AF12444) MAGE tumor antigen D1 [Homo sapiens]	Contains protein domain (PF01454) - MAGE family	UNCLASSIFIED	18108397, 56182575, 22278995, 35696286, 56994075, 22278997, 22278999, 264259, 60432049, 66714117, 29331825, 60432289, 35696052, 33656970, 29148499, 264508, 264905, 264508, 29331830, 264809, 264510, 264511, 264512, 265007, 265008, 265009, 60170831, 264756, 21906754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264750, 264681, 264682, 264683, 264764, 284369, 284288, 284686, 284788, 264769, 264689, 21906765, 21906766, 21906767, 55811957, 35695917, 265020, 265021, 265022, 52644150, 284691, 284692, 33657023, 264693, 263972, 18108376, 55811576, 35696423, 284952, 60170394, 264639, 83373044, 18108387, 65274727, 87168518, 60432113, 264482, 264563, 284564, 284588, 264487, 18108391, 22278995, 22278996, 22278997, 22278999, 29331824, 29331825, 29331826, 29331827, 33656970, 264905, 264908, 265008, 264910, 33657402, 265011, 265017, 265018, 264369, 21906768, 21906767, 21906768, 35695917, 265020, 60170815, 284691, 284692, 284693, 27486261, 27486262, 18108370, 60431528, 264634, 264636, 264639, 22279000, 264588, 264488, 29331822, 29331825, 60432289, 29331826, 35696052, 29331828, 29331830, 264594, 55812038, 33109954, 33657084, 87168474, 87168559, 52644229, 21906765, 21906767, 18108376, 35696423, 52644332, 264638, 60432113, 22279002, 264634, 264637, 264565
3096	87756128 (6191, 6192)	Novel Protein sim. GBank gij3882221dbjBAA34470.1  - (AB018293) KIAA0750 protein [Homo sapiens]	Contains protein domain (PF00307) - Calponin homology (CH) domain	struct	29331824, 29331825, 29331826, 29331827, 33656970, 264905, 264908, 265008, 264910, 33657402, 265011, 265017, 265018, 264369, 21906768, 21906767, 21906768, 35695917, 265020, 60170815, 284691, 284692, 284693, 27486261, 27486262, 18108370, 60431528, 264634, 264636, 264639, 22279000, 264588, 264488, 29331822, 29331825, 60432289, 29331826, 35696052, 29331828, 29331830, 264594, 55812038, 33109954, 33657084, 87168474, 87168559, 52644229, 21906765, 21906767, 18108376, 35696423, 52644332, 264638, 60432113, 22279002, 264634, 264637, 264565
3097	88264895 (6193, 6194)	Novel Protein sim. GBank gij4468288jmbjCAB37981  - (AL022395) dJ273N12.1 (PUTATIVE protein based on EST matches) [Homo sapiens]	Contains protein domain (PF00846) - F-box domain.	UNCLASSIFIED	29331824, 29331825, 29331826, 29331827, 33656970, 264905, 264908, 265008, 264910, 33657402, 265011, 265017, 265018, 264369, 21906768, 21906767, 21906768, 35695917, 265020, 60170815, 284691, 284692, 284693, 27486261, 27486262, 18108370, 60431528, 264634, 264636, 264639, 22279000, 264588, 264488, 29331822, 29331825, 60432289, 29331826, 35696052, 29331828, 29331830, 264594, 55812038, 33109954, 33657084, 87168474, 87168559, 52644229, 21906765, 21906767, 18108376, 35696423, 52644332, 264638, 60432113, 22279002, 264634, 264637, 264565
3098	80258024 (6195, 6196)	Novel Protein sim. GBank gij303603dbjBAA02145.1  - (D12621) cytochrome P-450 TBV [Homo sapiens]			264488, 35696286, 29331822, 29331824, 29331825, 29331827, 265007, 265008, 265010, 265011, 265018, 265019, 18108357, 21906768, 265020, 265022, 55811576, 56182323, 22279002, 264563
3099	91243325 (6197, 6198)	Novel Protein sim. GBank gij1083764 pirjB48013 - proline- rich proteoglycan 2 precursor, parotid - rat			29331825, 60432289, 35696052, 264910, 60432229, 264592, 284288, 284693, 283967, 264635
3100	87602421 (6199, 6200)			UNCLASSIFIED	
3101	79602134 (6201, 6202)			UNCLASSIFIED	264908, 284693, 264628, 264630, 264632



3102	91220892 (6203, 6204)	Novel Protein sim. GBank gi 5305705 gb AAD41781.1 AF12853 - (AF128536) cytoplasmic phosphoprotein PACSIN2 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	struct	35696286, 22278996, 22278999, 29331827, 35696052, 264909, 264512, 265008, 60170831, 60433356, 33109954, 18108351, 264684, 264689, 21906767, 60170815, 264692, 33657023, 264638, 22279000, 264482, 264564 35695917, 264565
3103	90938004 (6205, 6206)	Novel Protein sim. GBank gi 464564 sp P35292 RB17_MOUSE - RAS-RELATED PROTEIN RAB-17		UNCLASSIFIED	
3104	87340833 (6207, 6208)	Novel Protein sim. GBank gi 5032207 ref NP_005696.1 pTSSC - tumor-suppressing STF cDNA 6		UNCLASSIFIED	264259, 264684, 264532, 33657182, 264558
3105	94148603 (6209, 6210)				22278997, 264259, 29331824, 35696052, 29331828, 264508, 264509, 264905, 264908, 264907, 264908, 264511, 264910, 264591, 264594, 264758, 264760, 264681, 264762, 264764, 264288, 264766, 264768, 264687, 264769, 21906766, 21906768, 35695917, 33657023, 264692, 264693, 264628, 264629, 35695855, 264630, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 83373044, 264404, 22279002, 264563, 264565, 264566, 264486, 264567
3106	95361416 (6211, 6212)	Novel Protein sim. GBank gi 1938574 (U97190) - B0025.2 gene product [Caenorhabditis elegans]			22278996, 22278997, 22278998, 22278999, 264092, 264093, 264094, 29331822, 264905, 264907, 264908, 52644045, 56182435, 264112, 265008, 265009, 55812038, 265017, 285018, 264683, 264686, 264687, 264768, 52644229, 21906765, 21906768, 21906769, 55811957, 265020, 265022, 264690, 52644150, 264692, 264693, 18108370, 18108377, 55811576, 56182323, 18108385, 18108388, 22279000, 264563
3107	95343272 (6213, 6214)	Novel Protein sim. GBank gi 3341441 emb CAA76851  - (Y17794) winged-helix transcription factor [Gallus gallus]			22278995, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 264259, 29331822, 29331825, 29331826, 60432289, 29331827, 29331828, 33656970, 264105, 264512, 265009, 60433356, 60433438, 265011, 265017, 265018, 21906765, 21906768, 21906767, 21906769, 265021, 264691, 33657109, 27486261, 27486265, 18108370, 263972, 18108374, 55811576, 18108385, 56526486, 264482, 264487
3108	87340635 (6215, 6216)	Novel Protein sim. GBank gi 5032207 ref NP_005696.1 pTSSC - tumor-suppressing STF cDNA 6		UNCLASSIFIED	56182435, 264288, 264690, 264564

3109	94318461 (6217, 6218)	Novel Protein sim. GBank gl5002587[emb CAB44347.1] - (Y17454) LSFR1 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	Struct	264480, 264908, 265007, 264910, 264593, 264683, 264684, 264687, 21908767, 21906768, 264693, 18108370, 264629, 18108374, 264632, 264638, 22279000
3110	95080716 (6218, 6220)	Novel Protein sim. GBank gl1076211[pir S50755] - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	264488, 65274572, 22278995, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264908, 264510, 265006, 265007, 265008, 265009, 60432229, 33857402, 60433356, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264288, 264389, 21906766, 21906767, 21908768, 265020, 60170615, 264693, 65274620, 18108370, 264639, 18108384, 22279000, 264563, 18108390
3111	87754512 (6221, 6222)	Novel Protein sim. GBank gl3282231 (U75454) - C2H2 type zinc finger protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	264488, 18108398, 66712502, 265017, 265018, 265019, 264448, 21908767, 265020, 33857023, 18108385, 18108388, 35686423, 52644332, 18108385, 18108388
3112	88043639 (6223, 6224)	Novel Protein sim. GBank gl3900848 (AC005023) - match to EST AA361117 (NID:92013436) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	
3113	88207098 (6225, 6226)	Novel Protein sim. GBank gl2459910 (AF005856) - anon2A5 [Drosophila yakuba]		im7	18108397, 22278999, 264259, 29331824, 35686052, 264907, 264757, 60433438, 87168559, 264763, 264448, 18108354, 264288, 21908767, 21908769, 35695917, 264690, 264691, 264692, 264693, 18108365, 18108381, 18108384, 18108385, 18108388, 87168518, 22279000, 22279002
3114	79843167 (6227, 6228)	Novel Protein sim. GBank gl4966270[gb AA52261.2] - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh). Score=57.4, E-value=1.7e-18, N=2; contains similarity to Pfam domain PF00702 (hydrolase). Score=57.4, E-value=1e-13, N=1 [C...	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	hydrolase	
3115	94117898 (6229, 6230)	Novel Protein sim. GBank gl5032225[ref NP_005676.1]pWBSC - Williams-Beuren syndrome chromosome region 11		transcript factor	60424179, 56182575, 264259, 29331824, 60424269, 29331826, 66712502, 264510, 265007, 60431735, 60433356, 55612038, 55811388, 265019, 264288, 264689, 21908769, 264691, 33657023, 264693, 60431528, 263974, 80431850, 56182323, 264559, 22279000, 22279002
3116	79842855 (6231, 6232)			UNCLASSIFIED	264905, 264758, 21908764, 264690
3117	87711288 (6233, 6234)			UNCLASSIFIED	264510, 265011, 18108351, 264288, 264689, 264691, 18108368, 18108372, 263981, 264558, 264564

3118	94665848 (6235, 6236)	Novel Protein sim. GBank gj3880563[emb]CAB01444.11 - (Z78018) predicted using GeneFinder; similar to serine/threonine kinase; cDNA EST yk353310.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00008) - EGF-like domain	Ig1	52645156, 52646842, 65274572, 56182575, 22278995, 56994075, 22278996, 35698286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 264905, 264908, 29331830, 52644045, 56182435, 264510, 264511, 265007, 285008, 265009, 264757, 52646317, 21906754, 33657084, 52644298, 87168474, 87168559, 265017, 265018, 264805, 265019, 264762, 284448, 264882, 264884, 264288, 264766, 56181562, 21906765, 21906766, 21906768, 21906769, 265020, 265022, 264690, 52644150, 264691, 33657023, 264693, 33657109, 33657349, 264628, 18108370, 60431528, 18108374, 35698423, 65274791, 60170394, 83373044, 87168518, 22279000, 22279002, 264486, 265006, 264288
3119	85728786 (6237, 6238)		Contains protein domain (PF00328) - Histidine acid phosphatase		
3120	87344040 (6239, 6240)	Novel Protein sim. GBank gj5019819[gb]/AAD37863.1/AF14315 - (AF143152) putative NADH oxidoreductase complex I subunit [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264509, 264510, 264511, 264512, 264288, 264486
3121	94110735 (6241, 6242)	Novel Protein sim. GBank gj4501877[ref]NP_001088.1/pACRI - acrosin			52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278996, 22278999, 264259, 29331824, 29331827, 35696052, 52644045, 265008, 52646317, 87168474, 87168559, 21906765, 52644150, 33657023, 18108374, 264637
3122	11814528 (6243, 6244)			UNCLASSIFIED	264638
3123	88083003 (6245, 6246)	Novel Protein sim. GBank gj2439517 (AC002563) - putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860) [Homo sapiens]	Contains protein domain (PF00780) - CNH domain	kinase	18108392, 29331822, 29331824, 29331825, 264905, 265007, 55812038, 265019, 18108351, 264682, 264288, 264766, 21906764, 21906765, 21906768, 21906769, 55811957, 18108365, 18108366, 27486265, 18108374, 18108381, 18108384, 22279000, 22279002, 264482
3124	87788899 (6247, 6248)			UNCLASSIFIED	264905
3125	91216607 (6249, 6250)	Novel Protein sim. GBank gj4980826[gb]/AAD35412.1/AE00171 - (AE001714) oxidoreductase, short chain dehydrogenase/reductase family [Thermotoga maritima]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	56181686, 264259, 66714117, 60432289, 29331828, 29331827, 264907, 264908, 264828, 265009, 60433356, 33657402, 60433438, 264758, 18108351, 264288, 29148627, 25148628, 33657023, 33657109, 18108382, 56526488

3126	95337205 (6251, 6252)			UNCLASSIFIED	22278999, 264490, 264259, 60432049, 29331822, 60432289, 29148498, 52644045, 56182435, 285009, 60433438, 265010, 87168559, 265017, 265018, 55811150, 264763, 264883, 264389, 264686, 29148629, 33657023, 264893, 33657109, 18108374, 55811576, 18108385, 60432113, 22279002, 35686286, 22278986, 22278989, 28331828, 264908, 60433438, 87168559, 264604, 21908765, 21908769, 33657023, 33657349, 264629, 18108374, 18108377, 22279000, 22279002
3127	91639233 (6253, 6254)	Novel Protein sim. GBank gi 2828280 emb CAA16694.1  - (AL021687) putative protein [Arabidopsis thaliana]			
3128	87874330 (6255, 6256)	Novel Protein sim. GBank gi 3885828 (AF090133) - lin-7-A (Rattus norvegicus)	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	misc_channel	22278996, 264259, 52644045, 265008, 21908754, 265017, 265018, 21908768, 18108376, 18108387, 22279000, 22279002
3129	87755412 (6257, 6258)	Novel Protein sim. GBank gi 3135273 (AC003058) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	56182575, 284259, 29331825, 29331828, 52644045, 56182435, 60433358, 264600, 264682, 264763, 264764, 264369, 264280, 264686, 55811957, 264692, 33657023, 33657109, 60432113, 264564, 264568, 264636
3130	14993860 (6259, 6260)	Novel Protein sim. GBank gi 3329465 (AF084553) - NSD1 protein [Mus musculus]			
3131	95351469 (6261, 6262)	Novel Protein sim. GBank gi 1848277 (U86136) - telomerase-associated protein TP-1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	56182575, 284259, 29331824, 264807, 56182435, 264594, 60433438, 55812038, 33109954, 21908754, 33657084, 87168474, 264448, 264766, 21908769, 55811957, 265020, 265021, 265022, 60170615, 33657023, 33657109, 33657182, 27466261, 33657349, 65274791, 60170394, 56182323, 83373044, 87168518, 264584

3132	95415459 (6263, 6264)	Novel Protein sim. GBank gi 4680647 gb AAD27713.1 AF13293 - (AF13293) CGI-03 protein [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	ubiquitin	5264507, 5264684, 52646365, 65274572, 56182575, 22278994, 22278995, 35696286, 55994075, 22278996, 22278997, 22278998, 22278999, 60432048, 52645080, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 52644045, 56182435, 264910, 60170831, 60432229, 60433356, 33657402, 55812038, 52646317, 21906754, 52644296, 85658542, 87168559, 265017, 265018, 265019, 264448, 264288, 264389, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 264692, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 18108374, 18108376, 55811576, 35695855, 18108385, 18108387, 56526466, 87168518, 60432113, 22279002
3133	87379414 (6265, 6266)	Novel Protein sim. GBank gi 4507613 ref NP_003738.1 pTNKS - TANKYRASE		polymerase	22278994, 22278998, 264905, 265006, 265007, 87168559, 264760, 21906767, 18108374, 22279000, 22279002, 284563 264595, 264369, 284685, 284628, 264566
3134	94649816 (6267, 6268)	Novel Protein sim. GBank gi 1729827 sp P54633 ITALA_DICDI - FILOPODIN (TALIN HOMOLOG)			
3135	86389358 (6269, 6270)	Novel Protein sim. GBank gi 3093478 (AF012927) - fibrinogen-binding protein [Streptococcus equi]		struct	22278996, 264095, 29331826, 33657402, 18108348, 263974
3136	94845839 (6271, 6272)	Novel Protein sim. GBank gi 627101 pir S44092 - probable carrier protein c2 - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	22278998, 264259, 264828, 265006, 265008, 60433438, 265019, 264764, 284288, 264769, 264689, 265020, 27486262, 263972, 65274791, 264557, 264558
3137	88257947 (6273, 6274)	Novel Protein sim. GBank gi 3342730 (AC005331) - R31341_1 [Homo sapiens]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264510, 265008, 21906754, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264682, 264768, 21906765, 21906766, 21906767, 21906769, 55811857, 35695917, 265020, 265021, 52644150, 18108370, 18108374, 22279000, 22279002, 264482, 264486

3138	94130186 (6275, 6276)	Novel Protein sim. GBank gll4406759jbb[AA020070] - (AC006836) hypothetical protein [Arabidopsis thaliana]			264559, 264488, 264907, 264511, 264593, 33109954, 87188559, 284881, 284884, 264685, 264686, 264687, 264788, 264688, 264689, 264691, 264692, 264693, 33657109, 284631, 284634, 284635, 284636, 284637, 60170394, 83373044, 18108385, 18108388, 60432113, 22278000, 22278002
3139	87325503 (6277, 6278)	Novel Protein sim. GBank gll228938prj[1814452C - Hyp-rich glycoprotein [Zea diploperennis]		UNCLASSIFIED	22278997, 22278998, 22278999, 264905, 265018, 265019, 21906765, 265020, 264636, 264557
3140	91222692 (6279, 6280)	Novel Protein sim. GBank gll932[emb]CAA337773j - (X53744) 68kDa subunit of signal recognition particle [Canis familiaris]		stud	22278995, 56994075, 35696286, 264908, 264909, 60433356, 21906754, 52644296, 87188474, 87188559, 284693, 264286, 284885, 284886, 285022, 264693, 27486282, 35695855, 264630, 264555, 264566
3141	87323564 (6281, 6282)	Novel Protein sim. GBank gll3213227 (AF035209) - putative v-SNARE Vti1a [Mus musculus]		UNCLASSIFIED	56182575, 35696286, 28331828, 264909, 265009, 265018, 18108351, 284389, 21908766, 29148627, 265020, 264628, 264629, 284631, 18108385
3142	95418028 (6283, 6284)	Novel Protein sim. GBank gll2498197isp[Q95245]C561_P1G - CYTOCHROME B561 (CYTOCHROME B-561)		cytochrome	52645156, 52646365, 22278995, 35696286, 22278998, 22278999, 60432049, 264259, 28331822, 28331824, 28331827, 28148499, 56182435, 265007, 60170831, 60432229, 33657402, 264595, 60433438, 284758, 21906754, 284288, 284766, 264687, 52644229, 21906765, 21906767, 21906768, 60170815, 52844150, 65274620, 33657109, 35695763, 18108370, 18108376, 65274791, 35695855, 264631, 264557, 87168518, 60432113, 22278000
3143	95351475 (6285, 6286)	Novel Protein sim. GBank gll5420387[emb]CAB46679.1j - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 56182575, 22278996, 22278998, 22278999, 28331822, 28331824, 60432289, 35696052, 28331828, 264508, 264805, 264908, 264907, 264908, 264909, 52644045, 56182435, 264511, 264512, 285008, 264910, 60432229, 33657402, 60433356, 60433438, 55812038, 265011, 265019, 264760, 264763, 264448, 264764, 264884, 284288, 264685, 264686, 284768, 264889, 21906765, 21906768, 21906767, 21906769, 35695917, 264680, 33657023, 264683, 263967, 33657109, 264628, 264629, 18108374, 263976, 55811576, 35695855, 264630, 264631, 264632, 284634, 284635, 264636, 264637, 264558, 87168518, 60432113, 22278000, 22278002, 264563, 264586, 264488

3144	95336328 (6287, 6288)	Novel Protein sim. GBank gij484468[embjCAB43322.1] - (AL050225) hypothetical protein [Homo sapiens]			264488, 18108396, 22278996, 35696286, 22278997, 22278998, 29331826, 29331827, 35696052, 29331828, 264106, 265008, 265007, 265009, 33657402, 85658542, 265011, 18108351, 264448, 264369, 21906766, 21906768, 21906767, 265020, 265021, 52844150, 27486261, 18108370, 18108374, 35696423, 56182323, 83373044, 22279000, 22279002, 284567
3145	86611657 (6289, 6290)	Novel Protein sim. GBank gij3879709[embjCAB03330] - (ZB1118) Similarity to Human endosomal protein P162 (TR:Q15075); cDNA EST EMBL:Z14487 comes from this gene; cDNA EST EMBL:Z14556 comes from this gene; cDNA EST EMBL:D27011 comes from this gene; cDNA EST EMBL:D27015 comes from t...	UNCLASSIFIED		18108397, 29331824, 29148499, 20281100, 265006, 55812038, 265010, 21906766, 29148627, 21906769, 29148784, 264692, 33657023, 33657109, 35695763, 263981, 56182323, 87188518
3146	87756314 (6291, 6292)	Novel Protein sim. GBank gij2135746[pirjS68890 - mitogen inducible gene mig-2 - human	Contains protein domain (PF00169) - struct PH domain		264259, 29331826, 29331828, 29331830, 264510, 264511, 265007, 285009, 264600, 265017, 18108351, 264448, 264369, 21906766, 265021, 284692, 33657109, 18108374, 35696423, 35695855, 60432113, 264584
3147	94848512 (6293, 6294)	Novel Protein sim. GBank gij3874279[embjCAB07315.1] - (Z92825) predicted using GeneFinder; cDNA EST yk315e12.3 comes from this gene; cDNA EST yk315e12.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	56181686, 35696286, 60432049, 264259, 56182181, 29331825, 60432289, 35696052, 56182435, 265008, 264910, 60431735, 60433358, 60433438, 265010, 264448, 264288, 265022, 33657023, 33657109, 60431528, 55274791, 264631, 56182323, 264404, 22279002
3148	95362169 (6295, 6296)	Novel Protein sim. GBank gij5225322[gbjAAD0851.1] (AF083108) siruin type 3 [Homo sapiens]	UNCLASSIFIED		35696286, 35696052, 264511, 85658542, 87168474, 264764, 35696423, 264555, 264556, 264557, 264558, 83373044, 56526486, 60432113
3149	95308548 (6297, 6298)	Novel Protein sim. GBank gij4200448 (AF102777) - FYVE finger-containing phosphoinositide kinase [Mus musculus]		Contains protein domain (PF01363) - eph FYVE zinc finger	29331822, 35696052, 264109, 29148629, 18108381
3150	87655472 (6299, 6300)	Novel Protein sim. GBank gij3378454[embjCAA76893] - (Y17850) ganglioside-induced differentiation associated protein 1 [Mus musculus]		Contains protein domain (PF00043) - transferase Glutathione S-transferases.	264259, 29331822, 29331824, 29331825, 29331827, 52846317, 264686, 35695855, 56182323, 264639
3151	87772355 (6301, 6302)	Novel Protein sim. GBank gij172591 (M63577) - SFP1 [Saccharomyces cerevisiae]		Contains protein domain (PF00096) - oncogene Zinc finger, C2H2 type	29331822, 265008
3152	85698108 (6303, 6304)		UNCLASSIFIED		21906754, 87168559, 264605, 21906768, 52844150, 27486264, 35696423, 22279000

3153	95317298 (6305, 6306)	Novel Protein sim. GBank gi 4895041 gb AA032705.1 AF14395 - (AF14395) coronin-3 [Mus musculus]	Contains protein domain (PF00400) - struct WD domain, G-beta repeat	224488, 52846365, 35698286, 22278998, 22278997, 22278998, 60432048, 264259, 29331826, 60432289, 33658970, 264508, 264908, 33857402, 264595, 60433438, 87168474, 87168559, 264601, 265018, 264448, 264682, 264764, 284288, 264369, 264768, 21906765, 21906768, 21906767, 21906768, 21906769, 29148784, 265021, 265022, 60170615, 52844150, 264690, 264691, 33657023, 65274620, 33657109, 18108370, 35698555, 264638, 60170394, 87168518, 60432113, 22278000, 22278002, 22278988, 264259, 29331824, 68712502, 285008, 265010, 265017, 18108354, 284691, 33857023, 264693, 20281149, 18108374
3154	87718573 (6307, 6308)	Novel Protein sim. GBank gi 4680681 gb AA027720.1 AF13294 - (AF13294) CGI-11 protein [Homo sapiens]	ATPase-associated	22278998, 264259, 29331824, 68712502, 285008, 265010, 265017, 18108354, 284691, 33857023, 264693, 20281149, 18108374
3155	87762394 (6309, 6310)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	UNCLASSIFIED	29331828, 264509, 264805, 264808, 264510, 264511, 264512, 33657402, 264681, 284683, 33857023, 18108370, 264634, 284639, 18108385, 264563, 264488
3156	87737449 (6311, 6312)	Novel Protein sim. GBank gi 563007 gb AA045821.1 AC00601 - (AC00601) N-acetylglucosaminyltransferase; similar to Q10473 (PID.g1709559) [Homo sapiens]	transferase Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 68714117, 29331825, 29331826, 29331827, 35698052, 52844045, 285007, 265009, 60170831, 60432228, 60433356, 21906754, 33109954, 87168474, 265010, 265017, 265018, 265019, 18108351, 284448, 284288, 264689, 21906766, 21906768, 21906769, 35695917, 265020, 285022, 264682, 18108370, 35698423, 56182323, 22279002
3157	88259577 (6313, 6314)			18108396, 264259, 29331826, 35698052, 29146498, 87168559, 265017, 284448, 264288, 264691, 18108386, 52845129, 35698423, 52844332
3158	80034118 (6315, 6316)	Novel Protein sim. GBank gi 5306064 gb AA041895.1 AF15677 - (AF15677) ASB-3 protein [Homo sapiens]	kinase Contains protein domain (PF00023) - Ank repeat	264488, 263974
3159	84124114 (6317, 6318)	Novel Protein sim. GBank gi 5531272 emb CAB50897.1 - (AJ243800) WSC4 homologue [Kluyveromyces fragilis]	UNCLASSIFIED	56182575, 22278998, 29331824, 264106, 60433396, 264758, 285011, 87168559, 264448, 18108354, 264768, 21906788, 265020, 264691, 264692, 33657109, 18108374, 35698423, 284555, 60170394, 22279000
3160	80221068 (6318, 6320)	Novel Protein sim. GBank gi 3930525 (AF084447) - sex-determination protein homolog Fem1a [Mus musculus]	struct Contains protein domain (PF00023) - Ank repeat	18108351, 264555, 264556, 284557, 264558, 264559



3161	88074111 (6321, 6322)				284488, 22278995, 22278987, 22278988, 264259, 29331822, 60432289, 29331828, 52644045, 285017, 285018, 264448, 264288, 21906784, 21906767, 265020, 18108374, 284636, 264566
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Table 2

Tissue ID	Tissue Name	Tissue Information	Disease Association
20281069	192xN	Protein-protein Interactions	Any
20281071	192xN	Protein-protein Interactions	Any
20281149	192xN	Protein-protein Interactions	Any
20281152	192xN	Protein-protein Interactions	Any
264111	276xN	Protein-protein Interactions	Any
264112	276xN	Protein-protein Interactions	Any
263966	384xN	Protein-protein Interactions	Any
263967	384xN	Protein-protein Interactions	Any
264110	552xN	Protein-protein Interactions	Any
18108379	SPH 52.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108381	SPH 52.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108383	SPH 52.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108368	SPH 52.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108384	SPH 52.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108394	SPH 53.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108355	SPH 53.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108359	SPH 53.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108361	SPH 53.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108362	SPH 53.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108366	SPH 53.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108354	SPH 54.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108392	SPH 54.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108348	SPH 54.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108382	SPH 54.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108395	SPH 54.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108365	SPH 54.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108397	SPH 55.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108398	SPH 55.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108364	SPH 55.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	
18108388	SPH 55.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108358	SPH 55.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
20281099	SPH 56.2 (MG63)		
20281100	SPH 56.3 (U1SMC)		
264404	SPH.1 (Brain)	Whole Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264510	SPH.10 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264511	SPH.11 (Placenta)	Placenta	Infertility, birth defects
264512	SPH.12 (Thyroid)	Thyroid	Hyperparathyroidism, Hypoparathyroidism
264555	SPH.13 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft vesus host,
264556	SPH.14 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft vesus host,
264557	SPH.15 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft vesus host,
264558	SPH.16 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft vesus host,
264559	SPH.17 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft vesus host,
264569	SPH.19 (One Fetal tissue and two cell lines)	Mixed	
264687	SPH.19.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264688	SPH.19.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264689	SPH.19.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264690	SPH.19.4 (Fetal Liver)	Fetal liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264691	SPH.19.5 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264692	SPH.19.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft vesus host
264693	SPH.19.7 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264482	SPH.2 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264600	SPH.21 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264601	SPH.22 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264602	SPH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264603	SPH.24 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264604	SPH.25 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264605	SPH.26 (Placenta)	Placenta	Infertility, birth defects
264634	SPH.28 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264635	SPH.29 (Fetal Kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264483	SPH.3 (Bone Marrow)	Bone marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264636	SPH.30 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264637	SPH.31 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264638	SPH.32 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264639	SPH.33 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264484	SPH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264758	SPH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264760	SPH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation

264762	SPH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264764	SPH.44.4 (Prostate)	Prostate	Prostate Cancer
264766	SPH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264768	SPH.44.6 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264769	SPH.44.7 (Uterus)	Uterus	Infertility, birth defects
264905	SPH.48.1 (Burkitt's Lymphoma- Raji)	Burkitt's Lymphoma	Lymphoma, blood cancers
264906	SPH.48.2 (Thalamus- Brain)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264907	SPH.48.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
264908	SPH.48.4 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
264909	SPH.48.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
264910	SPH.48.6 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
265006	SPH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
265007	SPH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
265008	SPH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
265009	SPH.50.4 (fetal lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
265010	SPH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
265011	SPH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
18108385	SPH.51.1 (MCF-7)	Breast Cancer	Breast Cancer
18108370	SPH.51.2 (CCRF-CEM)	Cancer Cell line	Cancer
18108374	SPH.51.3 (K-562)	Cancer Cell line	Cancer
18108351	SPH.51.4 (OVCAR-3)	Ovarian cancer	Ovarian cancer
18108372	SPH.51.5 (HL-60)	Cancer Cell line	Cancer
264486	SPH.6 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host.

264508	SPH.8 (Fetal Brain)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264509	SPH.9 (Lymph Node)	Lymph Node	Lymphedema , Allergies
20798451	SRH.56.3 (Utricle)		
264487	SRH.1 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264534	SRH.11 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264535	SRH.12 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264563	SRH.19 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264488	SRH.2 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264564	SRH.20 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264565	SRH.21 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264566	SRH.22 (Placenta)	Placenta	Infertility, birth defects
264567	SRH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264591	SRH.25 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264592	SRH.26 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264593	SRH.27 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264594	SRH.28 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264595	SRH.29 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264489	SRH.3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264596	SRH.30 (Placenta)	Placenta	Infertility, birth defects
264628	SRH.33 (fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264629	SRH.34 (lymph Node)	Lymph Node	Lymphedema, Allergies
264630	SRH.35 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264631	SRH.36 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264632	SRH.37 (Fetal Brain)	Fetal Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264490	SRH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264681	SRH.43.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264682	SRH.43.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264683	SRH.43.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264684	SRH.43.4 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264685	SRH.43.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264686	SRH.43.7 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264757	SRH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264759	SRH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264761	SRH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264763	SRH.44.4 (Prostate)	Prostate	Prostate Cancer
264765	SRH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host

264767	SRH.44.6 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264828	SRH.46.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
264887	SRH.47.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
18108377	SRH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
18108380	SRH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
18108396	SRH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
18108391	SRH.50.4 (fetal lung)	Fetal Lung	Airway diseases, infection
18108357	SRH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
18108390	SRH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
264532	SRH.9 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
263974	736xN		
263976	736xN		
263981	736xN		
20281166	96xN		
20281169	96xN		
20281171	96xN		
263994	cDNA-ORF Selection		
264080	Mx96		
21906754	NQH 6.1 (HH729)		
22278996	NQH 6.10 (PrEC)	Endothelial cells	heart disease, cancer
22278997	NQH 6.11 (CAEC)	Endothelial cells	heart disease, cancer
22278998	NQH 6.12 (CSC)	Cancer Cell line	Cancer
22278999	NQH 6.13 (NHNPC)	Cancer Cell line	Cancer
22279000	NQH 6.14 (NHMC-RM)	Cancer Cell line	Cancer
22279002	NQH 6.15 (Hypothalamus)	Hypothalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
21906764	NQH 6.2 (In Dated Platelets)	Platelets	Clotting diseases, stroke
21906765	NQH 6.3 (HuVec)	Endothelial cells	heart disease, cancer
87168474	NQH 6.3 (Sized-HUVEC)	Endothelial cells	heart disease, cancer
21906766	NQH 6.4 (UMVEC- myo)	Cancer Cell line	Cancer
21906767	NQH 6.5 (NHEM-neo)	Cancer Cell line	Cancer
21906768	NQH 6.6 (NHEK)	Cancer Cell line	Cancer
21906769	NQH 6.7 (ByCAEC)	Endothelial cells	heart disease, cancer
22278994	NQH 6.8 (NHA)	Cancer Cell line	Cancer



22278995	NQH 6.9 (PrSC)	Cancer Cell line	Cancer
27486261	NQH 7.1 (Jurkat E6-untreated)	Cancer Cell line	Cancer
27486262	NQH 7.2 (TF1-untreated)	Cancer Cell line	Cancer
27486264	NQH 7.3 (U87-untreated)	Cancer Cell line	Cancer
27486265	NQH 7.4 (THP1-untreated)	Cancer Cell line	Cancer
29331822	NQH 8.1 (Brain- amygdala)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331824	NQH 8.2 (Brain-hippocampus)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331825	NQH 8.3 (Brain- substantia nigra)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331826	NQH 8.4 (small intestine)	Small intestine	digestive diseases, obesity, diabetes
29331827	NQH 8.5 (Spinal cord)	Spinal chord	paralysis, neurodegenerative disorders
29331828	NQH 8.6 (stomach)	Stomach	Stomach cancer
29331830	NQH 8.7 (Trachea)	Trachea	Airway diseases, infection
87168518	NQH 9.1 (Sized-MG-63_treatment pool)		
87168559	NQH 9.2 (Sized-HEPG2 untreated)		
35695763	NQH.10.1 (MCF-7untreated)	Cancer Cell line	Cancer
35695855	NQH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
35695917	NQH.10.3 (JAR)	Cancer Cell line	Cancer
35696052	NQH.10.4 (PA-1)	Cancer Cell line	Cancer
35696286	NQH.10.5 (CADMEC)	Endothelial cells	heart disease, cancer
35696423	NQH.10.6 (CADMEC_LA)	Endothelial cells	heart disease, cancer
52644045	NQH.11.1 (SK-PN-DW)	Cancer Cell line	Cancer
52644150	NQH.11.2 (Chorionic Villus Cells)	Chorionic villus	fertility, birth defects
52644229	NQH.11.3 (A549)	Cancer Cell line	Cancer
52644296	NQH.11.4 (U266B1)	Cancer Cell line	Cancer
52644332	NQH.11.5 (Daoy)	Cancer Cell line	Cancer
52644507	NQH.11.6 (SW1783)	Cancer Cell line	Cancer
52645080	NQH.12.1 (U-118MG)	Cancer Cell line	Cancer
52645129	NQH.12.2 (A204)	Cancer Cell line	Cancer
52645156	NQH.12.3 (T24)	Cancer Cell line	Cancer
52646317	NQH.12.4 (G-401)	Cancer Cell line	Cancer
52646365	NQH.12.5 (CaSki)	Cancer Cell line	Cancer
52646842	NQH.12.6 (SHP-77)	Cancer Cell line	Cancer

60424179	NQH.14.1 (Yale75_breast carcinoma)	Breast carcinoma	Breast Cancer
60424269	NQH.14.2 (Yale78B_ovarytumor)	Ovary tumor	Ovarian cancer
60431528	NQH.14.3 (Yale79_prostateBPH)	Prostate	Prostate Cancer
60431602	NQH.14.4 (Yale80_ProstateAdenocarcinoma)	Prostate	Prostate Cancer
60431735	NQH.14.5 (Yale86_UterineMyoma)	Uterine Myoma	Uterine Cancer
60431850	NQH.14.6 (Yale207_Myometrium)	Myometrium	Fertility
60432049	NQH.15.1 (Yale99_cervix)	Cervix	Osteoporosis, cervical cancer
60432113	NQH.15.2 (Yale45_spleenITP)		Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
60432229	NQH.15.3 (Yale16_Skin)	Skin	wound healing, melanoma
60432289	NQH.15.4 (Yale137_Parotid)		
60433356	NQH.15.5 (Yale38_SmallIntestine)	Small intestine	digestive diseases, obesity, diabetes
60433438	NQH.15.6 (Yale28_ColonAscending)	Colon	Colon cancer
65274444	NQH.17.1 (Larynx)	Larynx	Cancer
65274572	NQH.17.2 (Duodenum)	Duodenum	
65274620	NQH.17.3 (Kidney, Primary tumors)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
65274727	NQH.17.4 (Lung Pleura, normal)	Lung	Airway diseases, infection
65274791	NQH.17.5 (Lung, Normal Adult)	Lung	Airway diseases, infection
83373044	NQH.18.230 (Pooled adrenal gland, placenta)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
85658542	NQH.18.560 (Pooled uterus, BeWo pool)	Uterus	Infertility, birth defects
33656970	NQH.9.1 (MG-63_treatment pool)	Cancer Cell line	Cancer
33657023	NQH.9.2 (HEPG2 untreated)		Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
33657084	NQH.9.3 (PC3_untreated)	Cancer Cell line	Cancer
33657109	NQH.9.4 (TF-1_TPA)	Cancer Cell line	Cancer
33657182	NQH.9.5 (TF-1_TPO)	Cancer Cell line	Cancer
33657349	NQH.9.6 (TF-1_Hermin)	Cancer Cell line	Cancer
33657402	NQH.9.7 (HFDPC)	Cancer Cell line	Cancer
264259	NQH1 (Mixture of eight adult & two fetal tissues)		
264288	NQH2 (Ten tissues plus lymphocyte control)		
264448	NQH3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
265017	NQH4.1 (lymph node)	Lymph Node	Lymphedema, Allergies

265018	NQH4.2 (fetal kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
66712502	NQH4.2 (Sized)		
265019	NQH4.3 (pituitary gland)		Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
66714117	NQH4.3 (Sized)		
265020	NQH4.4 (testis)	testis	Infertility, birth defects
265021	NQH4.5 (fetal liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
265022	NQH4.6 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
18108376	NQH5.1 (MCF-7)	Breast cancer	Breast Cancer
18108387	NQH5.2 (CCRF-CEM)	Cancer Cell line	Cancer
264952	NRL1: HPLC FRACTIONATION OF RELIG		
263971	Old BB3 Baits		
263969	Old BB5 Baits		
263975	ORFSEL		
263972	OTHER Baits		
263978	pGALORF		
264106	PPBAITS		
264088	QC-YA7		
264089	QC-YA8		
264102	Resequenced Interactors		
264369	RRH.1		
60170394	RRH.10.1 (MCF-7untreated)	Breast cancer	Breast Cancer
60170615	RRH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
60170831	RRH.10.3 (JAR)	Cancer Cell line	Cancer
60174639	RRH.11.8 (HeLa)	Cancer Cell line	Cancer
264113	rrQEA Baits		
263973	RRQEA_B5 baits		
29146498	SRD 3.1 (SKMC)	Cancer Cell line	Cancer
29146499	SRD 3.2 (SKMC)	Cancer Cell line	Cancer
29147620	SRD 3.3 (RPTEC)	Cancer Cell line	Cancer
29148627	SRD 3.4 (HRCE)	Cancer Cell line	Cancer
29148629	SRD 3.6 (HRE)	Cancer Cell line	Cancer
29148784	SRD 3.7 (HRE)	Cancer Cell line	Cancer
55810764	SRD.7.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
55811150	SRD.7.2 (pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
55811386	SRD.7.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,

55811576	SRD.7.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
55811957	SRD.7.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
55812038	SRD.7.6 (Fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
56181562	SRD.8.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
56181686	SRD.8.2 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
56182181	SRD.8.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
56182323	SRD.8.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
56182435	SRD.8.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
56182575	SRD.8.6 (Fetal Kidney)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
32833986	SRD4: HL adapter		
56526486	SRD5.1:rr fragments		
33109954	SRD5: long-RXRJ		
56994075	SRD9.1 (CS/SC)	Cancer Cell line	Cancer
263977	TSC Screen 1		

## Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences

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 Pro Pro Pro Ile Ser Ala Ala Arg Leu Ser Arg Met Ser Leu Val Glu  
 50 55 60  
 Arg Cys Ser Ala Ser Ala Ser Cys Ser Ala Val Leu Arg Asp Trp Ala  
 65 70 75 80  
 Cys Ser Ser Ala Leu Val Arg Ala Ala Ser Met Ser Ala Lys Ser Asp  
 85 90 95  
 Ser Ala Phe Gly Ser Glu Thr Arg  
 100

<210> 3  
 <211> 987  
 <212> DNA  
 <213> Homo sapiens

<400> 3  
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 gctggcggtg taaagatcgc taagtccccg gccgaggcgg ctgaacgcgc cgaggccatc  
 120  
 ctcggtatgg acatcaaggg tcacaccgtt cacaagggtga tggtcgctga aggtgctgac  
 180  
 attgccgagg aatactactt ctcgatcttg ctcgaccgtg gagagcgtcg ctaccttgcg  
 240  
 atgtgctcgc gtgagggtgg catggacatc gagacccttg ctaaggagcg ccccgagggt  
 300  
 ctcgccaagg tgccggtcga cccgattgac ggcgttgacg atgctaaagc ccgcgaaatc  
 360  
 cttagcgagg caggggtccc cgactctgag caggacgcta tcgtcccggc tgttctcaag  
 420  
 ctgtgggaga cctaccgtga cgaggatgcc accctcgtcg aggtcaacct gatgatcaag  
 480  
 accggcgatg gacgcacatc ggctatcgac ggcaagatga ctggtgacaa caacgcaccc  
 540  
 ttccgccagc ctgaccgcgc cggcttggtg gatcgcgcca ccaccgaccc gctcgagttg  
 600  
 cgtgccggcg agctcgggtc caactacgtc aagcttgacg gcaacgtcgg cgtcatcgga  
 660  
 aacggtgctg gtctgggtcat gagcaccctt gactgcgttg cgtacgccgg tgagaacttc  
 720  
 ccgggatctc cagctcccgc taacttcctc gacatcggtg gcggcgccct gcccgagatc  
 780  
 atggccaacg gccttgacct catcatgagt gacgagcagg tgcgttcggt gttcgtcaac  
 840  
 gtctttggcg gtatcaccgc ctgtgaccag gtggcgcttg gtatcaaggg cgctctcgag  
 900  
 aagttggggc acaaggccgt gaagccgctc gtcgtccgtc tggacggcaa cgctgtggcc  
 960  
 gagggcagaa agattctcga ggaattc  
 987

<210> 4  
 <211> 329  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Glu Leu Gly Thr Pro Val Val Ala Val Lys Ala Gln Val Lys Val Gly  
 1 5 10 15  
 Gly Arg Gly Lys Ala Gly Gly Val Lys Ile Ala Lys Ser Pro Ala Glu  
 20 25 30  
 Ala Ala Glu Arg Ala Glu Ala Ile Leu Gly Met Asp Ile Lys Gly His  
 35 40 45

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Thr Val His Lys Val Met Val Ala Glu Gly Ala Asp Ile Ala Glu Glu
  50                      55                      60
Tyr Tyr Phe Ser Ile Leu Leu Asp Arg Gly Glu Arg Arg Tyr Leu Ala
  65                      70                      75                      80
Met Cys Ser Arg Glu Gly Gly Met Asp Ile Glu Thr Leu Ala Lys Glu
                      85                      90                      95
Arg Pro Glu Ala Leu Ala Lys Val Pro Val Asp Pro Ile Asp Gly Val
                      100                      105                      110
Asp Asp Ala Lys Ala Arg Glu Ile Leu Ser Glu Ala Gly Phe Pro Asp
                      115                      120                      125
Ser Glu Gln Asp Ala Ile Val Pro Ala Val Leu Lys Leu Trp Glu Thr
                      130                      135                      140
Tyr Arg Asp Glu Asp Ala Thr Leu Val Glu Val Asn Pro Met Ile Lys
  145                      150                      155                      160
Thr Gly Asp Gly Arg Ile Leu Ala Ile Asp Gly Lys Met Thr Val Asp
                      165                      170                      175
Asn Asn Ala Ser Phe Arg Gln Pro Asp Arg Ala Gly Leu Val Asp Arg
                      180                      185                      190
Ala Thr Thr Asp Pro Leu Glu Leu Arg Ala Gly Glu Leu Gly Leu Asn
                      195                      200                      205
Tyr Val Lys Leu Asp Gly Asn Val Gly Val Ile Gly Asn Gly Ala Gly
  210                      215                      220
Leu Val Met Ser Thr Leu Asp Cys Val Ala Tyr Ala Gly Glu Asn Phe
  225                      230                      235                      240
Pro Gly Ser Pro Ala Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala
                      245                      250                      255
Ser Ala Glu Ile Met Ala Asn Gly Leu Asp Leu Ile Met Ser Asp Glu
                      260                      265                      270
Gln Val Arg Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ala Cys
                      275                      280                      285
Asp Gln Val Ala Leu Gly Ile Lys Gly Ala Leu Glu Lys Leu Gly Asp
  290                      295                      300
Lys Ala Val Lys Pro Leu Val Val Arg Leu Asp Gly Asn Ala Val Ala
  305                      310                      315                      320
Glu Gly Arg Lys Ile Leu Glu Glu Phe
                      325

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&lt;210&gt; 5

&lt;211&gt; 622

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

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acgcgtggcc tagacctgaa tccattcctc acaaaacagt ctccctcctt gccatgggat
  60
tccctgggggt ttccacaggc cacagctcta atgggtctgca gcagggttacc ttgttcccca
  120
gaacatagct tgtcataaca tctctgcagg gttctcccaa acccctttct gcctggcaac
  180
agctgacatc acacctagct gtaagtcctt gtagatcgca aattactttt tggagactgg
  240
gggtagcagg ggcattgggg taatagcctt ctagcccttt ttgagggaaa cacatgggtg
  300

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aggtattttt ggggctggga agtggggggcc tgggtgcccc tggatggctg tgetggcctc  
 360  
 tggctgcaag ggagaggggc acaggcaagg acatgacccc cgtcaaccct gagccccctc  
 420  
 cagaaattta accagagcct gtcctcctt tcttgctgc ccccaacatc tcacaatccc  
 480  
 tcctgtgatg gcagatgtct ccattactc tacagacacc tgcaactatc attccttga  
 540  
 tccgtggtaa ttaggagggga actcctctgt gaagaaccgc ttctaccatc ctcttttaga  
 600  
 aactctttct cactgggat cc  
 622

<210> 6  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
 Met Ser Leu Pro Val Pro Leu Ser Leu Ala Ala Arg Gly Gln His Ser  
 1 5 10 15  
 His Pro Gly Asp Thr Arg Pro Pro Leu Pro Ser Pro Lys Ile Ala Ser  
 20 25 30  
 Pro Met Cys Phe Pro Gln Lys Gly Leu Glu Gly Tyr Tyr Pro Asn Ala  
 35 40 45  
 Pro Ala Thr Pro Ser Leu Gln Lys Val Ile Cys Asp Leu Gln Gly Leu  
 50 55 60  
 Thr Ala Arg Cys Asp Val Ser Cys Cys Gln Ala Glu Arg Gly Leu Gly  
 65 70 75 80  
 Glu Pro Cys Arg Asp Val Met Thr Ser Tyr Val Leu Gly Asn Lys Val  
 85 90 95  
 Thr Cys Cys Arg Pro Leu Glu Leu Trp Pro Val Lys Thr Pro Gly Asn  
 100 105 110  
 Pro Met Ala Arg Arg Glu Thr Val Leu  
 115 120

<210> 7  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

<400> 7  
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 agaaaaccca cacctctcct cccctcccca gtggctgtgg ctttcctagg gacaatagga  
 120  
 tgaatgggct ttcagtgtgg ggacagcaaa acatgcacta gggcccagag tggcagttct  
 180  
 cttggtgtgg agagtgcctg ccacaggcct tggccagagc ccgtgagggga gtggtgtgtg  
 240  
 aaaggccacc tccacgtggg taagcgtgag gacttggact tctctggcac tgagatggga  
 300  
 cctcctgcct gtgggagtca tctggccacc accctggggc cagtaaaggt tggagctaga  
 360



agggtcgtcc tccctgactt gagctctgag ggctttgcct gccagccag agcggcaagg  
 420  
 cacaggggac cctcggggac gcccatggcc accctgggga agacagggct cctcacgcgt  
 480

<210> 8  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
 Met Gly Phe Gln Cys Gly Asp Ser Lys Thr Cys Thr Arg Ala Gln Ser  
 1 5 10 15  
 Gly Ser Ser Leu Gly Val Glu Ser Ala Cys His Arg Pro Trp Pro Glu  
 20 25 30  
 Pro Val Arg Glu Trp Cys Val Lys Gly His Leu His Val Gly Lys Arg  
 35 40 45  
 Glu Asp Leu Asp Phe Ser Gly Thr Glu Met Gly Pro Pro Ala Cys Gly  
 50 55 60  
 Ser His Leu Ala Thr Thr Leu Gly Pro Val Lys Val Gly Ala Arg Arg  
 65 70 75 80  
 Val Val Leu Pro Asp Leu Ser Ser Glu Gly Phe Ala Cys Pro Ala Arg  
 85 90 95  
 Ala Ala Arg His Arg Gly Pro Ser Gly Thr Pro Met Ala Thr Leu Gly  
 100 105 110  
 Lys Thr Gly Leu Leu Thr Arg  
 115

<210> 9  
 <211> 428  
 <212> DNA  
 <213> Homo sapiens

<400> 9  
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 120  
 tcccagggat gctggatgac ctctttcagt ccatgttcct gtgcgccctg ctgctcttct  
 180  
 ggctgtgcgt gtaccacggg attcgtgtcc agggagaaag aaagtgttta actttctatt  
 240  
 tgctaaatt cttcattgtt ggactattgt ggttggttc tgttacgcta ggaatatggc  
 300  
 aaacagttaa cgaattacat gatccaatgt accagtatcg agttgatacc ggaaattttc  
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 420  
 tgatagtg  
 428

<210> 10  
 <211> 138  
 <212> PRT

<213> Homo sapiens

<400> 10

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Met Arg Asp Trp Gly Ile Glu Gln Lys Trp Met Ser Val Leu Leu Pro
 1          5          10          15
Leu Leu Leu Leu Tyr Asn Asp Pro Phe Phe Pro Leu Ser Phe Leu Val
          20          25          30
Asn Ser Trp Leu Pro Gly Met Leu Asp Asp Leu Phe Gln Ser Met Phe
          35          40          45
Leu Cys Ala Leu Leu Leu Phe Trp Leu Cys Val Tyr His Gly Ile Arg
          50          55          60
Val Gln Gly Glu Arg Lys Cys Leu Thr Phe Tyr Leu Pro Lys Phe Phe
          65          70          75          80
Ile Val Gly Leu Leu Trp Leu Ala Ser Val Thr Leu Gly Ile Trp Gln
          85          90          95
Thr Val Asn Glu Leu His Asp Pro Met Tyr Gln Tyr Arg Val Asp Thr
          100          105          110
Gly Asn Phe Gln Gly Met Lys Val Phe Phe Met Val Val Ala Ala Val
          115          120          125
Tyr Ile Leu Tyr Leu Leu Phe Leu Ile Val
          130          135

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<210> 11

<211> 453

<212> DNA

<213> Homo sapiens

<400> 11

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60
gaatggttgca ggcaaactca agaccggtgg ccttggtgaa ggtccaggtc agctcggcgg
120
acttgccccg ctcgaccagc acgctgttgg ggtcgtcatg cttcatgccg cccatatacg
180
catgccccat ggcggcgtgg tccatcttgc ccatgccggt ggccgtgagc atgccgctgg
240
cttgcacatt gagcatttct ttctggtgtt cggcgtgcat cgccgcatca cccagattga
300
attcgtgcag taactggcct ttgttgacca gcacaaagcg cacggtctca ccggctttta
360
catccagagc cttgggcgaa aaggaaatgt cctgcagggt gacttcacg gtgcgcgtgg
420
ctttatcggc cggtgccggg tggccaaacg cgt
453

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<210> 12

<211> 130

<212> PRT

<213> Homo sapiens

<400> 12

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Met Leu Gln Ala Asn Ser Arg Pro Val Ala Leu Val Lys Val Gln Val
 1          5          10          15
Ser Ser Ala Asp Leu Pro Gly Ser Thr Ser Thr Leu Leu Gly Ser Ser

```

[illegible]

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<210> 13
<211> 2034
<212> DNA
<213> Homo sapiens
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<400> 13
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120
tgggccctac catgctggca ttttcctcca tgtgtcaaac acatgggttc agccagcgaa
180
gattccatgg gacctcctcg tgtgggacgt gtgctcccca ccacaaatgg aacgttcctt
240
gtttgcatct ggagggggtg gtggtcctgc tggctggagc agcctggggc cagaggaagc
300
cgtatcaacc ggctctgcag cgcttcagcg aggggtgccct ggagtaccta gccaacctgg
360
accgagcccc agaccccacg gtcaggaagg acgcctttgc caccgacatc ttcagcgctt
420
acgatgttct cttccatcag tggctgcaga gtcgagaagc caagctccgt cttgccgtgg
480
tggaggctct ggggcctatg agccatctgc tgcccagtga gaggttgga gagcagctgc
540
ccaagctect ccctgggatt ctcgccctct acaagaagca cgcagagacc ttctacttgt
600
ccaagagcct gggccagatc ctcgaggcag ctgtgagtgt gggcagccgc acactggaga
660
cccagctgga tgccctcttg gctgcactgc actccagat ctgtgtgcct gtggagtect
720
caagcccect ggtgatgagt aaccagaagg aggtgctgcg ctgcttact gtgctggcct
780
gcagctcgcc tgaccgccta ctggccttcc tgctgccag gctggacacc accaatgaga
840
ggacccgcgt gggcaccctg cagggggcca aacatgtcat caactcaact gctgctcaaa
900
tggaagataa aaagcccttt atcctgtctt ccatgaggct tcctctctg aacaccaaca
960

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gcaaggtgaa gcgggcagtg gtgcaggtga ttagcgccca tggcccacca cggctacctg  
 1020  
 gagcagcctg gaggtgaggc gatgatcgag taaatcgtgc agcagtgccg gctgcccccc  
 1080  
 gagcaggagc ctgagaagcc agggccccgc agcaaggacc ccaaggccga cagcgtgcgg  
 1140  
 gccatcagcg tgcgcaccct ctacctgggc agcaccaccg tggacaggat gagtcacgtc  
 1200  
 ctctggccat acctgctcca gttcctcacc cctgtgcgct tcaactggggc cctgactccg  
 1260  
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 1320  
 ctcatccagt acgacgcccc tgcgagcctc ccgtctccct atgctgtaac cggaagactg  
 1380  
 ttggttggtg cttccagccc ctacctaggg gacggacgtg gggcagcggc gctgcgccctc  
 1440  
 ctacgtgttc tgcacccaaa cattcacctt ttgctgggtc agcattggga aacgactgtc  
 1500  
 ccgctgctgc tggggtacct ggatgagcac acagaagaga ccctgccaca ggaggagtgg  
 1560  
 gaggagaagc tgttgatggt gagggccggg gtacggccca tcctgggcct taagggtgtg  
 1620  
 tctggcctgg ggggtgctgg ggtggcagag gctgggccac ctgcctcgac ctcacctcgt  
 1680  
 gggttggtg gggagccaag gatcaggcag catcaaggct gaagaccca gcagccttgc  
 1740  
 agcggggggc ttgctgtgac aaggcaccgg ccctctagca gtcgcagccc caagcgtcgg  
 1800  
 gggcaacctc tcacctgcc tggtagacca actgtggcat ggctgtcccc tgagggttgg  
 1860  
 ctctgccgcc cccggcctcc gctggaaggc ggtctgcagc ccctgcagcc acagcacatg  
 1920  
 gggatgtgcc caggctccag ccagccctgt gaggggtcgg gctcccagcc cctcagtggc  
 1980  
 atcttgccct gcagttcctg cgagacaccc tggccatcat ttctgacaac gcgt  
 2034

<210> 14

<211> 222

<212> PRT

<213> Homo sapiens

<400> 14

Ile	Val	Gln	Gln	Cys	Ala	Leu	Pro	Pro	Glu	Gln	Glu	Pro	Glu	Lys	Pro
1				5					10					15	
Gly	Pro	Gly	Ser	Lys	Asp	Pro	Lys	Ala	Asp	Ser	Val	Arg	Ala	Ile	Ser
			20					25					30		
Val	Arg	Thr	Leu	Tyr	Leu	Val	Ser	Thr	Thr	Val	Asp	Arg	Met	Ser	His
		35				40					45				
Val	Leu	Trp	Pro	Tyr	Leu	Leu	Gln	Phe	Leu	Thr	Pro	Val	Arg	Phe	Thr
	50					55				60					
Gly	Ala	Leu	Thr	Pro	Leu	Cys	Arg	Ser	Leu	Val	His	Leu	Ala	Gln	Lys
65				70					75					80	
Arg	Gln	Glu	Ala	Gly	Ala	Asp	Ala	Phe	Leu	Ile	Gln	Tyr	Asp	Ala	His

```

      85              90              95
Ala Ser Leu Pro Ser Pro Tyr Ala Val Thr Gly Arg Leu Leu Val Val
      100          105          110
Ser Ser Ser Pro Tyr Leu Gly Asp Gly Arg Gly Ala Ala Ala Leu Arg
      115          120          125
Leu Leu Ser Val Leu His Pro Asn Ile His Pro Leu Leu Gly Gln His
      130          135          140
Trp Glu Thr Thr Val Pro Leu Leu Leu Gly Tyr Leu Asp Glu His Thr
      145          150          155          160
Glu Glu Thr Leu Pro Gln Glu Glu Trp Glu Glu Lys Leu Leu Met Val
      165          170          175
Arg Ala Gly Val Arg Pro Ile Leu Gly Leu Lys Val Leu Ser Gly Leu
      180          185          190
Gly Gly Ala Gly Val Ala Glu Ala Gly Pro Pro Ala Ser Thr Ser Pro
      195          200          205
Arg Gly Leu Ala Gly Glu Pro Arg Ile Arg Gln His Gln Gly
      210          215          220

```

&lt;210&gt; 15

&lt;211&gt; 363

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 15

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naccgcttgc tggctcgcca cggcaagggc catgtcggct gcgatatctg caagccggcg
60
gtgggttcga tccttgccctc gtgctggaac cagccgatca tggaccgggc gttggtgccg
120
ttgcaggaca ccaatgacac cttcatggcc aacatgcaga agaacggtag ctattcgatc
180
atccccgcgtg tcgccggcgg cgagatcacc ccggacaaac tgatcgccct cggcgcggtg
240
gcgaagaaat acgatctgta caccaagatc accggcggcc agcggatcga cctgttcggc
300
gccagttgc acgaattgcc gcagatctgg ggcgagctgg tggatgccgg attcgagacc
360
ggt
363

```

&lt;210&gt; 16

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

```

Xaa Ala Leu Leu Ala Arg His Gly Lys Gly His Val Gly Cys Asp Ile
1      5      10      15
Cys Lys Pro Ala Val Gly Ser Ile Leu Ala Ser Cys Trp Asn Gln Pro
      20      25      30
Ile Met Asp Pro Ala Leu Val Pro Leu Gln Asp Thr Asn Asp Thr Phe
      35      40      45
Met Ala Asn Met Gln Lys Asn Gly Thr Tyr Ser Ile Ile Pro Arg Ile
50      55      60
Ala Gly Gly Glu Ile Thr Pro Asp Lys Leu Ile Ala Leu Gly Ala Val

```

```

65              70              75              80
Ala Lys Lys Tyr Asp Leu Tyr Thr Lys Ile Thr Gly Gly Gln Arg Ile
              85              90              95
Asp Leu Phe Gly Ala Gln Leu His Glu Leu Pro Gln Ile Trp Gly Glu
              100              105              110
Leu Val Asp Ala Gly Phe Glu Thr Gly
              115              120

```

<210> 17  
 <211> 682  
 <212> DNA  
 <213> Homo sapiens

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<400> 17
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tgttcatctt tgttttgaat ataattggct agaagatata catatatcta tgtaacttcc
120
tctagcatcc tccagtatgg aggctgcatt aagactgcat gaaggagagg gagagaaggg
180
agaaacagag cagctggaca agaggacagg tatagggaaat aagggagaag ccagtaaggc
240
aggaaagacc ctccgtgaca aaggggcagg gaacagaact caaacattta atggcaggta
300
acccagggtta gaatggtaaa ttgaaagggtg aatataaagg gagaatgggtg aaatgaattt
360
tctgaaatta attgctgtgt ttatagtttt tagccatgca tcggaatcac ctcaggactc
420
cactcccaat caattatata tctggggggag gaccaaggcg ttggtatttt tcagaagctc
480
cactggtgat tctgacagca cagctaggat taagaaactg atcaatggga acagcatgcc
540
tgttgcagag gagcttccct gggaaatgtc acacacagaa catcaatctt ccttccccac
600
tcctgagatc cctcattctt tggcaccagg aacagttgca attagtaaac cctggttccc
660
tgctgtctca caaatcgcaa ga
682

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<210> 18  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

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<400> 18
Met Asn Phe Leu Lys Leu Ile Ala Val Phe Ile Val Phe Ser His Ala
1              5              10              15
Ser Glu Ser Pro Gln Asp Ser Thr Pro Asn Gln Leu Tyr Ile Trp Gly
20              25              30
Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp
35              40              45
Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Ser Met Pro Val
50              55              60
Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser

```

```

65              70              75              80
Phe Pro Thr Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala
              85              90              95
Ile Ser Lys Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg
              100              105              110

```

<210> 19  
 <211> 515  
 <212> DNA  
 <213> Homo sapiens

```

<400> 19
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60
ccccatctc aactatgtta gccagtctgg ctgttcactt agtcactaca gtttcttct
120
cgtctgcagt gcagtcttgg gctataagaa aactggggcc actcaatacc tcccccttt
180
tggcccttct cctcctctgg tccatgggtg gggttggggg gagcccagtt tcagcaccag
240
cagctgggagc ccataccaca ctcatcttct agttctggct gtgggagccc ctcccacagg
300
tttcagttcc ccaagcccca ggctgagtt tttttattg caaaagctgg ttgttgtgtg
360
ggctagctcc caggcgtgtg aggtgcagct tgctaagtaa gagctaggaa agagaatagg
420
gtcctgctgt aggtgtccag tctgaaggaa tgctgggat acttcctcaa gcagttcctt
480
ctcacagtct cctggctgct ccgcatgtca gatct
515

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<210> 20  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

```

<400> 20
Met Gly Pro Ala Ser Leu Leu His Pro Ser Leu Gly Lys Asp His Ala
1      5      10      15
Pro Ile Ser Thr Met Leu Ala Ser Leu Ala Val His Leu Val Thr Thr
20      25      30
Val Cys Phe Ser Ser Ala Val Gln Ser Trp Ala Ile Arg Asn Thr Gly
35      40      45
Pro Leu Asn Thr Ser Pro Leu Leu Ala Leu Leu Leu Trp Ser Met
50      55      60
Gly Gly Val Gly Gly Ser Pro Val Ser Ala Pro Ala Ala Gly Ala His
65      70      75      80
Thr Thr Leu Ile Phe Gln Phe Trp Leu Trp Glu Pro Leu Pro Gln Val
85      90      95
Ser Val Pro Gln Ala Pro Gly Leu Ser Phe Phe Tyr Cys Lys Ser Trp
100     105     110
Leu Leu Leu Trp Leu Ala Pro Arg Arg Val Arg Cys Ser Leu Leu Ser
115     120     125
Lys Ser

```

130

&lt;210&gt; 21

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

gtgcgcacaa aagagcacgt tcgcaagggg aggaagagcg tgccaccggt tctgccgagc  
 60  
 tagacgcggt gcctatgggt gcggaggacc atggagtga gcgagtaaga ctagatgatg  
 120  
 caacaaatgt gcctgagggg gaaatggcac gagccagtgc caatgagggc atgacacctg  
 180  
 ttaaccacga caaataccct tctgtccttt taaatgaagc ggcccaggct tcattactgg  
 240  
 atacaatgac tgcttgcaat gatgggttca caattgagca attggagctt acacgatctc  
 300  
 tatgttatga aagagtatta gcacatcgat cctcatggga tcgttcagcc ctgggtcaag  
 360  
 aattaaagca agttgtccaa ggcacccatn  
 390

&lt;210&gt; 22

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 22

Met	Val	Ala	Glu	Asp	His	Gly	Val	Lys	Arg	Val	Arg	Leu	Asp	Asp	Ala
1				5					10				15		
Thr	Asn	Val	Pro	Glu	Gly	Glu	Met	Ala	Arg	Ala	Ser	Ala	Asn	Glu	Gly
		20						25				30			
Met	Thr	Pro	Val	Asn	His	Asp	Lys	Tyr	Pro	Ser	Val	Leu	Leu	Asn	Glu
		35					40					45			
Ala	Ala	Gln	Ala	Ser	Leu	Leu	Asp	Thr	Met	Thr	Ala	Cys	Thr	Asp	Gly
	50					55					60				
Phe	Thr	Ile	Glu	Gln	Leu	Glu	Leu	Thr	Arg	Ser	Leu	Cys	Tyr	Glu	Arg
65				70					75					80	
Val	Leu	Ala	His	Arg	Ser	Ser	Trp	Asp	Arg	Ser	Ala	Leu	Ala	Gln	Glu
			85						90					95	
Leu	Lys	Gln	Val	Val	Gln	Gly	Ile	His							
		100					105								

&lt;210&gt; 23

&lt;211&gt; 385

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 23

ntctcggagg ccgacagcct ggccggctgg aagccctcgg tgtaccacgt gctgctcatc  
 60  
 ctgggcctgt tcgccgtgct gctgtcctgc tgcgcctcgg ccatgtacac cagcgtggag  
 120



ggctgggact acgtggactc gctctacttc tgettcgtca ccttcagcac catcggttc  
 180  
 ggggacctgg tgagcagcca gcacgcgcc taccggaacc aggggctcta ccgcctgggc  
 240  
 aacttctct tcatcctgct cggcgtgtgc tgcatttact cgctcttcaa cgtcatctcc  
 300  
 atcctcatca agcaggtgct caactggatg ctgcgcaagc tgagctgccg ctgctgcgcg  
 360  
 cgctgctgcc cggctcctgg cgcgc  
 385

<210> 24

<211> 128

<212> PRT

<213> Homo sapiens

<400> 24

Xaa	Ser	Glu	Ala	Asp	Ser	Leu	Ala	Gly	Trp	Lys	Pro	Ser	Val	Tyr	His
1				5					10					15	
Val	Leu	Leu	Ile	Leu	Gly	Leu	Phe	Ala	Val	Leu	Leu	Ser	Cys	Cys	Ala
			20					25					30		
Ser	Ala	Met	Tyr	Thr	Ser	Val	Glu	Gly	Trp	Asp	Tyr	Val	Asp	Ser	Leu
		35					40					45			
Tyr	Phe	Cys	Phe	Val	Thr	Phe	Ser	Thr	Ile	Gly	Phe	Gly	Asp	Leu	Val
	50					55					60				
Ser	Ser	Gln	His	Ala	Ala	Tyr	Arg	Asn	Gln	Gly	Leu	Tyr	Arg	Leu	Gly
65				70					75					80	
Asn	Phe	Leu	Phe	Ile	Leu	Leu	Gly	Val	Cys	Cys	Ile	Tyr	Ser	Leu	Phe
			85					90					95		
Asn	Val	Ile	Ser	Ile	Leu	Ile	Lys	Gln	Val	Leu	Asn	Trp	Met	Leu	Arg
		100					105					110			
Lys	Leu	Ser	Cys	Arg	Cys	Cys	Ala	Arg	Cys	Cys	Pro	Ala	Pro	Gly	Ala
		115					120					125			

<210> 25

<211> 337

<212> DNA

<213> Homo sapiens

<400> 25

ccatgggaga gaccgtgcat tttcttctag gtctgcgtgg gaagtcactg cagagtttcg  
 60  
 aggaggggag ttcccagctc tgtatttttg aagggtcagt cttgttgctt ggaccagtga  
 120  
 ggagccccgt gggatccaga ctcgagtggg tggagccggg gcaggtggga gcagagacac  
 180  
 tggaggaaag ctggtcgaat gcactgtgta tttggaggca gaaccagcag agggtcctct  
 240  
 ggggttgagt tagggcaaaa gagaaagaag gcaccaagcc tggggtctgg gttttctctc  
 300  
 ttacacttgc tgggtggacg gtggtgccac tgaatga  
 337

<210> 26

<211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 26  
 Met Gly Glu Thr Val His Phe Leu Leu Gly Leu Arg Gly Lys Ser Leu  
 1 5 10 15  
 Gln Ser Phe Glu Glu Gly Ser Ser Gln Leu Cys Ile Phe Glu Gly Ser  
 20 25 30  
 Val Leu Leu Leu Gly Pro Val Arg Ser Pro Val Gly Ser Arg Leu Glu  
 35 40 45  
 Trp Val Glu Pro Gly Gln Val Gly Ala Glu Thr Leu Glu Glu Ser Trp  
 50 55 60  
 Ser Asn Ala Leu Cys Ile Trp Arg Gln Asn Gln Gln Arg Val Leu Trp  
 65 70 75 80  
 Val Glu Cys Arg Ala Lys Glu Lys Glu Gly Thr Lys Pro Gly Val Trp  
 85 90 95  
 Val Phe Ser Leu Thr Leu Ala Gly Trp Thr Val Val Pro Leu Asn  
 100 105 110

<210> 27  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 ccgacgtcga atatccatgc agccgcgccg aggatggaga gagcgatgga gcaactcaac  
 60  
 cgccctgacgc gctcgctgcg ccgcgcgcgc accgtggagt tgcccgagga taatgaaact  
 120  
 gctgtttata cattaatgcc aatggttatg gctgatcaac acaggctctgt ttctgaaacta  
 180  
 ctatcaaatt caaaatttga tgtcaattat gcattcggac gtgtgaaaag aagcttgctt  
 240  
 cacattgcag caaattgtgg atcgggtggaa tgcttggttt tgctgttaaa gaaaggagca  
 300  
 aatcctaact atcaagatat ttcaggctgt aca  
 333

<210> 28  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 28  
 Pro Thr Ser Asn Ile His Ala Ala Pro Arg Met Glu Arg Ala Met  
 1 5 10 15  
 Glu Gln Leu Asn Arg Leu Thr Arg Ser Leu Arg Arg Ala Arg Thr Val  
 20 25 30  
 Glu Leu Pro Glu Asp Asn Glu Thr Ala Val Tyr Thr Leu Met Pro Met  
 35 40 45  
 Val Met Ala Asp Gln His Arg Ser Val Ser Glu Leu Ser Asn Ser  
 50 55 60  
 Lys Phe Asp Val Asn Tyr Ala Phe Gly Arg Val Lys Arg Ser Leu Leu

```

65              70              75              80
His Ile Ala Ala Asn Cys Gly Ser Val Glu Cys Leu Val Leu Leu Leu
              85              90              95
Lys Lys Gly Ala Asn Pro Asn Tyr Gln Asp Ile Ser Gly Cys Thr
              100              105              110

```

<210> 29  
 <211> 375  
 <212> DNA  
 <213> Homo sapiens

```

<400> 29
ncgccgtccg tgctggctat tatgacggcg ggtagcgacc agggcgagga ggtcaactcg
60
gagagctatt tgagcgccgt gacgccgctg agtcccaaag agattcgta gctgccccgc
120
tacaatatca cgatcaagcg cgtcgtgaac atgacgggca agggccgcac gccgagctgg
180
tactcgctcg tcgtggctgg caatggctcg ggctcgtgg gctatggcga aggcaaagat
240
actaacatca gccgcgcgaa caaaaaggcg ttccacgccg cggtgaaaaa catggacttg
300
gtatcgggcc accggtcgaa gaggggcgcc aacacgctcg agccccccgt cgagggcgcc
360
tggggcgcta cgcgt
375

```

<210> 30  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

```

<400> 30
Xaa Pro Ser Val Leu Ala Ile Met Thr Ala Gly Ser Asp Gln Gly Glu
1      5      10      15
Glu Val Asn Ser Glu Ser Tyr Leu Ser Ala Val Thr Pro Leu Ser Pro
20     25     30
Lys Glu Ile Arg Gln Leu Pro Arg Tyr Asn Ile Thr Ile Lys Arg Val
35     40     45
Val Asn Met Thr Gly Lys Gly Arg Thr Pro Ser Trp Tyr Ser Leu Val
50     55     60
Val Ala Gly Asn Gly Arg Gly Leu Val Gly Tyr Gly Glu Gly Lys Asp
65     70     75     80
Thr Asn Ile Ser Arg Ala Asn Lys Lys Ala Phe His Ala Ala Val Lys
85     90     95
Asn Met Asp Leu Val Ser Val His Arg Ser Lys Ser Gly Ala Asn Thr
100    105    110
Leu Glu Pro Pro Val Glu Gly Arg Trp Gly Ala Thr Arg
115    120    125

```

<210> 31  
 <211> 375  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 31

accggtcttg gcctcagctt tgctctgaaa ttgaagtcgg tgccaaaagt ggggaagagc  
 60  
 gggagcaggc acttacgagc ctgcgcgtca gggatgcttc ctgggccctt gagagtgcag  
 120  
 agattcctgg atccagagct gcggctgggc ggctgcagct gcgcctggga gtgcagggct  
 180  
 cccgccctgc cagctcaaaa ggaaatgggg gctcctgcct gttcctggct cctgttggcc  
 240  
 ctgcagagtg cacaaccta gccgcgcttc ctccactgca gcttacgtct ttgcagcagc  
 300  
 cactcccgat gggctgccac tgccatctgt gagaccataa tgtgtgcaat ttgagactca  
 360  
 tggcctgcat tgttt  
 375

&lt;210&gt; 32

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 32

Met	Gln	Ala	Met	Ser	Leu	Lys	Leu	His	Thr	Leu	Trp	Ser	His	Arg	Trp
1			5						10					15	
Gln	Trp	Gln	Pro	Ile	Gly	Ser	Gly	Cys	Cys	Lys	Asp	Val	Ser	Cys	Ser
			20					25					30		
Gly	Gly	Ser	Ala	Ala	Arg	Phe	Val	His	Ser	Ala	Gly	Pro	Thr	Gly	Ala
		35				40					45				
Arg	Asn	Arg	Gln	Glu	Pro	Pro	Phe	Pro	Phe	Glu	Leu	Ala	Gly	Arg	Glu
	50					55				60					
Pro	Cys	Thr	Pro	Arg	Arg	Ser	Cys	Ser	Arg	Pro	Ala	Ala	Ala	Leu	Asp
65				70					75					80	
Pro	Gly	Ile	Ser	Ala	Leu	Ser	Gly	Ala	Gln	Glu	Ala	Ser	Leu	Thr	Arg
			85					90					95		
Arg	Leu	Val	Ser	Ala	Cys	Ser	Arg	Ser	Ser	Pro	Leu	Leu	Ala	Pro	Thr
			100				105						110		
Ser	Ile	Ser	Glu	Gln	Ser										
			115												

&lt;210&gt; 33

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 33

ccatgcagcc caaccgttgg cgataaagtc cgtttaggcg ataccaattt atgggcaacc  
 60  
 attgaacaag atttattaac caaagggtgat gagtgtaaat ttggtggcgg taaaagtgtg  
 120  
 cgtgatggta tggcgcaaag cggcaccgca actcgcgaca atccaaatgt attggatttt  
 180  
 gtgattacca atgtgatgat cattgatgcc aaattaggca ttatcaaagc cgatattggg  
 240

attcgcgatg gtcgtattgt cggatcggga caagcaggta accctgacac catggatgac  
 300  
 gtcacgccaa acatgattat cggtgctagc acagaagtac ataacggtgc a  
 351

<210> 34  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
 Pro Cys Ser Pro Thr Val Gly Asp Lys Val Arg Leu Gly Asp Thr Asn  
 1 5 10 15  
 Leu Trp Ala Thr Ile Glu Gln Asp Leu Leu Thr Lys Gly Asp Glu Cys  
 20 25 30  
 Lys Phe Gly Gly Gly Lys Ser Val Arg Asp Gly Met Ala Gln Ser Gly  
 35 40 45  
 Thr Ala Thr Arg Asp Asn Pro Asn Val Leu Asp Phe Val Ile Thr Asn  
 50 55 60  
 Val Met Ile Ile Asp Ala Lys Leu Gly Ile Ile Lys Ala Asp Ile Gly  
 65 70 75 80  
 Ile Arg Asp Gly Arg Ile Val Gly Ile Gly Gln Ala Gly Asn Pro Asp  
 85 90 95  
 Thr Met Asp Asp Val Thr Pro Asn Met Ile Ile Gly Ala Ser Thr Glu  
 100 105 110  
 Val His Asn Gly Ala  
 115

<210> 35  
 <211> 355  
 <212> DNA  
 <213> Homo sapiens

<400> 35  
 nngctagctg caccaccacc tggtcatgca ggcagagcgg ccaccctca tggaagaaga  
 60  
 ggaatccact gtattgggca caggcttcct gctggacctt ggcaagcagg tgcttggtg  
 120  
 gtaccaggaa gtccagcgtg tacctcagtg cgtcctcccg ataagtcctc tccaccacct  
 180  
 ggaacacctg gcccacagg gtgggggctg ttgcctcaaa ggggtggatac agggcggcga  
 240  
 gagtgctctg cacacagtcc tccactggct caggctccat ggctcggcgc cgggccgcgt  
 300  
 ccgacgcttg gtcgggcggg cggggccggg cgcgccaccg cctcccttca cgcgt  
 355

<210> 36  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
 Xaa Leu Ala Ala Pro Pro Pro Val His Ala Gly Arg Ala Ala Thr Pro

```

      1           5           10           15
His Gly Arg Arg Gly Ile His Cys Ile Gly His Arg Leu Pro Ala Gly
      20           25           30
Pro Trp Gln Ala Gly Ala Trp Leu Val Pro Gly Ser Pro Ala Cys Thr
      35           40           45
Ser Val Arg Pro Pro Asp Lys Ser Ser Pro Pro Pro Gly Thr Pro Gly
50-----55-----60-----
Pro Thr Gly Trp Gly Leu Leu Pro Gln Arg Val Asp Thr Gly Arg Arg
65           70           75           80
Glu Cys Ser Ala His Ser Pro Pro Leu Ala Gln Ala Pro Trp Leu Gly
      85           90           95
Ala Gly Pro Arg Pro Thr Leu Gly Arg Ala Gly Gly Ala Gly Arg Ala
      100          105          110
Thr Ala Ser Leu His Ala
      115

```

<210> 37  
 <211> 492  
 <212> DNA  
 <213> Homo sapiens

```

<400> 37
acgcgtggcc ttcgtctgcc accaggaccg actcagcccc accgggtttc cggacccgcc
60
gcaaccatga caagggcgat gttgtgatct ggggtggattc cttctccgac atgctcgagg
120
gatcggatct ctccggcgga gtcacgggtgc ttgccgaggc cggctatcgc ccacgggtcc
180
tcgccgacga cgtctgctgc gggttgacgt ggatcactac cggtcagctc gacggtgctc
240
ggcgtcggct gcgcgtggt ctccgacgtgc tggcaccctc gtcagacgcc agcgtcccag
300
tcgttgggct agagccgtcc tgcactaccg tctggcgtga tgacgcactc cgcctcctgc
360
cagatgatcc gcgcgtccac cgggtagcca gaaacatgca taccgtcgcc gagatgcttg
420
aggcagcaca gtggacccca ccctcgctag caggccacac cctcgtcgct cagccccatt
480
gtcateccgc gg
492

```

<210> 38  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

```

<400> 38
Met Leu Glu Gly Ser Asp Leu Ser Ala Val Val Thr Val Leu Ala Glu
      1           5           10           15
Ala Gly Tyr Arg Pro Arg Val Leu Ala Asp Asp Val Cys Cys Gly Leu
      20           25           30
Thr Trp Ile Thr Thr Gly Gln Leu Asp Gly Ala Arg Arg Arg Leu Arg
      35           40           45
Ala Gly Leu Asp Val Leu Ala Pro Leu Ser Asp Ala Ser Val Pro Val

```

```

      50              55              60
Val Gly Leu Glu Pro Ser Cys Thr Thr Val Trp Arg Asp Asp Ala Leu
65              70              75              80
Arg Leu Leu Pro Asp Asp Pro Arg Val His Arg Val Ala Arg Asn Met
      85              90              95
His Thr Val Ala Glu Met Leu Glu Ala Ala Gln Trp Thr Pro Pro Ser
      100             105             110
Leu Ala Gly His Thr Leu Val Ala Gln Pro His Cys His Pro Ala
      115             120             125

```

<210> 39  
 <211> 412  
 <212> DNA  
 <213> Homo sapiens

```

<400> 39
aacgaaggtt ccgtacgcgc tctgaaagcc ctgcgtaaaag agcgttccga tcgccgggaa
60
gtgatngca ccgcaaaaat gcaggtggtc gaagccgcga gttcaggcaa gattgtcttt
120
gaaatggaag acgtttatta cagcattgcc ggaaaacaac tggtagagcaa cttctctgcg
180
caagtcatgc gtggtgataa aattgcgctg attggcccga acggttgttg taaaacgacg
240
ttgctgaaac tgatgttaag taagattcag gcagacagcg gccgtgttca ctgcggtact
300
aaactggaag ttgcgtactt cgaccagcac cgtgctgagc tggatcctga gcgtacggtg
360
atggataacc tggccgaagg taagcaggaa gtgatggtaa atggccgtgt an
412

```

<210> 40  
 <211> 137  
 <212> PRT  
 <213> Homo sapiens

```

<400> 40
Asn Glu Gly Xaa Val Arg Ala Leu Lys Ala Leu Arg Lys Glu Arg Ser
1      5      10      15
Asp Arg Arg Glu Val Met Xaa Thr Ala Lys Met Gln Val Val Glu Ala
20     25     30
Ala Ser Ser Gly Lys Ile Val Phe Glu Met Glu Asp Val Tyr Tyr Ser
35     40     45
Ile Ala Gly Lys Gln Leu Val Ser Asn Phe Ser Ala Gln Val Met Arg
50     55     60
Gly Asp Lys Ile Ala Leu Ile Gly Pro Asn Gly Cys Gly Lys Thr Thr
65     70     75     80
Leu Leu Lys Leu Met Leu Ser Lys Ile Gln Ala Asp Ser Gly Arg Val
85     90     95
His Cys Gly Thr Lys Leu Glu Val Ala Tyr Phe Asp Gln His Arg Ala
100    105    110
Glu Leu Asp Pro Glu Arg Thr Val Met Asp Asn Leu Ala Glu Gly Lys
115    120    125
Gln Glu Val Met Val Asn Gly Arg Val

```

130

135

&lt;210&gt; 41

&lt;211&gt; 1080

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 41

gaattcaagt ggacacaggc tccacgcccg cgtctcaccg ataagagcta caagcacaac  
 60  
 tactatgacg agcgggtttc gtcgaagag cgtcttgagc gcactgtggc taaggatttc  
 120  
 gtcacgacgg aggtcgagcc catgtgggat gcggctgatg tcatgcggat gggtaaggat  
 180  
 ctcttcatcc agcacggtct gacgacaaat cggaagtcaa tggagtgggt taagcgttac  
 240  
 taccocgatt tccgcgttca cgcggtgaat ttccttgggg atccgtaccc gatccatata  
 300  
 gacgcgacct ttgtgccgct tcgtccgggg ctcatcatca acaaccgaa tcgtccactg  
 360  
 ccgcaggagc agaggaagat cttcgaggcc aatgactggc agatcggtga tgctgctcag  
 420  
 ccggcgacag acacgcctcc agaattgtgc tactcgtctg tgtggctatc aatgaactgc  
 480  
 ttggtacttg atccgaagac ggtcatctgc gaggcctcgg aagttcatca gatggagcag  
 540  
 atggacaagc tgggtatgaa cgtcatcccc gtcgccttcc gtgacgcgta cccattcggg  
 600  
 ggaggtctcc actgcgccac agctgatgta tatcggaag gtacctgtga ggactacttc  
 660  
 ccgaatcagg tcgacgaccc gaccttgggt tgagaaaacc ccgtgggtcat gtcatgactg  
 720  
 acggatctcg gtggctcggg acggaactta cgttgtccgt taccgggccg ccgggtctga  
 780  
 tatggcagta tcacgcctag caaaaaggag catgtcatgg acatggagcc gggcatcatc  
 840  
 aacgtcaaac aggaagttcc aggcgtcggg acgatgaacc agaaagtggg attcgtgtcc  
 900  
 atgcttcttt ctgcaacggg tatgggggtg gtgggtactt tcgggcgtct cagcactcct  
 960  
 gtggatccca cgacgggcag taagtacatc atcggtgatt ttttgccac tggtaggatg  
 1020  
 atagtcgggg tcctgggatt tctgcttatt atcgtcatac ttggaaaatg gtctgagctc  
 1080

&lt;210&gt; 42

&lt;211&gt; 230

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 42

Glu Phe Lys Trp Thr Gln Ala Pro Arg Pro Arg Leu Thr Asp Lys Ser  
 1 5 10 15  
 Tyr Lys His Asn Tyr Tyr Asp Glu Arg Val Ser Leu Glu Glu Arg Leu



```

          20          25          30
Glu Arg Thr Val Ala Lys Asp Phe Val Thr Thr Glu Val Glu Pro Met
          35          40          45
Trp Asp Ala Ala Asp Val Met Arg Met Gly Lys Asp Leu Phe Ile Gln
          50          55          60
His Gly Leu Thr Thr Asn Arg Lys Ser Met Glu Trp Phe Lys Arg Tyr
          65          70          75          80
Tyr Pro Asp Phe Arg Val His Ala Val Asn Phe Pro Gly Asp Pro Tyr
          85          90          95
Pro Ile His Ile Asp Ala Thr Phe Val Pro Leu Arg Pro Gly Leu Ile
          100          105          110
Ile Asn Asn Pro Asn Arg Pro Leu Pro Gln Glu Gln Arg Lys Ile Phe
          115          120          125
Glu Ala Asn Asp Trp Gln Ile Val Asp Ala Ala Gln Pro Ala His Asp
          130          135          140
Thr Pro Pro Glu Leu Cys Tyr Ser Ser Val Trp Leu Ser Met Asn Cys
          145          150          155          160
Leu Val Leu Asp Pro Lys Thr Val Ile Cys Glu Ala Ser Glu Val His
          165          170          175
Gln Met Glu Gln Met Asp Lys Leu Gly Met Asn Val Ile Pro Val Ala
          180          185          190
Phe Arg Asp Ala Tyr Pro Phe Gly Gly Gly Leu His Cys Ala Thr Ala
          195          200          205
Asp Val Tyr Arg Glu Gly Thr Cys Glu Asp Tyr Phe Pro Asn Gln Val
          210          215          220
Asp Asp Pro Thr Leu Val
          225          230

```

<210> 43  
 <211> 358  
 <212> DNA  
 <213> Homo sapiens

```

<400> 43
gggcccccca catagtggac acagggtttct gggatgtcag catggagtgc caagaggtgg
60
gtgaccacct ggtggggaat aaggcgcttc tgggacatag aggctgcctt ccagctgcgc
120
ctggcagagc tgttgacaca acagcatggt ctgcagtgcc gggccactgc caccacacc
180
gatgtccttt aaggatggat ttgggttttc ggattcgcgt ggcctatcag cgggagtcctc
240
agatcctgaa ggaagtgcag agcccagagg ggatgatctc gctgagggac acagctgcct
300
ccctccgct tgagagagac acaaggcagt tgccactgct caccagtgcc ctgcacgn
358

```

<210> 44  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

```

<400> 44
Met Glu Cys Gln Glu Val Gly Asp His Leu Val Gly Asn Lys Ala Leu

```

1	5	10	15
Leu Gly His Arg Gly Cys Leu Pro Ala Ala Pro Gly Arg Ala Val Asp			
	20	25	30
Thr Thr Ala Trp Ser Ala Val Pro Gly His Cys His Ala His Arg Cys			
	35	40	45
Pro Leu Arg Met Asp Leu Gly Phe Arg Ile Arg Val Ala Tyr Gln Arg			
	50	55	60
Glu Ser Gln Ile Leu Lys Glu Val Gln Ser Pro Glu Gly Met Ile Ser			
65	70	75	80
Leu Arg Asp Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp Thr Arg Gln			
	85	90	95
Leu Pro Leu Leu Thr Ser Ala Leu His			
	100	105	

&lt;210&gt; 45

&lt;211&gt; 905

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 45

gtcgacgata aaggagtatt tgcgcagcag cagtatgatg ctctcgttga ggcgggtttc  
 60  
 gcggctcctg gaatcccaga gcagtatggt ggcgacggtg cggatgcgat tgcgtccgca  
 120  
 ataatcatgg aaggagtcgc tcgagtctgt gcgtcgtcgt ccaccgtcat atcgtccaat  
 180  
 gagcttggtta ccgtccctct cctcaaatac ggtagcgagg agcagaggaa acgttatctt  
 240  
 tctgaagttg cttcgggtaa ggcacttttc ggatatgcgc tctccgaggc tgatgctgga  
 300  
 tcagatccag ctgcacttaa gtgtcgagcc gacgaagatg gggacagttt cgtcctgaat  
 360  
 ggcgttaagg cttgggtcac ggaggctggc gaggccaagt acctggtgat atttgcggtt  
 420  
 actgacccag acgatccgcg ccacagaatc agcgcgttga tgggtccatgc agatgacccg  
 480  
 ggcattagct acggggctcc ggagcacaaa atggggatag gcgggtcagt taccagggaa  
 540  
 gtggttttca agaatacgcg tatccccaag gaacgagtaa ttggccgtcg agggcacggt  
 600  
 ctgagtgttg ctctaggtac gcttgataac tctcgtgtct cgattgctgc tcaagcagtg  
 660  
 ggaattgccc aaggagcttt agacattgcc acggattacg tccagaagcg caagcagttt  
 720  
 ggccagccac tgtccaattt tgagggaatc cagttcatgc tcgcagacat ggcaatgcgt  
 780  
 ttggaggcgg cgcgagcgct gacatactct gcagctgac gtagtgggcy ccagactgac  
 840  
 gatgtgagtt atttcggcgc ggcggccaaa tgtttcgctt ccgacacagc gatggcagtg  
 900  
 tgcac  
 905

&lt;210&gt; 46

<211> 301  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
 Val Asp Asp Lys Gly Val Phe Ala Gln Gln Gln Tyr Asp Ala Leu Val  
 1 5 10 15  
 Glu Ala Gly Phe Ala Ala Pro Gly Ile Pro Glu Gln Tyr Gly Gly Asp  
 20 25 30  
 Gly Ala Asp Ala Ile Ala Ser Ala Ile Ile Met Glu Glu Val Ala Arg  
 35 40 45  
 Val Cys Ala Ser Ser Ser Thr Val Ile Ser Ser Asn Glu Leu Gly Thr  
 50 55 60  
 Val Pro Leu Leu Lys Tyr Gly Ser Glu Glu Gln Arg Lys Arg Tyr Leu  
 65 70 75 80  
 Ser Glu Val Ala Ser Gly Lys Ala Leu Phe Gly Tyr Ala Leu Ser Glu  
 85 90 95  
 Ala Asp Ala Gly Ser Asp Pro Ala Ala Leu Lys Cys Arg Ala Asp Glu  
 100 105 110  
 Asp Gly Asp Ser Phe Val Leu Asn Gly Val Lys Ala Trp Val Thr Glu  
 115 120 125  
 Ala Gly Glu Ala Lys Tyr Leu Val Ile Phe Ala Val Thr Asp Pro Asp  
 130 135 140  
 Asp Pro Arg His Arg Ile Ser Ala Leu Met Val His Ala Asp Asp Pro  
 145 150 155 160  
 Gly Ile Ser Tyr Gly Ala Pro Glu His Lys Met Gly Ile Arg Gly Ser  
 165 170 175  
 Val Thr Arg Glu Val Val Phe Lys Asn Thr Arg Ile Pro Lys Glu Arg  
 180 185 190  
 Val Ile Gly Arg Arg Gly His Gly Leu Ser Val Ala Leu Gly Thr Leu  
 195 200 205  
 Asp Asn Ser Arg Val Ser Ile Ala Ala Gln Ala Val Gly Ile Ala Gln  
 210 215 220  
 Gly Ala Leu Asp Ile Ala Thr Asp Tyr Val Gln Lys Arg Lys Gln Phe  
 225 230 235 240  
 Gly Gln Pro Leu Ser Asn Phe Glu Gly Ile Gln Phe Met Leu Ala Asp  
 245 250 255  
 Met Ala Met Arg Leu Glu Ala Ala Arg Ala Leu Thr Tyr Ser Ala Ala  
 260 265 270  
 Asp Arg Ser Gly Arg Gln Thr Asp Asp Val Ser Tyr Phe Gly Ala Ala  
 275 280 285  
 Ala Lys Cys Phe Ala Ser Asp Thr Ala Met Ala Val Cys  
 290 295 300

<210> 47  
 <211> 379  
 <212> DNA  
 <213> Homo sapiens

<400> 47  
 aagcttgtag agctagtccg aagcggactg tcggtacgcc aagctgctaa aagatgtggg  
 60  
 atgcatactta ccgctgcgta tgccgtagct acggaagctg ggtgccatat ccggttaagt  
 120

cagtatgctc ggaaagtccg ccagacgcag ttaagagtgg aatacctgcg ccttcggctg  
 180  
 gcgagcctgc ctggtggtga tgctggcgcg gcagtaggaa ttgatcgctg actgcgttta  
 240  
 gatttcgaaa aaggactcac caaatcccag ggctgcagcag aagagttcat acccgctggc  
 300  
 gaagacgcca gcäcgtataa cagacttatg aaagcgctgc gccaacgcca tgatgtcatc  
 360  
 aaatccggaa agcttgccc  
 379

<210> 48  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 48  
 Met His Leu Thr Ala Ala Tyr Ala Val Ala Thr Glu Ala Gly Cys His  
 1 5 10 15  
 Ile Arg Leu Ser Gln Tyr Ala Arg Lys Val Arg Gln Thr Gln Leu Arg  
 20 25 30  
 Val Glu Tyr Leu Arg Leu Arg Leu Ala Ser Leu Pro Gly Gly Asp Ala  
 35 40 45  
 Gly Ala Ala Val Gly Ile Asp Arg Arg Leu Arg Leu Asp Phe Glu Lys  
 50 55 60  
 Gly Leu Thr Lys Ser Gln Gly Arg Arg Glu Glu Phe Ile Pro Val Gly  
 65 70 75 80  
 Glu Asp Ala Ser Thr Tyr Asn Arg Leu Met Lys Ala Leu Arg Gln Arg  
 85 90 95  
 His Asp Val Ile Lys Ser Gly Lys Leu Ala  
 100 105

<210> 49  
 <211> 309  
 <212> DNA  
 <213> Homo sapiens

<400> 49  
 tgatcatgat gctggcatgg actattctgg tccctgttcc tctctcacct gctgaaggac  
 60  
 atccctctaa tttttgtgtc tccttctgta tcatcaaatt tccctctct actgagtctc  
 120  
 ttgcatctcc ttggaagcat gctgtactat gtcccatcct taaagaactc cccttgctcg  
 180  
 cacattaccc tctgccagct ggctcatttt tctgctcccc ttacaggga aactcttcaa  
 240  
 aaagtatatc ccacctcctt ccattctcatg ttctcttgaa cctgcagtac tgggtgctcc  
 300  
 ctccttttg  
 309

<210> 50  
 <211> 101  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 50

```

Met Met Leu Ala Trp Thr Ile Leu Val Pro Val Pro Leu Ser Pro Ala
 1             5             10             15
Glu Gly His Pro Ser Asn Phe Cys Val Ser Phe Cys Ile Ile Lys Phe
 20             25             30
Ser Leu Ser Thr Glu Ser Leu Ala Ser Pro Trp Lys His Ala Val Leu
 35             40             45
Cys Pro Ile Leu Lys Glu Leu Pro Leu Ser Ala His Tyr Pro Leu Pro
 50             55             60
Ala Gly Ser Phe Phe Cys Ser Pro Leu Gln Gly Asn Ser Ser Lys Ser
 65             70             75             80
Tyr Leu His Leu Leu Pro Ser His Val Leu Leu Asn Leu Gln Tyr Trp
 85             90             95
Val Leu Pro Pro Phe
 100

```

&lt;210&gt; 51

&lt;211&gt; 512

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 51

```

agatctttga agaattgccca cactgtcttc ctccctgctt ataatttcct tattccctag
60
gatgtgatcc ttgttcttgg ggccctcacat ggcagctgga tctctggcga ttgcatctga
120
gttccagaca ccaggatgga aaagaaaaga aggaggggca agaggaaccc ccagatgctc
180
cttaagagct actgctggc attccactt gcatctcatt tgctcgatcg ctgtcactgt
240
gccctaacga gctgcaagga cactggggaa atgagtctgt cttgtacttc atgtgccctt
300
caaaatcttc tggtgctgag ggagaagagg ccagccggta ttgaggaaca actagcactt
360
tctgcttccg cgtcccaggg ggacgtgggt gtgttgaatc cacaccgggg gtgcggacct
420
ctgaggctgg gctggatggg acatcaggtg ggccctctgt ttcatttatg tgacctccca
480
tcaggctcttc tggttggatc ctgctttcta ga
512

```

&lt;210&gt; 52

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 52

```

Met Glu Lys Lys Arg Arg Arg Gly Lys Arg Asn Pro Gln Met Leu Leu
 1             5             10             15
Lys Ser Tyr Cys Val Ala Phe Pro Leu Ala Ser His Leu Leu Asp Arg
 20             25             30
Cys His Cys Ala Leu Thr Ser Cys Lys Asp Thr Gly Glu Met Ser Leu

```

```

      35          40          45
Ser Cys Thr Ser Cys Ala Pro Gln Asn Leu Leu Leu Leu Arg Glu Lys
  50          55          60
Arg Pro Ala Gly Ile Glu Gln Leu Ala Leu Ser Ala Ser Ala Ser
  65          70          75          80
Gln Gly Asp Val Gly Val Leu Asn Pro His Arg Gly Cys Gly Pro Leu
      85          90          95
Arg Leu Gly Trp Met Gly His Gln Val Gly Pro Leu Phe His Leu Cys
      100          105          110
Asp Leu Pro Ser Gly Leu Leu Val Gly Ser Cys Phe Leu
      115          120          125

```

<210> 53  
 <211> 474  
 <212> DNA  
 <213> Homo sapiens

```

<400> 53
accggtacac ctacgtcacc cgtaaaaacc gacgcaatac ccggatcgcc tcgtcctcaa
60
aaaattcgat cccgtcgtgc gtcgtcacat tgagttcaag gaggcccgct aatggccaaa
120
aagccaaga ttgtcgccca gaagaaacgt gagaagctcg tagcccaata cgccgaaagg
180
cgcgccgaac tcaaggccat catgaagtgc ccaactgcct cattggacga acgcatggag
240
gcatcgcgta agctgtctcg cctgccgcgc gattcatccc ccgtgcgggtt acgtaaccgt
300
gaccaagtcg acgggcgtcc ccgcggctac gttggcaagg ccggtgtgtc ccgtatccgt
360
ttccgtgaga tggcccaccg cggcgaactc cccggaatcg cgaagtcaag ctggtgaagc
420
catggcagta ccgaagcgaa agaagtcctg ttccgaccacg cgtcataggc gggc
474

```

<210> 54  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

```

<400> 54
Met Ala Lys Lys Ser Lys Ile Val Ala Gln Lys Lys Arg Glu Lys Leu
  1          5          10          15
Val Ala Gln Tyr Ala Glu Arg Arg Ala Glu Leu Lys Ala Ile Met Lys
      20          25          30
Cys Pro Thr Ala Ser Leu Asp Glu Arg Met Glu Ala Ser Arg Lys Leu
      35          40          45
Ser Arg Leu Pro Arg Asp Ser Ser Pro Val Arg Leu Arg Asn Arg Asp
      50          55          60
Gln Val Asp Gly Arg Pro Arg Gly Tyr Val Gly Lys Ala Gly Val Ser
      65          70          75          80
Arg Ile Arg Phe Arg Glu Met Ala His Arg Gly Glu Leu Pro Gly Ile
      85          90          95
Ala Lys Ser Ser Trp

```

100

<210> 55  
 <211> 378  
 <212> DNA  
 <213> Homo sapiens

<400> 55  
 ccatggccca ggacagccgg catatcggct acgactacgg tacaccggtg gcgccacagt  
 60  
 tcggcgccagc caagcccgca gcgtgctgcc aggcgcaagc gacaaacacc ggcccggtggg  
 120  
 tgggtgttcca ccatgtgcgt tgcacccacg acacctttct gatcgacgtc tttctcaacc  
 180  
 agcccgatgc caccgcgcag cagggtcaatg ccgacaaccc gcactacgtc gggcgtttca  
 240  
 gccgcacggt catgggcctg gtggatgaca agggccggtg cattacccag ggcgtatcgc  
 300  
 gcgcgttgaa tgcggcgcg cagaccaagg cgctgaacct gggaccgagt gacgcggcgc  
 360  
 agttatcggg gaggcgta  
 378

<210> 56  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 56  
 Met Ala Gln Asp Ser Arg His Ile Gly Tyr Asp Tyr Gly Thr Pro Val  
 1 5 10 15  
 Ala Pro Gln Phe Gly Ala Ala Lys Pro Ala Ala Cys Cys Gln Ala Gln  
 20 25 30  
 Ala Thr Asn Thr Gly Pro Trp Val Val Phe Asp His Val Arg Cys Thr  
 35 40 45  
 His Asp Thr Phe Leu Ile Asp Val Phe Leu Asn Gln Pro Asp Ala Thr  
 50 55 60  
 Ala Gln Gln Val Asn Ala Asp Asn Pro His Tyr Val Gly Arg Phe Ser  
 65 70 75 80  
 Arg Ile Gly Met Gly Leu Val Asp Asp Lys Gly Arg Cys Ile Thr Gln  
 85 90 95  
 Gly Val Ser Arg Ala Leu Asn Ala Ala Arg Ser Thr Lys Ala Leu Asn  
 100 105 110  
 Leu Gly Pro Ser Asp Ala Ala Gln Leu Ser Val Arg Arg  
 115 120 125

<210> 57  
 <211> 388  
 <212> DNA  
 <213> Homo sapiens

<400> 57  
 agaccacccc gacacagatc aggagtcgtc atgtccagaa agaagaaggc cggcatcctc  
 60

accgcaggcg gtgattgccc cgggctcaac gccgctatcc gcggatttgg caaggctgcc  
 120  
 atccgccagc acgacatgga gctcatcggt attcaggacg gctttcttgg attggcggga  
 180  
 aaccgcacca tctcccttgg cccgcgtgcc ctctcaggca tcttgacggt cggcgggacc  
 240  
 atcctgggaa ctagccgtga caaggtaaat cacatgatta tcgacggcga ggaacgggat  
 300  
 atggtcccca ccaccgtcga gaattacgag aagctggggc ttgacgcttt ggtgactttg  
 360  
 ggtggcgggtg gcaccgcca gaacgcgt  
 388

<210> 58

<211> 129

<212> PRT

<213> Homo sapiens

<400> 58

Arg	Pro	Thr	Arg	His	Arg	Ser	Gly	Val	Val	Met	Ser	Arg	Lys	Lys	Lys
1				5					10					15	
Val	Gly	Ile	Leu	Thr	Ala	Gly	Gly	Asp	Cys	Pro	Gly	Leu	Asn	Ala	Ala
			20					25					30		
Ile	Arg	Gly	Phe	Gly	Lys	Ala	Ala	Ile	Arg	Gln	His	Asp	Met	Glu	Leu
		35					40					45			
Ile	Gly	Ile	Gln	Asp	Gly	Phe	Leu	Gly	Leu	Ala	Gly	Asn	Arg	Thr	Ile
	50					55				60					
Ser	Leu	Gly	Pro	Arg	Ala	Leu	Ser	Gly	Ile	Leu	Thr	Val	Gly	Gly	Thr
65				70					75					80	
Ile	Leu	Gly	Thr	Ser	Arg	Asp	Lys	Val	Asn	His	Met	Ile	Ile	Asp	Gly
			85					90					95		
Glu	Glu	Arg	Asp	Met	Val	Pro	Thr	Thr	Val	Glu	Asn	Tyr	Glu	Lys	Leu
			100				105						110		
Gly	Leu	Asp	Ala	Leu	Val	Thr	Leu	Gly	Gly	Gly	Gly	Thr	Ala	Lys	Asn
		115					120					125			
Ala															

<210> 59

<211> 417

<212> DNA

<213> Homo sapiens

<400> 59

ggtaccatcg gagctcgaca agaaatgggtt ggggtgaagtc gtggcttctg ctccaccag  
 60  
 tgccctcatg ggtcagccca cctgaatatc ttcatgcctg tgcatttctc ctgatgttca  
 120  
 cgtgtgccct gtgtttttac gcatctgtga tcgtgcaccc acgcgtctca gagaggagcc  
 180  
 cgtttgggaa tccggagaat gtgcgctggc ggaagagcgt cacacactgg aagcaaacct  
 240  
 cagaccgcgt ggacaagacc aaggatgaaa tggaacacga ggccttggtg gaagggaacc  
 300



tggcaaccga ggcaagccta gtggttcttg acacactgga gatcatcgtg cagacggtga  
 360  
 tgctttcaga agcccgagg agcgtcttgg gggcagtgt gaaggttgtg ctgtaca  
 417

<210> 60  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 60  
 Met Phe Thr Cys Ala Leu Cys Phe Tyr Ala Ser Val Ile Val His Pro  
 1 5 10 15  
 Arg Val Ser Glu Arg Ser Pro Phe Gly Asn Pro Glu Asn Val Arg Trp  
 20 25 30  
 Arg Lys Ser Val Thr His Trp Lys Gln Thr Ser Asp Arg Val Asp Lys  
 35 40 45  
 Thr Lys Asp Glu Met Glu His Glu Ala Leu Val Glu Gly Asn Leu Ala  
 50 55 60  
 Thr Glu Ala Ser Leu Val Val Leu Asp Thr Leu Glu Ile Ile Val Gln  
 65 70 75 80  
 Thr Val Met Leu Ser Glu Ala Arg Glu Ser Val Leu Gly Ala Val Leu  
 85 90 95  
 Lys Val Val Leu Tyr  
 100

<210> 61  
 <211> 304  
 <212> DNA  
 <213> Homo sapiens

<400> 61  
 agatcttcac agccttagac ttttttcatg ggtgccttac agttttggag gtccctatcc  
 60  
 gcacacatat ttgcaggctt ggagagagtg tgtgggggca tgtactttcg gtgggtcaag  
 120  
 tatgaagaag caggccttat aaacacatat tctgacctta acctgtactt cagaagagga  
 180  
 ccgtgactc accaaggagg cctgaaggac aaggcagcat ctctgtcttc acatgagtcc  
 240  
 tcccctagac cgggcccatt gccaggcctg accacagagc tcccattgcc tttcctgcac  
 300  
 gcgt  
 304

<210> 62  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 62  
 Met Gly Ala Leu Gln Phe Trp Arg Ser Leu Ser Ala His Ile Phe Ala  
 1 5 10 15

Gly Leu Glu Arg Val Cys Gly Gly Met Tyr Phe Arg Trp Val Lys Tyr  
 20 25 30  
 Glu Glu Ala Gly Leu Ile Asn Thr Tyr Ser Asp Leu Asn Leu Tyr Phe  
 35 40 45  
 Arg Arg Gly Pro Leu Thr His Gln Gly Gly Leu Lys Asp Lys Ala Ala  
 50 55 60  
 Ser Leu Ser Ser His Glu Ser Ser Pro Arg Pro Gly Pro Trp Pro Gly  
 65 70 75 80  
 Leu Thr Thr Glu Leu Pro Leu Pro Phe Leu His Ala  
 85 90

<210> 63  
 <211> 577  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
 cgcgtcaagg gggctctacac cgggacgatt aacgcctcgg tgggagtatt catcaccgcg  
 60  
 ctgacgggtgc tagctgggtg gctcacccta gccgggcgta tcagtgtcgg ggaactcgtc  
 120  
 accgtgggtcg ggctggccca aaccctcggc cctccgctgc gagcactggg cgctgacacc  
 180  
 gcgacgatgt tggccaccgc ccacgcctcc ggggaccgat tctgtgagtt gcgtgatagc  
 240  
 ccggcagcct ggcagatcca ccccacgac ggtgcccga ccacaccggg tgatggcccc  
 300  
 gtggagttgc acatcccggg cagggatttc cagcttgacg tcgccggcgg caccatgtg  
 360  
 ggtatcatgg cgctcaatc ggtctgtgac gccttgccg aggcgataga ccacggctcc  
 420  
 gagaccgtct tgaatggggg tcccggcagt cgctcaacc ctgcccacg gcgtcgtctg  
 480  
 gtgctgggtg ctccccgctc ccccgaaactg ttcgacgata ctgcccgctg gaacatcgtg  
 540  
 cttgacagcc agacgactgt cgccaggctg aatgcat  
 577

<210> 64  
 <211> 192  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Arg Val Lys Gly Val Tyr Thr Gly Thr Ile Asn Ala Ser Val Gly Val  
 1 5 10 15  
 Phe Ile Thr Ala Leu Thr Val Leu Ala Gly Trp Leu Thr Leu Ala Gly  
 20 25 30  
 Arg Ile Ser Val Gly Glu Leu Val Thr Val Val Gly Leu Ala Gln Thr  
 35 40 45  
 Leu Gly Pro Pro Leu Arg Ala Leu Gly Val Asp Thr Ala Thr Met Leu  
 50 55 60  
 Ala Thr Ala His Ala Ser Gly Asp Arg Phe Cys Glu Leu Arg Asp Ser  
 65 70 75 80

```

Pro Ala Ala Trp Gln Ile His Pro Asp Asp Gly Ala Arg Thr Thr Pro
      85          90          95
Gly Asp Gly Pro Val Glu Leu His Ile Pro Val Arg Asp Phe Gln Leu
      100        105        110
Asp Val Ala Gly Gly Thr His Val Gly Ile Met Ala Pro Gln Ser Val
      115        120        125
Cys Asp Ala Leu Ala Glu Ala Ile Asp His Gly Ser Glu Thr Val Leu
      130        135        140
Asn Gly Val Pro Ala Ser Arg Leu Asn Pro Ala Gln Arg Arg Arg Leu
      145        150        155        160
Val Leu Val Ala Pro Arg Ser Pro Glu Leu Phe Asp Asp Thr Ala Arg
      165        170        175
Ala Asn Ile Val Leu Asp Ser Gln Thr Thr Val Ala Arg Leu Asn Ala
      180        185        190

```

&lt;210&gt; 65

&lt;211&gt; 339

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 65

```

gtcgaccgcg ccttgggatac gctcgaaggg gccagcctgg accaggtagc ggaagaagtc
60
aagaaggccg ctttcaagat caccgcgccc gggcaactag tgggcacccat ggccctccgag
120
cgccttggcg tacccttcgg catcatcgac ctttcgcttg cccctactgc cgaattggga
180
gattcggggg cccacatcct tgagcatatg ggattggacc aagtaggcac gcacggcaca
240
actgctgctt tggctctgct taacgacgcc gtaaagaaag gcggcatgat ggccctgcccc
300
cgcgtcggcg gtttgtctgg ctcccttcac ccgggctcc
339

```

&lt;210&gt; 66

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 66

```

Val Asp Arg Ala Leu Gly Ser Leu Glu Gly Ala Ser Leu Asp Gln Val
  1          5          10          15
Ala Glu Glu Val Lys Lys Ala Ala Phe Lys Ile Thr Arg Ala Gly Gln
      20        25        30
Leu Val Gly Thr Met Ala Ser Glu Arg Leu Gly Val Pro Phe Gly Ile
      35        40        45
Ile Asp Leu Ser Leu Ala Pro Thr Ala Glu Leu Gly Asp Ser Gly Ala
      50        55        60
His Ile Leu Glu His Met Gly Leu Asp Gln Val Gly Thr His Gly Thr
      65        70        75        80
Thr Ala Ala Leu Ala Leu Asn Asp Ala Val Lys Lys Gly Gly Met
      85        90        95
Met Ala Cys Pro Arg Val Gly Gly Leu Ser Gly Ser Phe Ile Pro Gly
      100       105       110

```

Ser

&lt;210&gt; 67

&lt;211&gt; 446

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 67

tgatcataaa ccacgcgtca ccgaggggat gtggcacacc tacctgcgcg tcgcagatgc  
 60  
 cgcacaggga cgggtcaggg gcgttcgagg cgccagctgg cacaacttcg cgaccggtga  
 120  
 caaggggtcc ttgcagccca acgagcttgc cgtaactcct gatactgaca ccgtcatcca  
 180  
 gggagtcggg cccgccctag ccctcctcga ttcagcgtgg ggacgccaga tccacgtgga  
 240  
 gacaacaggg tgtcccagtg ccgtggtctg gaatccacgc tcctcgtcga cacatgccga  
 300  
 taaccgcaca gccagggcat ggcgcgattt cgtatgcgtc gagaccgggg cctgcaagga  
 360  
 caatgcggtc attgttgccc cacacagcga cctcaccatg tccacacgga ttagcgtcga  
 420  
 aacgttgtga tcgctgcatg gatatt  
 446

&lt;210&gt; 68

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

Met Trp His Thr Tyr Leu Arg Val Ala Asp Ala Ala Gln Ala Arg Val  
 1 5 10 15  
 Arg Gly Val Arg Gly Ala Ser Trp His Asn Phe Ala Thr Gly Asp Lys  
 20 25 30  
 Gly Ser Phe Asp Ala Asn Glu Leu Ala Val Thr Pro Asp Thr Asp Thr  
 35 40 45  
 Val Ile Gln Gly Val Gly Pro Ala Leu Ala Leu Asp Ser Ala Trp  
 50 55 60  
 Gly Arg Gln Ile His Val Glu Thr Thr Gly Cys Pro Ser Ala Val Val  
 65 70 75 80  
 Trp Asn Pro Arg Ser Ser Ser Thr His Ala Asp Asn Pro Thr Ala Gln  
 85 90 95  
 Ala Trp Arg Asp Phe Val Cys Val Glu Thr Gly Ala Cys Lys Asp Asn  
 100 105 110  
 Ala Val Ile Val Ala Pro His Ser Asp Leu Thr Met Ser Thr Arg Ile  
 115 120 125  
 Ser Val Glu Thr Leu  
 130

&lt;210&gt; 69

&lt;211&gt; 552

&lt;212&gt; DNA

<213> Homo sapiens

<400> 69

nnaagggttaa ggagaaaagc aaggaccttg caaagagagc ctctgtgccg gagaggctgg  
60  
ccctcaagga ggagccaaaa gaagacccca gtggagcagc tgtgcccagag atgccaaaaa  
120  
agtcctccaa gattgccagc ttcattccca aaggggggaa gctcaacagt gccagaagg  
180  
agcnccatgg ccccttcctt cagtgggaata ccaaaaccag gaatgaaaag catgcccggg  
240  
aaatccccaa gtgcccagc gccttccaag gaaggggagc ggagccggag tgggaagctg  
300  
agctcaggac tccccagca gaagccccag ctggacggca gacactccag ttcctcttcc  
360  
agcctggcgt cctcagaagg aaaaggccca ggagggacca ccctgaacca cagcatcagc  
420  
agccagactg tcagtgggtc tgtcgggacc acccagacca caggaagcaa tnnaccgtca  
480  
gtgttcagct acctcagccc cagcagcaat acaaccatcc caaactgcc acggttgac  
540  
ctttcctgta ca  
552

<210> 70

<211> 184

<212> PRT

<213> Homo sapiens

<400> 70

Xaa	Arg	Val	Arg	Arg	Lys	Ala	Arg	Thr	Leu	Gln	Arg	Glu	Pro	Leu	Cys
1				5					10					15	
Arg	Arg	Gly	Trp	Pro	Ser	Arg	Arg	Ser	Gln	Lys	Lys	Thr	Pro	Val	Glu
		20						25					30		
Gln	Leu	Cys	Pro	Arg	Cys	Gln	Lys	Ser	Pro	Pro	Arg	Leu	Pro	Ala	Ser
		35					40					45			
Ser	Pro	Lys	Gly	Gly	Ser	Ser	Thr	Val	Pro	Arg	Arg	Ser	Xaa	Met	Ala
		50				55					60				
Pro	Ser	Leu	Ser	Gly	Ile	Pro	Lys	Pro	Gly	Met	Lys	Ser	Met	Pro	Gly
65					70				75					80	
Lys	Ser	Pro	Ser	Ala	Pro	Ala	Pro	Ser	Lys	Glu	Gly	Glu	Arg	Ser	Arg
				85					90					95	
Ser	Gly	Lys	Leu	Ser	Ser	Gly	Leu	Pro	Gln	Gln	Lys	Pro	Gln	Leu	Asp
			100					105					110		
Gly	Arg	His	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Ala	Ser	Ser	Glu	Gly	Lys
		115					120					125			
Gly	Pro	Gly	Gly	Thr	Thr	Leu	Asn	His	Ser	Ile	Ser	Ser	Gln	Thr	Val
		130				135						140			
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Val	Phe	Ser	Tyr	Leu	Ser	Pro	Ser	Ser	Asn	Thr	Thr	Ile	Pro	Thr	Leu
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<211> 799

<212> PRT

<213> Homo sapiens

<400> 78

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Thr	Ala	Ser	Ile	Ile	Gly	Asp	Val	Met	Gly	Pro	Thr	Leu	Asn	His	Leu	35	40	45	
Asn	Asn	Leu	Leu	Arg	Leu	Pro	Phe	Gly	Cys	Gly	Glu	Gln	Asn	Met	Ile	50	55	60	
His	Phe	Ala	Pro	Asn	Val	Phe	Val	Leu	Lys	Tyr	Leu	Gln	Lys	Thr	Gln	65	70	75	80
Gln	Leu	Ser	Pro	Glu	Val	Glu	Arg	Glu	Thr	Thr	Asp	Tyr	Leu	Val	Gln	85	90	95	
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Val	Leu	Lys	Ser	Phe	Ala	Gln	Ala	Arg	Ser	Phe	Ile	Phe	Val	Asp	Pro	130	135	140	
Arg	Glu	Leu	Ala	Ala	Ala	Lys	Ser	Trp	Ile	Ile	Gln	Gln	Gln	Gln	Ala	145	150	155	160
Asp	Gly	Ser	Phe	Leu	Ala	Val	Gly	Arg	Val	Leu	Asn	Lys	Asp	Ile	Gln	165	170	175	
Gly	Gly	Ile	His	Gly	Ile	Val	Pro	Leu	Thr	Ala	Tyr	Val	Val	Val	Ala	180	185	190	
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Lys	Ala	Arg	His	Phe	Leu	Glu	Ser	Ala	Ala	Pro	Leu	Ala	Met	Asp	Pro	210	215	220	
Tyr	Ser	Cys	Ala	Leu	Thr	Thr	Tyr	Ala	Leu	Thr	Leu	Leu	Arg	Ser	Pro	225	230	235	240
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Gly	Thr	Phe	Leu	Ser	Phe	Ser	Asp	Arg	Val	Ser	Gln	Ser	Val	Val	Ser	275	280	285	
Ala	Glu	Val	Glu	Met	Thr	Ala	Tyr	Ala	Leu	Leu	Thr	Tyr	Thr	Leu	Leu	290	295	300	
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Phe Glu Leu His Arg Thr Asn Gln Lys Val Leu Gln Thr Ala Ala Ile
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<212> DNA
<213> Homo sapiens
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 cctctatgag tggaatccag tctcatggcc ccccccattg ctctgtttac cctggaggag  
 180  
 gctactccat gaggttggt ccggtggcac tgcctcgggg ctgcatgtac atgtgtgtgc  
 240  
 atgnntgtgt gcatgtgcgt gtgcacgtgt nngtgtgtgc ccgtgtgcat gtgcccgtgt  
 300  
 gcgtgtctgt gctgtgtgtg tgcgtgcatg tgtgcgtgtc tgtgcgtgnc tgtgtgtgtg  
 360  
 cgtgcatgtg tgtgcacgtg tgtgcatgtg cacgtgtgcg caccctgtgt catgtccgtg  
 420  
 tgcacgcgt  
 429

&lt;210&gt; 82

&lt;211&gt; 79

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 82

Gly	Trp	Leu	Arg	Trp	His	Cys	Leu	Gly	Ala	Ala	Cys	Thr	Cys	Val	Cys
1				5				10						15	
Met	Xaa	Val	Cys	Met	Cys	Val	Cys	Thr	Cys	Xaa	Cys	Val	Pro	Val	Cys
			20					25					30		
Met	Cys	Pro	Cys	Ala	Cys	Leu	Cys	Val	Cys	Ala	Cys	Met	Cys	Ala	
		35				40					45				
Cys	Leu	Cys	Val	Xaa	Val	Cys	Val	Arg	Ala	Cys	Val	Cys	Thr	Cys	Val
	50					55				60					
His	Val	His	Val	Cys	Ala	Pro	Val	Cys	Met	Ser	Val	Cys	Thr	Arg	
65					70					75					

&lt;210&gt; 83

&lt;211&gt; 411

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 83

gtgcacttct tcggacgagg gtccttcggc gcccgcgata acgagagggt gcggagattt  
 60  
 cgtgcgctct ttaaaaagcg caaaggcttt tataagtctg atgtgctttt tttcaggccc  
 120  
 ggaaagacgc gatccgtaga taaaataggg ccgctttatc gcaaatggct ttatggttac  
 180  
 cgtttccgca tcgatttgca gctgcggaaa aaaaggcctg tggtcgatgc cgttgtggat  
 240  
 gatttcgatt ttcgctttgt cgatgccaaag ccctatcaaa tcgttttcgca aaaactcgct  
 300  
 cgcggcgacg atcttttgca cctttgtaag ccccgcttt atctgcatgc gcatcatgag  
 360  
 gtcgctcttt tctttgagca tgacggaaac gatggaattg acgacggcga c  
 411

<210> 84  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
 Met Leu Lys Glu Lys Ser Asp Arg Met Met Arg Met Gln Ile Lys Arg  
 1 5 10 15  
 Gly Leu Thr Lys Val Gln Lys Ile Val Ala Ala Ser Glu Phe Leu Arg  
 20 25 30  
 Asn Asp Leu Ile Gly Leu Gly Ile Asp Lys Ala Lys Ile Glu Ile Ile  
 35 40 45  
 His Asn Gly Ile Asp His Arg Pro Phe Phe Pro Gln Leu Gln Ile Asp  
 50 55 60  
 Ala Glu Thr Val Thr Ile Lys Pro Phe Ala Ile Lys Arg Pro Tyr Phe  
 65 70 75 80  
 Ile Tyr Gly Ser Arg Leu Ser Gly Pro Glu Lys Lys His Ile Glu Leu  
 85 90 95  
 Ile Lys Ala Phe Ala Leu Phe Lys Glu Arg Thr Lys Ser Pro His Pro  
 100 105 110  
 Leu Val Ile Ala Gly Ala Glu Gly Pro Ser Ser Glu Glu Val His  
 115 120 125

<210> 85  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
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 atcctcgacg cggtgaaact gctgagttcg ctcggettca aggtgatcgc cacctcgggc  
 120  
 acccagcggt tcttggtgga gaacggagta ccggcggaag agatcaacaa ggtgctggaa  
 180  
 ggccgcccgc acattgttga cgcaattacc aacggcgagg tgcaactcgt tttcaatacc  
 240  
 accgaggggc cacaggcgct ggctgacagc cgctcgttgc gacgcgctgc cctcttgcac  
 300  
 aaagtgccat attacaccac tctttcaggt gca  
 333

<210> 86  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 86  
 Xaa Arg Val Pro Arg Lys Gly Thr Met Phe Val Ser Val Arg Glu Thr  
 1 5 10 15  
 Asp Lys Ala Arg Ile Leu Asp Ala Val Lys Leu Leu Ser Ser Leu Gly  
 20 25 30  
 Phe Lys Val Ile Ala Thr Ser Gly Thr Gln Arg Phe Leu Val Glu Asn



## ATTORNEY DOCKET NO.: 15966-543

```

      35          40          45
Gly Val Pro Ala Glu Lys Ile Asn Lys Val Leu Glu Gly Arg Pro His
      50          55          60
Ile Val Asp Ala Ile Thr Asn Gly Glu Val Gln Leu Val Phe Asn Thr
65          70          75          80
Thr Glu Gly Pro Gln Ala Leu Ala Asp Ser Arg Ser Leu Arg Arg Ala
      85          90          95
Ala Leu Leu His Lys Val Pro Tyr Tyr Thr Thr Leu Ser Gly Ala
      100          105          110

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<210> 87  
 <211> 355  
 <212> DNA  
 <213> Homo sapiens

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<400> 87
acgcgtgagg aaatgggggc cgcaggcctg gatcgcaagg tatggcagtg cccggtcgtc
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ctcctgagcg atgttcattc ggtaggggta cagggtgacg ggcgtactta tggttctccc
120
attgtgcttc gcccggtgac gagtgaggac gccatgactg cggactgggc acgtatccca
180
tatgacgtac tggaaaagat ctcgactcgc attacgaatg cgtgtccgca aatcaaccgg
240
gtggtactcg atatcacatc taaaccgccg gccaccatcg agtgggaatg agccccgtct
300
cacctgaac atgacatggc ccgcaccttt cttggggcgg gccatgccgt gttag
355

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<210> 88  
 <211> 96  
 <212> PRT  
 <213> Homo sapiens

```

<400> 88
Thr Arg Glu Glu Met Gly Ala Ala Gly Leu Asp Arg Lys Val Trp Gln
1      5      10      15
Cys Pro Val Val Leu Leu Ser Asp Val His Ser Val Gly Val Gln Gly
      20      25      30
Asp Gly Arg Thr Tyr Gly Ser Pro Ile Val Leu Arg Pro Val Thr Ser
      35      40      45
Glu Asp Ala Met Thr Ala Asp Trp Ala Arg Ile Pro Tyr Asp Val Leu
      50      55      60
Glu Lys Ile Ser Thr Arg Ile Thr Asn Ala Cys Pro Gln Ile Asn Arg
65      70      75      80
Val Val Leu Asp Ile Thr Ser Lys Pro Pro Ala Thr Ile Glu Trp Glu
      85      90      95

```

<210> 89  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 89

## ATTORNEY DOCKET NO.: 15966-543

nacgcgtcaa caccaggcta cgggtgggtat gatcatgata agggctggga cccgcaggag  
 60  
 agggcaagag ttatataata gacgggtgta tgggtttaag gtatacatgg tgatgagaca  
 120  
 ggtgattgga taaggccaga ggggtgggag ggggtctgcc cctgctgaag cctgggtggg  
 180  
 cccaggctctg tgatctggga ccggaacaac acatctgctc tgggcctgct ggatgtggcg  
 240  
 caagccctgg aacagaacca cagcctcaag tccatgccgc tgccactgaa tgacgtaacc  
 300  
 caggctcatc gcagccggcc agaactcaca actcgagcgg tccatcagat c  
 351

<210> 90  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

<400> 90  
 Ser Leu Val Gly Pro Arg Ser Val Ile Trp Asp Arg Asn Asn Thr Ser  
 1 5 10 15  
 Ala Leu Gly Leu Leu Asp Val Ala Gln Ala Leu Glu Gln Asn His Ser  
 20 25 30  
 Leu Lys Ser Met Pro Leu Pro Leu Asn Asp Val Thr Gln Ala His Arg  
 35 40 45  
 Ser Arg Pro Glu Leu Thr Thr Arg Ala Val His Gln Ile  
 50 55 60

<210> 91  
 <211> 327  
 <212> DNA  
 <213> Homo sapiens

<400> 91  
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 60  
 acgtcgaagc ccagcagggc ctccctgcagg tccctggggc agccagcaca cacaaagtcc  
 120  
 cggaaggggc tgtagactcc ctgccagcgg ctttcccggg gaaggcacc acgcccagct  
 180  
 gcctcttgca ggtactgctc ggggtctggtg ggagggcagc cgtgtccagc acaccctgtg  
 240  
 tgtgcagtcc tctccctgcc ccaactgccga acgagccctc cacggtgaag ccattgggga  
 300  
 acgtgacctt gcccttcccc atgaggt  
 327

<210> 92  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 92  
 Met Gly Lys Gly Lys Val Thr Phe Pro Asn Gly Phe Thr Val Glu Gly

## ATTORNEY DOCKET NO.: 15966-543

```

      1             5             10             15
Ser Phe Gly Ser Gly Ala Gly Arg Gly Leu His Thr Gln Gly Val Leu
      20             25             30
Asp Thr Ala Ala Leu Pro Pro Asp Pro Ser Ser Thr Cys Lys Arg Gln
      35             40             45
Leu Gly Val Gly Ala Phe Pro Gly Lys Ala Ala Gly Arg Glu Ser Thr
      50             55             60
Ala Pro Ser Gly Thr Leu Cys Val Leu Ala Ala Pro Gly Thr Cys Arg
      65             70             75             80
Arg Pro Cys Trp Ala Ser Thr Cys Arg Ala Pro Gly Ser Cys Val Gly
      85             90             95
Leu Arg Ile Thr Cys Pro Ala Arg Gly Pro Thr
      100             105

```

&lt;210&gt; 93

&lt;211&gt; 394

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 93

```

nccgcgtacg acaagcagta cctcgagggg cgttacggtg cggacccata cctgagcaac
60
atgctcgaat gggacggcgg acatgagcaa taggccgcca aagcacagcg agaggaaggc
120
ggcgcgctct gcggcctcgc ggatgaagga ggggtggtcg cgcaagagac gccccgcgcc
180
ttttgtaccg ataaatcccc ggcgccacct gatcgtgacc gagggtagca aaacggaacc
240
gctctatttc gaggctatca ggttgctgtt caacaaccgt taccacggcc agtgggtgac
300
aatggaagtt gtcgttaccg gcaagcatac caggggactt ctcgatcgtg cagtcactct
360
ggcgggaagaa agtgccacag gattcactca cgta
394

```

&lt;210&gt; 94

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 94

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Met Leu Ala Gly Asn Asp Asn Phe His Cys His Pro Leu Ala Val Ile
      1             5             10             15
Thr Val Val Asp Thr Gln Pro Asp Ser Leu Glu Ile Glu Arg Phe Arg
      20             25             30
Phe Arg Thr Leu Gly His Asp Gln Val Ala Pro Gly Ile Tyr Arg Tyr
      35             40             45
Lys Arg Arg Gly Ala Ser Leu Ala Arg Pro Pro Leu Leu His Pro Arg
      50             55             60
Gly Arg Arg Ala Arg Arg Leu Pro Leu Ala Val Leu Trp Arg Pro Ile
      65             70             75             80
Ala His Val Arg Arg Pro Ile Arg Ala Cys Cys Ser Gly Met Gly Pro
      85             90             95
His Arg Asn Ala Pro Arg Gly Thr Ala Cys Arg Thr Arg

```

100

105

<210> 95  
 <211> 531  
 <212> DNA  
 <213> Homo sapiens

<400> 95  
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 tgcttgatc ctaaaatgga ctggtcttgg gtgtgtaacc ccggtgaagt tatagcctcc  
 120  
 ccaaattgag gtgacagaag gaagacaaga ggtgtaagct ggagagggaa gggaagaaat  
 180  
 cagtggcttt ggccagcctc tgtgccaccc agtacgacag aggagtggga actggccctc  
 240  
 tggggctctg cttggccata ggcactgcac attgtgccac ctgctcatca cctcctctag  
 300  
 tctcacactg agcatcggag tacctgttgt gcagacagga aaactgagga gctctgagag  
 360  
 gctgagcatg gagctcacc ccatgcatag ggtgtgggaa gagggcacag gaggcctcat  
 420  
 ccatggggga aagggttgag gatggacatg ggtggggaga gggcatagac atcccttctt  
 480  
 aatctctgtt cccaccacat ttcataaggag atgagttagg agatgacagc t  
 531

<210> 96  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 96  
 Met Arg Pro Pro Val Pro Ser Ser His Thr Leu Trp His Gly Val Ser  
 1 5 10 15  
 Ser Met Leu Ser Leu Ser Glu Leu Leu Ser Phe Pro Val Cys Thr Thr  
 20 25 30  
 Gly Thr Pro Met Leu Ser Val Arg Leu Glu Glu Val Met Ser Arg Trp  
 35 40 45  
 His Asn Val Gln Cys Leu Trp Pro Ser Arg Ala Pro Glu Gly Gln Phe  
 50 55 60  
 Pro Leu Leu Cys Arg Thr Gly Trp His Arg Gly Trp Pro Lys Pro Leu  
 65 70 75 80  
 Ile Ser Ser Leu Pro Ser Pro Ala Tyr Thr Ser Cys Leu Pro Ser Val  
 85 90 95  
 Thr Ser Ile Trp Gly Gly Tyr Asn Phe Thr Gly Val Thr His Pro Arg  
 100 105 110  
 Pro Val His Phe Arg Ile Gln Ala Lys Phe Pro Glu  
 115 120

<210> 97  
 <211> 405  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 97

ggctcgggcca gtcgaacttc attcccgtt cgagggtctt gctgcggatg ggccgtacgc  
 60  
 tcgcggtgcc ttgcgcgcgg gctggttagt ggagaagccg cgcgagtacg cgccgtagag  
 120  
 cgacatcgtg tctgagacgt cgaagctcag gccagctttt ggcgtccagg cgcgctcgg  
 180  
 cggtcgcgcc tcttgcggca attgattcag cgcaatcccg gccatcacat gccagcgctt  
 240  
 gtccagggtc atgaaatcct gggcataggc gcgcgaggag cgcagcggcg aattggacag  
 300  
 gcgctcgata ttgggcgtga tgtccgaaga cgggaacggg acccgggggg agaagacgtt  
 360  
 gcccgggaaa agatcccccg acgccatcgt ggtgtcgacc gagat  
 405

&lt;210&gt; 98

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 98

Met	Ala	Ser	Gly	Asp	Leu	Phe	Pro	Gly	Asn	Val	Phe	Ser	Pro	Arg	Val
1				5					10					15	
Pro	Phe	Pro	Ser	Ser	Asp	Ile	Thr	Pro	Asn	Ile	Glu	Arg	Leu	Ser	Asn
		20						25					30		
Ser	Pro	Leu	Arg	Ser	Ser	Arg	Ala	Tyr	Ala	Gln	Asp	Phe	Met	Thr	Leu
		35					40					45			
Asp	Lys	Arg	Trp	His	Val	Met	Ala	Gly	Ile	Ala	Leu	Asn	Gln	Leu	Pro
	50					55					60				
Gln	Glu	Gly	Gly	Pro	Thr	Glu	Arg	Ala	Trp	Thr	Pro	Lys	Leu	Gly	Leu
65				70						75				80	
Ser	Phe	Asp	Val	Ser	Asp	Thr	Met	Ser	Leu	Tyr	Gly	Ala	Tyr	Ser	Arg
			85					90					95		
Gly	Phe	Ser	Thr	Tyr	Gln	Pro	Ala	Arg	Lys	Ala	Pro	Arg	Ala	Tyr	Gly
			100					105					110		
Pro	Ser	Ala	Ala	Arg	Pro	Ser	Lys	Arg	Glu						
		115						120							

&lt;210&gt; 99

&lt;211&gt; 545

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 99

acgcgtccgc tcccgatgtc gttgacgagc tgcgctcagc gatgacggta ctcacccatc  
 60  
 tgccccgacg acccagcaaa cgtccccggc tgttcctcat tgaccacgcc gaccggatcg  
 120  
 tcgatcccat cactcgggat ttgctggaat ccctgggttcg cgaagccggc gaggctcggg  
 180  
 tgatcttggg tgcccagcgt cgcggtcgca tcgattggct cccccacag atcatccaca  
 240

acctggccga acaccatttt gagtcgtcct ctggagggtac tcgatgatga ctgaacgttc  
 300  
 ccattccacg atcagggttaa ggtggccggc ggtgggtggt ctcgtcctcg ttccgctgct  
 360  
 ggtggtcgcc ggattggtcc gggacgacct ggcataccac cgaccgggtg ggccgggtga  
 420  
 aagcggccgt cgtcaacgag gacaaggccg tcaaggtgcg tggacaactg gttccgatgg  
 480  
 gccgccaaact caccgcccgc ttgatggact ctggctcgca caccactgat ggccacaccg  
 540  
 tcgac  
 545

<210> 100

<211> 101

<212> PRT

<213> Homo sapiens

<400> 100

Met	Gly	Thr	Phe	Ser	His	His	Arg	Val	Pro	Pro	Glu	Asp	Asp	Ser	Lys
1				5					10					15	
Trp	Cys	Ser	Ala	Arg	Leu	Trp	Met	Ile	Cys	Gly	Glu	Ser	Gln	Ser	Met
			20					25					30		
Arg	Pro	Arg	Arg	Trp	Ala	Pro	Lys	Ile	Thr	Ala	Ala	Ser	Pro	Ala	Ser
			35				40					45			
Arg	Thr	Arg	Asp	Ser	Ser	Lys	Ser	Arg	Val	Met	Gly	Ser	Thr	Ile	Arg
			50			55					60				
Ser	Ala	Trp	Ser	Met	Arg	Asn	Ser	Arg	Gly	Arg	Leu	Leu	Gly	Arg	Arg
65					70				75					80	
Gly	Arg	Trp	Val	Ser	Thr	Val	Ile	Ala	Glu	Arg	Ser	Ser	Ser	Thr	Thr
			85						90					95	
Ser	Gly	Ala	Asp	Ala											
															100

<210> 101

<211> 619

<212> DNA

<213> Homo sapiens

<400> 101

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 tcattgcacga tccggacttc gatccgatcc ccatggtgaa caaggagctt gacgccttcg  
 120  
 aagctgccgg ggggtgactat ctcatcctcg ccacggattc cggacgcaag ggatacacga  
 180  
 ccgcccgtcc tcacgaggcc ggcggaaaac gctattacca acctggacca gatccgcgaa  
 240  
 gtctgcgcca gccgcaacgt caccgcctgt ctacaccccc attggggaac gatgggtccag  
 300  
 aaccgtgacg aagtgatccg cgtgctcgag aactcctcga tcgggctgtg cctggacact  
 360  
 ggtcatctgg cctgtggtgg taccgatgtc gttgagctgg tgcgtaagta cgccaaccgc  
 420

gtcgacattg tccacgcca agatgtccat aaggagatgg ccgacaagct tttgcctggc  
 480  
 gagatcacct ggtccgaagg cattcgcgcc gggatgttcg caccatcgg cgacggtgat  
 540  
 atcgactttg cagccatcgt gaggtcctt gatgaagccg gggtcgatgg ttattacgtc  
 600  
 ctagagcagg acatcatga  
 619

<210> 102

<211> 173

<212> PRT

<213> Homo sapiens

<400> 102

Thr	Arg	Ser	Leu	Thr	Pro	Ser	Lys	Leu	Pro	Gly	Val	Thr	Ile	Ser	Ser
1				5					10					15	
Ser	Pro	Arg	Ile	Pro	Asp	Ala	Arg	Asp	Thr	Arg	Pro	Pro	Val	Leu	Thr
			20					25					30		
Arg	Pro	Ala	Glu	Asn	Ala	Ile	Thr	Asn	Leu	Asp	Gln	Ile	Arg	Glu	Val
		35					40					45			
Cys	Ala	Ser	Arg	Asn	Val	Thr	Ala	Cys	Leu	His	Pro	His	Trp	Gly	Thr
	50					55				60					
Met	Val	Gln	Asn	Arg	Asp	Glu	Val	Ile	Arg	Val	Leu	Glu	Asn	Ser	Ser
65					70					75				80	
Ile	Gly	Leu	Cys	Leu	Asp	Thr	Gly	His	Leu	Ala	Cys	Gly	Gly	Thr	Asp
				85					90					95	
Val	Val	Glu	Leu	Val	Arg	Lys	Tyr	Ala	Asn	Arg	Val	Asp	Ile	Val	His
			100					105					110		
Ala	Lys	Asp	Val	His	Lys	Glu	Met	Ala	Asp	Lys	Leu	Leu	Pro	Gly	Glu
		115					120					125			
Ile	Thr	Trp	Ser	Glu	Gly	Ile	Arg	Ala	Gly	Met	Phe	Ala	Pro	Ile	Gly
	130				135						140				
Asp	Gly	Asp	Ile	Asp	Phe	Ala	Ala	Ile	Val	Arg	Leu	Leu	Asp	Glu	Ala
145					150					155				160	
Gly	Phe	Asp	Gly	Tyr	Tyr	Val	Leu	Glu	Gln	Asp	Ile	Met			
				165						170					

<210> 103

<211> 321

<212> DNA

<213> Homo sapiens

<400> 103

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 gccattgggg ggagaccct gccgtgggga aagaccctg ccattggggca gaccctgcc  
 120  
 actgggggga gaccctgcc gctgggggga gaccgagcc attgggggga gaccctgcc  
 180  
 atggggaaag acccctgcca ttgggggaga ntacctgcca ttgggggaga tcctgccc  
 240  
 tggggggaga tcctgctgt tgggggga ntccctcctg taggggaaga cccctgcagg  
 300

agtgggtggg gcgaagaccc c  
321

<210> 104

<211> 107

<212> PRT

<213> Homo sapiens

<400> 104

Xaa His Gly Gly Arg Gln Gln Pro Cys Gly Gly Asp Pro Ser His Trp  
1 5 10 15  
Gly Glu Thr Pro Ala Ile Gly Gly Arg Pro Leu Pro Trp Gly Lys Thr  
20 25 30  
Pro Ala Met Gly Gln Thr Pro Ala Thr Gly Gly Arg Pro Leu Pro Leu  
35 40 45  
Gly Gly Asp Pro Ser His Trp Gly Glu Thr Pro Ala Met Gly Lys Asp  
50 55 60  
Pro Cys His Trp Gly Arg Xaa Pro Ala Ile Gly Gly Asp Pro Cys Arg  
65 70 75 80  
Trp Gly Glu Ile Pro Ala Val Gly Gly Arg Xaa Pro Pro Val Gly Glu  
85 90 95  
Asp Pro Cys Arg Ser Gly Trp Gly Glu Asp Pro  
100 105

<210> 105

<211> 344

<212> DNA

<213> Homo sapiens

<400> 105

nnntctctcc gaccgcgtcc agatccaccg tggcccgcac gaaccagtcg ttgttgccct  
60  
ccgggtcaac gagggtttgg cgcacggtcc actccgtggc gcccgggggtg atgtgcaaca  
120  
gggcggggccc gcgcgcggcc gggcctgatt ccagcctctc gtgctcgtcc cagtacccat  
180  
ccagcgcacg gccccagcgg tcggcatccc agccgtggtc gccgtcgagc gccccaggg  
240  
cctcaatgtc gtcacggcg gccagttcca cccggcgga catctcgttg cggaccatga  
300  
cccggaaggc gcgggaattc tcggtcagtt tcggcggtgc cggc  
344

<210> 106

<211> 62

<212> PRT

<213> Homo sapiens

<400> 106

Cys Ala Thr Gly Arg Ala Arg Ala Arg Pro Gly Leu Ile Pro Ala Ser  
1 5 10 15  
Arg Ala Arg Pro Ser Thr His Pro Ala His Arg Pro Ser Gly Arg His  
20 25 30  
Pro Ser Arg Gly Arg Arg Arg Ala Pro Pro Gly Pro Gln Cys Arg His



35 40 45  
 Arg Arg Pro Val Pro Pro Gly Gly Thr Ser Arg Cys Gly Pro  
 50 55 60

<210> 107

<211> 549

<212> DNA

<213> Homo sapiens

<400> 107

acgcgttcct cggacgctgc tagtttgagc gcacaggcat tgggcggggc tcacggggga  
 60  
 gccgcttaat aaccgaccaa catgaaactc aagggtgccc ccttcctagc ggggacctg  
 120  
 cacagaccgc aaaataaggc gttttgctct gccctcctca gttcacgtgg gcaccttgga  
 180  
 acactgaaga aggcattttc cgaactcact gtccctacgga cttattctcc gcactgtttt  
 240  
 cgctccttc gccctgttct cgtgactgac aggagcaggg gtcacaagca ggcagcccg  
 300  
 gagctctgct cacctggaaa agcatttttg ttagcttaa atgtgaaggc ctcaggcagt  
 360  
 ggctgttgt cctcctccac atgcgcccat cttactctt tcatgtgact ggctgtttt  
 420  
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 agggtaggc  
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<210> 108

<211> 108

<212> PRT

<213> Homo sapiens

<400> 108

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 20 25 30  
 Gly Thr Leu Lys Lys Ala Phe Ser Glu Leu Thr Val Leu Arg Thr Tyr  
 35 40 45  
 Ser Pro His Cys Phe Arg Leu Leu Arg Pro Val Leu Val Thr Asp Arg  
 50 55 60  
 Ser Arg Gly His Lys Gln Ala Ala Arg Glu Leu Cys Ser Pro Gly Lys  
 65 70 75 80  
 Ala Phe Leu Cys Ser Leu Asn Val Lys Ala Ser Gly Ser Gly Leu Leu  
 85 90 95  
 Ser Ser Ser Thr Cys Ala His Leu His Ser Phe Met  
 100 105

<210> 109

<211> 748

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 109

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120
gatattgggg taagttacca atttacttta cagcccttaa gtataataatc tgctttcctc
180
agcatcatag acttttgaag aggattaatt aagcgcttaa aaaacctgta gactctatta
240
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748

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&lt;210&gt; 110

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 110

```

Met Gln Leu Phe Tyr Phe Arg Gln Glu Cys Ser Lys Leu Arg Glu Glu
1      5      10      15
Leu Arg Leu Gln His Glu Glu Asp Lys Lys Ser Ala Met Ser Gln Leu
20     25     30
Leu Gln Leu Lys Asp Arg Glu Lys Asn Ala Ala Arg Asp Ser Trp Gln
35     40     45
Lys Lys Val Glu Asp Leu Leu Asn Gln Ile Ser Leu Leu Lys Gln Asn
50     55     60
Leu Glu Ile Gln Leu Ser Gln Ser Gln Thr Ser Leu Gln Gln Leu Gln
65     70     75     80
Ala Gln Phe Thr Gln Glu Arg Gln Arg Leu Thr Gln Glu Leu Glu Glu
85     90     95
Leu Glu Glu Gln His Gln Gln Arg His Lys Ser Leu Lys Glu Ala His
100    105    110
Val Leu Ala Phe Gln Thr Met Glu Glu Lys Glu Lys Glu Gln Arg
115    120    125
Ala Leu Glu Asn His Leu Gln Gln Lys His Ser Ala Glu Leu Gln Ser

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<210> 111  
 <211> 429  
 <212> DNA  
 <213> Homo sapiens

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 180  
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 240  
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 ggtccggc  
 429

<210> 112  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<400> 112  
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 Ile Thr Gly Phe Asp Gly Ile Leu Ser Ala Tyr Xaa Arg His Gln His  
 35 40 45  
 Xaa Thr Leu Ala Glu Ile Ile Ala Pro Phe Gly His Leu Val Met Ile  
 50 55 60  
 Asp Gly Thr Asp Ser Phe Asp Leu Met Ala Phe Lys Ser Lys Ser Leu  
 65 70 75 80  
 Thr Val Thr Ser Glu Ser Met Phe Ser Arg Pro Gln Phe Ala Thr Pro  
 85 90 95  
 Asp Val Ala Glu Gln Gly Arg Ala Leu Ala Ser Ile Ala Asp Leu Val  
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 Glu Lys Gly Gln Ile Arg Pro Thr Met Thr Arg His Ile Glu Gly Leu  
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 Thr Thr Gln His Val Arg Glu Ala Thr Ala Ala Val Glu Ser Gly  
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<210> 113  
 <211> 382

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 113

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240  
ctgtccctgg ggggcagcca cctgcgagtc tccttctgcg cccctgggac ccccgggcgc  
300  
agtatgctgg ccgctctcat cggtgcccag gccacggccc tcaatcgggg gcagggagtc  
360  
ctccccgagc ccaacatcct gc  
382

&lt;210&gt; 114

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 114

Met	Leu	Gly	Ser	Gly	Arg	Thr	Pro	Cys	Pro	Arg	Leu	Arg	Ala	Val	Ala
1				5					10					15	
Trp	Ala	Thr	Met	Arg	Ala	Ala	Ser	Ile	Leu	Arg	Pro	Gly	Val	Pro	Gly
			20					25					30		
Ala	Gln	Lys	Glu	Thr	Arg	Arg	Trp	Leu	Pro	Pro	Arg	Asp	Arg	Pro	Ser
		35					40				45				
Ala	Cys	Cys	Cys	Ala	Ser	Ser	Ala	Ile	Ser	Ala	Val	Ser	Tyr	Ser	Ser
	50				55						60				
Thr	Ala	Lys	Pro	Phe	Ser	Cys	Pro	Ser	Trp	Pro	His	Ala	Ser	Trp	Gln
65					70				75					80	
Lys	Val	Gly	Leu	Trp	Thr	Ala	Asp	Ser	Ala	Arg	His	Arg	Ala	Ser	Thr
			85					90					95		
Ser	Leu	Lys	Pro	Gly	Gly	Arg	Arg	Ser	Thr	Gln	Arg	Gln	Gln	Glu	Trp
			100					105					110		
Arg	Arg	Ala	Gly	Leu	Ser	Ser	Pro	Ala	Ser	Val	Gln	Cys			
		115					120					125			

&lt;210&gt; 115

&lt;211&gt; 4798

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 115

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120  
ccccatcctt cctccccacca acctagaggc tttgtctcgt aaatgctggc cctttccttc  
180

atgggctcca ccctctgagt gtgtcatgaa ctcttcact tccttgccctt ggttcgtatt  
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360  
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&lt;210&gt; 116

&lt;211&gt; 1062

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 116

Met Met Gly Thr Ser Gln Gly His Val Ala Arg Lys Ser Arg Asn Trp

1	5	10	15
Gly Leu Asn Pro Ser Arg Leu Ser Ser Ile Pro Leu Ser Ser Thr Pro			
20	25	30	
Cys His Leu Ser Pro Ser Ser Leu Ser Pro Phe Ser Val Ala Glu Arg			
35	40	45	
Lys Pro Pro Leu Phe Asn Met Asn Ala Met Ser Ala Leu Tyr His Ile			
50	55	60	
Ala Gln Asn Glu Ser Pro Val Leu Gln Ser Gly His Trp Ser Glu Tyr			
65	70	75	80
Phe Arg Asn Phe Val Asp Ser Cys Leu Gln Lys Ile Pro Gln Asp Arg			
85	90	95	
Pro Thr Ser Glu Val Leu Leu Lys His Arg Phe Val Leu Arg Glu Arg			
100	105	110	
Pro Pro Thr Val Ile Met Asp Leu Ile Gln Arg Thr Lys Asp Ala Val			
115	120	125	
Arg Glu Leu Asp Asn Leu Gln Tyr Arg Lys Met Lys Lys Ile Leu Phe			
130	135	140	
Gln Glu Ala Pro Asn Gly Pro Gly Ala Glu Ala Pro Glu Glu Glu Glu			
145	150	155	160
Glu Ala Glu Pro Tyr Met His Arg Ala Gly Thr Leu Thr Ser Leu Glu			
165	170	175	
Ser Ser His Ser Val Pro Ser Met Ser Ile Ser Ala Ser Ser Gln Ser			
180	185	190	
Ser Ser Val Asn Ser Leu Ala Asp Ala Ser Asp Asn Glu Glu Glu Glu			
195	200	205	
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Pro Glu Ala Arg			
210	215	220	
Glu Met Ala Met Met Gln Glu Gly Glu His Thr Val Thr Ser His Ser			
225	230	235	240
Ser Ile Ile His Arg Leu Pro Gly Ser Asp Asn Leu Tyr Asp Asp Pro			
245	250	255	
Tyr Gln Pro Glu Ile Thr Pro Ser Pro Leu Gln Pro Pro Ala Ala Pro			
260	265	270	
Ala Pro Thr Ser Thr Thr Ser Ser Ala Arg Arg Arg Ala Tyr Cys Arg			
275	280	285	
Asn Arg Asp His Phe Ala Thr Ile Arg Thr Ala Ser Leu Val Ser Arg			
290	295	300	
Gln Ile Gln Glu His Glu Gln Asp Ser Ala Leu Arg Glu Gln Leu Ser			
305	310	315	320
Gly Tyr Lys Arg Met Arg Arg Gln His Gln Lys Gln Leu Leu Ala Leu			
325	330	335	
Glu Ser Arg Leu Arg Gly Glu Arg Glu Glu His Ser Ala Arg Leu Gln			
340	345	350	
Arg Glu Leu Glu Ala Gln Arg Ala Gly Phe Gly Ala Glu Ala Glu Lys			
355	360	365	
Leu Ala Arg Arg His Gln Ala Ile Gly Glu Lys Glu Ala Arg Ala Ala			
370	375	380	
Gln Ala Glu Glu Arg Lys Phe Gln Gln His Ile Leu Gly Gln Gln Lys			
385	390	395	400
Lys Glu Leu Ala Ala Leu Leu Glu Ala Gln Lys Arg Thr Tyr Lys Leu			
405	410	415	
Arg Lys Glu Gln Leu Lys Glu Glu Leu Gln Glu Asn Pro Ser Thr Pro			
420	425	430	
Lys Arg Glu Lys Ala Glu Trp Leu Leu Arg Gln Lys Glu Gln Leu Gln			



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      435      440      445
Gln Cys Gln Ala Glu Glu Glu Ala Gly Leu Leu Arg Arg Gln Arg Gln
  450      455      460
Tyr Phe Glu Leu Gln Cys Arg Gln Tyr Lys Arg Lys Met Leu Leu Ala
  465      470      475      480
Arg His Ser Leu Asp Gln Asp Leu Leu Arg Glu Asp Leu Asn Lys Lys
      485      490      495
Gln Thr Gln Lys Asp Leu Glu Cys Ala Leu Leu Leu Arg Gln His Glu
      500      505      510
Ala Thr Arg Glu Leu Glu Leu Arg Gln Leu Gln Ala Val Gln Arg Thr
      515      520      525
Arg Ala Glu Leu Thr Arg Leu Gln His Gln Thr Glu Leu Gly Asn Gln
      530      535      540
Leu Glu Tyr Asn Lys Arg Arg Glu Gln Glu Leu Arg Gln Lys His Ala
  545      550      555      560
Ala Gln Val Arg Gln Gln Pro Lys Ser Leu Lys Val Arg Ala Gly Gln
      565      570      575
Arg Pro Pro Gly Leu Pro Leu Pro Ile Pro Gly Ala Leu Gly Pro Pro
      580      585      590
Asn Thr Gly Thr Pro Ile Glu Gln Gln Pro Cys Ser Pro Gly Gln Glu
      595      600      605
Ala Val Leu Asp Gln Arg Met Leu Gly Glu Glu Glu Ala Val Gly
      610      615      620
Glu Arg Arg Ile Leu Gly Lys Glu Gly Ala Thr Leu Glu Pro Lys Gln
  625      630      635      640
Gln Arg Ile Leu Gly Glu Glu Ser Gly Ala Pro Ser Pro Ser Pro Gln
      645      650      655
Lys His Gly Ser Leu Val Asp Glu Glu Val Trp Gly Leu Pro Glu Glu
      660      665      670
Ile Glu Glu Leu Arg Val Pro Ser Leu Val Pro Gln Glu Arg Ser Ile
      675      680      685
Val Gly Gln Glu Glu Ala Gly Thr Trp Ser Leu Trp Gly Lys Glu Asp
      690      695      700
Glu Ser Leu Leu Asp Glu Glu Phe Glu Leu Gly Trp Val Gln Gly Pro
  705      710      715      720
Ala Leu Thr Pro Val Pro Glu Glu Glu Glu Glu Glu Glu Gly Ala
      725      730      735
Pro Ile Gly Thr Pro Arg Asp Pro Gly Asp Gly Cys Pro Ser Pro Asp
      740      745      750
Ile Pro Pro Glu Pro Pro Pro Thr His Leu Arg Pro Cys Pro Ala Ser
      755      760      765
Gln Leu Pro Gly Leu Leu Ser His Gly Leu Leu Ala Gly Leu Ser Phe
      770      775      780
Ala Val Gly Ser Ser Ser Gly Leu Leu Pro Leu Leu Leu Leu Leu
  785      790      795      800
Leu Pro Leu Leu Ala Ala Gln Gly Gly Gly Leu Gln Ala Ala Leu
      805      810      815
Leu Ala Leu Glu Val Gly Leu Val Gly Leu Gly Ala Ser Tyr Leu Leu
      820      825      830
Leu Cys Thr Ala Leu His Leu Pro Ser Ser Leu Phe Leu Leu Leu Ala
      835      840      845
Gln Gly Thr Ala Leu Gly Ala Val Leu Gly Leu Ser Trp Arg Arg Gly
      850      855      860
Leu Met Gly Val Pro Leu Gly Leu Gly Ala Ala Trp Leu Leu Ala Trp

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865		870		875		880
Pro Gly Leu Ala Leu Pro Leu Val Ala Met Ala Ala Gly Gly Arg Trp						
	885		890		895	
Val Arg Gln Gln Gly Pro Arg Val Arg Arg Gly Ile Ser Arg Leu Trp						
	900		905		910	
Leu Arg Val Leu Leu Arg Leu Ser Pro Met Ala Phe Arg Ala Leu Gln						
	915		920		925	
Gly Cys Gly Ala Val Gly Asp Arg Gly Leu Phe Ala Leu Tyr Pro Lys						
	930		935		940	
Thr Asn Lys Asp Gly Phe Arg Ser Arg Leu Pro Val Pro Gly Pro Arg						
945		950		955		960
Arg Arg Asn Pro Arg Thr Thr Gln His Pro Leu Ala Leu Leu Ala Arg						
	965		970		975	
Val Trp Val Leu Cys Lys Gly Trp Asn Trp Arg Leu Ala Arg Ala Ser						
	980		985		990	
Gln Gly Leu Ala Ser His Leu Pro Pro Trp Ala Ile His Thr Leu Ala						
	995		1000		1005	
Ser Trp Gly Leu Leu Arg Gly Glu Arg Pro Thr Arg Ile Pro Arg Leu						
	1010		1015		1020	
Leu Pro Arg Ser Gln Arg Gln Leu Gly Pro Pro Ala Ser Arg Gln Pro						
1025		1030		1035		1040
Leu Pro Gly Thr Leu Ala Gly Arg Arg Ser Arg Thr Arg Gln Ser Arg						
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Ala Leu Pro Pro Trp Arg						
	1060					

&lt;210&gt; 117

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 117

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 acgcctactt cgatcttggt gacgggtgtt ttcatttgtt tgtgcgcaa tgcggtgaat  
 240  
 ttcattgatg gacttgacgg cctggcatcc ggtgtggtgg ccatcgggtc cttggctttc  
 300  
 ttctcataca cctacctgct ggctcacgaa caggactttg ttgttgcgac gactaccagt  
 360  
 ctcattacgg ctgcgacggc gggcgccgtg ctcggttttt tgccccacaa ctggcatccg  
 420  
 gcgaggatgt tcatgggtga ttccggagct ctgctacttg gcttattgct a  
 471

&lt;210&gt; 118

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 118

Xaa Ala Leu Thr Ile Cys Leu Ala Gly Val Val Ile Cys Ala Val Gly  
 1 5 10 15  
 Val Val Asp Asp Leu Leu Asp Leu Pro Ala Leu Ala Lys Ala Ala Gly  
 20 25 30  
 Gln Val Leu Ala Ala Gly Ile Val Val Thr Gly Gly Val Arg Met Phe  
 35 40 45  
 Trp Ile Pro Leu Pro Asn Ser Ile Ile Ala Leu Gly Thr Pro Thr Ser  
 50 55 60  
 Ile Leu Val Thr Val Phe Phe Ile Val Leu Cys Ala Asn Ala Val Asn  
 65 70 75 80  
 Phe Ile Asp Gly Leu Asp Gly Leu Ala Ser Gly Val Val Ala Ile Gly  
 85 90 95  
 Ser Leu Ala Phe Phe Ser Tyr Thr Tyr Leu Leu Ala His Glu Gln Asp  
 100 105 110  
 Phe Val Val Ala Thr Thr Thr Ser Leu Ile Thr Ala Ala Thr Ala Gly  
 115 120 125  
 Ala Cys Leu Gly Phe Leu Pro His Asn Trp His Pro Ala Arg Met Phe  
 130 135 140  
 Met Gly Asp Ser Gly Ala Leu Leu Leu Gly Leu Leu Leu  
 145 150 155

&lt;210&gt; 119

&lt;211&gt; 302

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 119

ntcaaacatg agcagtcgtg gcggccgagg ccgcggtggc tattatcgcg agctttatgg  
 60  
 tagccgaggt cgaggcagta aatctaataa aactttcgca aaaaattcgg atgtctactc  
 120  
 tcagaaaaag actcgaacag tacgaggcac ctccgaagat ttagcacgat cgctccataa  
 180  
 gcttcatatg cgcccgatcc ctgcgtatca tgacattgag ggtatgtggg ctttcccagc  
 240  
 ctttactttt tatctggatc atgcacaagc agaccatac gctgccccaa ataaggcacg  
 300  
 cn  
 302

&lt;210&gt; 120

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 120

Met Ser Ser Arg Gly Gly Arg Gly Arg Gly Tyr Tyr Arg Glu Leu  
 1 5 10 15  
 Tyr Gly Ser Arg Gly Arg Gly Ser Lys Ser Asn Glu Thr Phe Ala Lys  
 20 25 30  
 Asn Ser Asp Val Tyr Ser Gln Lys Lys Thr Arg Thr Val Arg Gly Thr  
 35 40 45  
 Ser Glu Asp Leu Ala Arg Ser Leu His Lys Leu His Met Arg Pro Tyr

```

      50              55              60
Pro Ala Tyr His Asp Ile Glu Gly Met Trp Ala Phe Pro Ala Phe Thr
65              70              75              80
Phe Tyr Leu Asp His Ala Gln Ala Asp Pro Tyr Ala Ala Pro Asn Lys
      85              90              95
Ala Arg

```

```

<210> 121
<211> 318
<212> DNA
<213> Homo sapiens

```

```

<400> 121
ngcatggggg gccctgggac cgcacttggtg cccctttttt ttttagggaa aaaattgagc
60
cctaaaggat ttgccgcatt acaggaaagt tttttggtaa gtttgggggtt gtttctgtgc
120
tgtgtgagaa ggagtagaag cagctccagt agagtgggcc ttttcatttt tatccagagg
180
aaatttgtag gctgtggcta ttacttcctt ttttttcttt tttttttttg ttttagagaca
240
gagtcctgnet ctgtcgccag gctggagtga agtggcacga tctcagctca ctgcaacctc
300
tgcctcccag gttcaagc
318

```

```

<210> 122
<211> 89
<212> PRT
<213> Homo sapiens

```

```

<400> 122
Xaa Met Gly Gly Pro Gly Thr Ala Leu Val Pro Leu Phe Phe Leu Gly
1              5              10              15
Lys Lys Leu Ser Pro Lys Gly Phe Ala Ala Leu Gln Glu Ser Phe Leu
20              25              30
Val Ser Leu Gly Leu Phe Leu Cys Cys Val Arg Arg Ser Arg Ser Ser
35              40              45
Ser Ser Arg Val Gly Leu Phe Ile Phe Ile Gln Arg Lys Phe Val Gly
50              55              60
Cys Gly Tyr Tyr Phe Leu Phe Phe Leu Phe Phe Phe Cys Leu Glu Thr
65              70              75              80
Glu Ser Xaa Ser Val Ala Arg Leu Glu
85

```

```

<210> 123
<211> 338
<212> DNA
<213> Homo sapiens

```

```

<400> 123
acgcgtctag ggtagaaatc aactccagta actgtcatc aacctcagca atgctgggga
60

```

cgggcagagg cagggcagct gtgtgccaca ttcctgccag ggctggtcag gccccggctc  
 120  
 tcaccactcc tcttcctgc tttgaacctg tggaacaaag ggcccctgca ccccaactca  
 180  
 ttcctctttg ccacataagg gcctcaagtc atgctgtccc ctctgcctgg gttgcttttt  
 240  
 ctccctctgc ttgggtcact gttcacacca ctggccactt tctcagggga agggccctca  
 300  
 ctgcccacac acctaaacat gccccctgct cctccata  
 338

<210> 124

<211> 96

<212> PRT

<213> Homo sapiens

<400> 124

Met	Leu	Gly	Thr	Gly	Arg	Gly	Arg	Ala	Ala	Val	Cys	His	Ile	Pro	Ala
1				5				10					15		
Arg	Ala	Gly	Gln	Ala	Pro	Ala	Leu	Thr	Thr	Pro	Pro	Pro	Cys	Phe	Glu
			20					25					30		
Pro	Val	Glu	Gln	Arg	Ala	Pro	Ala	Pro	Gln	Leu	Ile	Pro	Leu	Cys	His
		35					40					45			
Ile	Arg	Ala	Ser	Ser	His	Ala	Val	Pro	Ser	Ala	Trp	Val	Ala	Phe	Ser
		50				55					60				
Pro	Ser	Ala	Trp	Val	Thr	Val	His	Thr	Thr	Gly	His	Phe	Pro	Gln	Gly
65					70					75				80	
Arg	Ala	Leu	Thr	Ala	His	Thr	Pro	Lys	His	Ala	Pro	Cys	Ser	Ser	Ile
			85						90					95	

<210> 125

<211> 280

<212> DNA

<213> Homo sapiens

<400> 125

ccatggacct ggccagccac catcacctgc ctctgcctc acccaccctg ggtgcctgcc  
 60  
 ggcaaggatt ggagggcaga ctgctggagc gtgagaccag gccaatctgt ctttctggga  
 120  
 accttcagcc tccaactgga gctgactgtc aactttcggg tgagaagtca cttttctgca  
 180  
 ttcccaccac actatctatc tgtgcaatac ggcagcgtga cagcactcac cttattgagg  
 240  
 gcttctgctg tcttgccca ttctggatag gctgatcta  
 280

<210> 126

<211> 92

<212> PRT

<213> Homo sapiens

<400> 126

Met Asp Leu Ala Ser His His His Leu Pro Pro Ala Ser Pro Thr Leu

```

      1           5           10           15
Gly Ala Cys Arg Gln Gly Leu Glu Gly Arg Leu Leu Glu Arg Glu Thr
      20           25           30
Arg Pro Ile Cys Leu Ser Gly Asn Leu Gln Pro Pro Thr Gly Ala Asp
      35           40           45
Cys Gln Leu Ser Gly Glu Lys Ser Leu Phe Cys Ile Pro Thr Thr Leu
      50           55           60
Ser Ile Cys Ala Ile Arg Gln Arg Asp Ser Thr His Leu Ile Glu Gly
      65           70           75           80
Phe Cys Cys Pro Gly Pro Phe Trp Ile Gly Leu Ile
      85           90

```

<210> 127  
 <211> 444  
 <212> DNA  
 <213> Homo sapiens

```

<400> 127
cgcgatgatcg ccgtggcgga gggccgcggc gccgactcga tcgcccagct gacaaccgag
60
ctgcaaagcc gtcactgccc tgcggagcag atcacgtccg tcagcatcga catgtcgcca
120
gcgttcacga ggggctgcgc cgagcacctg cccaacgcgc gcgtcacctt cgacaagtcc
180
cacgtcatcg ggcacgcca tgccggcgtg gacaggatgc gccgcatcga gcagcgagc
240
gacaagtccc tcaaggggat gcgctggctg ctgctgaaga accgcgccag cctcaagccc
300
gaggctgccc ccgatctgga tgcctgatc gccaggatgg ccaactgtgc caccgcgcgc
360
gcctgggtct acaaggagca gctgcgcgag atcctcgcgc gcaagcagat caactgggca
420
cgcgacatgc tcaagcactg gtgc
444

```

<210> 128  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

```

<400> 128
Arg Val Ile Ala Val Ala Glu Gly Arg Gly Ala Asp Ser Ile Ala Gln
1           5           10           15
Leu Thr Thr Glu Leu Gln Ser Arg His Cys Pro Ala Glu Gln Ile Thr
      20           25           30
Ser Val Ser Ile Asp Met Ser Pro Ala Phe Ile Arg Gly Cys Ala Glu
      35           40           45
His Leu Pro Asn Ala Arg Val Thr Phe Asp Lys Phe His Val Ile Gly
      50           55           60
His Ala Asn Ala Ala Val Asp Arg Met Arg Arg Ile Glu Gln Arg Ser
      65           70           75           80
Asp Lys Ser Leu Lys Gly Met Arg Trp Ser Leu Leu Lys Asn Arg Ala
      85           90           95
Ser Leu Lys Pro Glu Ala Ala Ala Asp Leu Asp Ala Leu Ile Ala Arg

```

100 105 110  
 Met Ala Thr Val Arg Thr Ala Arg Ala Trp Val Tyr Lys Glu Gln Leu  
 115 120 125  
 Arg Glu Ile Leu Ala Arg Lys Gln Ile Asn Val Ala Arg Asp Met Leu  
 130 135 140  
 Lys His Trp Cys  
 145

<210> 129  
 <211> 291  
 <212> DNA  
 <213> Homo sapiens

<400> 129  
 gaggagggac gtaccgtccc cgttatagcc aagctcgaga agccgcaagc tatcgagaac  
 60  
 ttggacgaga ttattgacgt ctttgacgcc gtcattggtg cccgtggcga tatggccgtc  
 120  
 gagggtcccgc tcgaggaagt tccgctgacg caaaagcaga tcatcgagaa ggctcgttta  
 180  
 caggctaagc ccgtcattgt ggccacccag atgcttgagt cgatgatcca cgctccccgt  
 240  
 ccgacccgcg ctgaggccgc cgacgtcgcg aacgccatcc ttgacggcgc g  
 291

<210> 130  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 130  
 Glu Glu Gly Arg Thr Val Pro Val Ile Ala Lys Leu Glu Lys Pro Gln  
 1 5 10 15  
 Ala Ile Glu Asn Leu Asp Glu Ile Ile Asp Val Phe Asp Ala Val Met  
 20 25 30  
 Val Ala Arg Gly Asp Met Ala Val Glu Cys Pro Leu Glu Glu Val Pro  
 35 40 45  
 Leu Ile Gln Lys Gln Ile Ile Glu Lys Ala Arg Leu Gln Ala Lys Pro  
 50 55 60  
 Val Ile Val Ala Thr Gln Met Leu Glu Ser Met Ile His Ala Pro Arg  
 65 70 75 80  
 Pro Thr Arg Ala Glu Ala Ala Asp Val Ala Asn Ala Ile Leu Asp Gly  
 85 90 95  
 Ala

<210> 131  
 <211> 416  
 <212> DNA  
 <213> Homo sapiens

<400> 131  
 tccggagcgt ccgtggccct catgggtgtg tcagcgtggt tgctgtctcg ggccgcagag  
 60

attccaccgg tgctctacct ggaggccgca gccgtcgggg ttcgattctt cggcatctcc  
 120  
 cgcggtgtct tccgctacgc cgaacgtctg gtaggccacg acctggctct gcggatgcag  
 180  
 ggggcattgc ggatgcgggt ctacgaccgg ctgtcacgta ccnaccctgc tggggnnacgt  
 240  
 cgccgggggtg acctgctggt acgggttact gccgacgtcg acgcggtgtt ggacatggtc  
 300  
 gtgcgggtga tcgttccggc gtgcgcgtca agcctcgtca tcattggcac cacggtcctt  
 360  
 ctttgtccga gagaagggtg agttttctta gccggattcc aacacagcct gggggc  
 416

<210> 132  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<400> 132  
 Ser Gly Ala Ser Val Ala Leu Met Gly Val Ser Ala Trp Leu Leu Ser  
 1 5 10 15  
 Arg Ala Ala Glu Ile Pro Pro Val Leu Tyr Leu Glu Ala Ala Ala Val  
 20 25 30  
 Gly Val Arg Phe Phe Gly Ile Ser Arg Gly Val Phe Arg Tyr Ala Glu  
 35 40 45  
 Arg Leu Val Gly His Asp Leu Ala Leu Arg Met Gln Gly Ala Leu Arg  
 50 55 60  
 Met Arg Val Tyr Asp Arg Leu Ser Arg Thr Xaa Pro Ala Gly Xaa Arg  
 65 70 75 80  
 Arg Arg Gly Asp Leu Leu Val Arg Val Thr Ala Asp Val Asp Ala Val  
 85 90 95  
 Leu Asp Met Val Val Arg Val Ile Val Pro Ala Cys Ala Ser Ser Leu  
 100 105 110  
 Val Ile Ile Gly Thr Thr Val Leu Leu Cys Pro Arg Glu Gly  
 115 120 125

<210> 133  
 <211> 327  
 <212> DNA  
 <213> Homo sapiens

<400> 133  
 gccgttgcta tcgctgctgg tatgcgtgca gacgtcactg tttttgatat caatategct  
 60  
 gcggtgaaga gactcgccga catctaccag ggctcgtgtc acacagtagt atccaccgc  
 120  
 gccgaaattg cgaaggcgct agaaaccgct gacgttgatga tcggttctgt ccttattccg  
 180  
 ggtagttcta ccccgaaagt tggtactacc gatatggttg ctcacatgca gcctgggtct  
 240  
 gttcttattg atattgctat agaccaaggc ggctgcttcg aggattcgca cccaccact  
 300  
 tacgatgacc ccactttcac tgtgcac  
 327



<210> 134  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 134  
 Ala Val Ala Ile Ala Ala Gly Met Arg Ala Asp Val Thr Val Phe Asp  
 1 5 10 15  
 Ile Asn Ile Ala Ala Leu Lys Arg Leu Ala Asp Ile Tyr Gln Gly Arg  
 20 25 30  
 Val His Thr Val Val Ser Thr Arg Ala Glu Ile Ala Lys Ala Leu Glu  
 35 40 45  
 Thr Ala Asp Val Val Ile Gly Ser Val Leu Ile Pro Gly Ser Ser Thr  
 50 55 60  
 Pro Lys Leu Val Thr Thr Asp Met Val Ala His Met Gln Pro Gly Ser  
 65 70 75 80  
 Val Leu Ile Asp Ile Ala Ile Asp Gln Gly Gly Cys Phe Glu Asp Ser  
 85 90 95  
 His Pro Thr Thr Tyr Asp Asp Pro Thr Phe Thr Val His  
 100 105

<210> 135  
 <211> 560  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
 taagatgtgg tcctgccctg ttctgaagg ggctgcagct ctgatggaaa atacagggat  
 60  
 ttacactcag ggctacagcc acggggggct gaggcccaag gctgcaatct cgggggaagg  
 120  
 ggaagtggc ttttctggt ggattggaaa catcctcttg gaggcaaaga cttttcctgg  
 180  
 atcttacaga ctccccgga tttttagatt agaattattg gggcaaagga ggctgtcttg  
 240  
 ttttaaagca atgctacata gacacagtgg ggaagacctg gttcgacggc agataagcag  
 300  
 tgggtgatgg gcttgaggag gagagtcagg gcaaagtcta agactgagca gaaaggaatt  
 360  
 ccccatctc ccatggataa gtacgttcta gaacattctc tttgggtcta atactctgaa  
 420  
 atgacatctt gtcttcatgc tcgagagaga attacttcac tggctccact tggagtgcc  
 480  
 gtgttcagac accaagcctg actgggaggg ttccgttttc ttaacacctt cccaccgccg  
 540  
 atttccaagt cccacgcgt  
 560

<210> 136  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 136

```

Met Trp Ser Cys Pro Val Pro Glu Gly Ala Ala Ala Leu Met Glu Asn
 1           5           10           15
Thr Gly Ile Tyr Thr Gln Gly Tyr Ser His Gly Gly Leu Arg Pro Lys
          20           25           30
Ala Ala Ile Ser Gly Glu Gly Glu Val Gly Phe Ser Trp Trp Ile Gly
          35           40           45
Asn Ile Leu Leu Glu Ala Lys Thr Phe Pro Gly Ser Tyr Arg Leu Pro
          50           55           60
Gly Ile Phe Arg Leu Glu Tyr Trp Gly Gln Arg Arg Leu Ser Cys Phe
65           70           75           80
Lys Ala Met Leu His Arg His Ser Gly Glu Asp Leu Val Arg Arg Gln
          85           90           95
Ile Ser Ser Gly
          100

```

&lt;210&gt; 137

&lt;211&gt; 429

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

```

accggttgga tggcctgcag gccaaagcgt tcctgcaaac tcagcaggcc ttcagcgcaa
60
gaggcaaaaca gctggtcgcg cacctgcttg aggtccaccg attgcgcata gcccttgagc
120
aaggcgcgcc agttggtttt gtcggccact tggctgcgga acaggtcttc gacaaaaccg
180
gactgctggc gggtcgcaac gcgcatgata ggcagcgccct ggctggcgcc ctggtcgagc
240
cagcgcgctg gcagttgggt ggcccgggtg ataccgacct tgatccccga cgaattggcc
300
aggtacacca catggtcggc catgcagaat gtttcgcccc agccgggata acggcaagtg
360
cggcgctcgt aatggcaacg ttcggggctc atgatgcaca ggtcacactg ggccagcttg
420
gtcatgccc
429

```

&lt;210&gt; 138

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 138

```

Met Thr Lys Leu Ala Gln Cys Asp Leu Cys Ile Met Ser Pro Glu Arg
 1           5           10           15
Cys His Tyr Asp Ala Gly Thr Cys Arg Asp Pro Gly Trp Gly Glu Thr
          20           25           30
Phe Cys Met Thr Asp His Val Val Tyr Leu Ala Asn Ser Ser Gly Ile
          35           40           45
Lys Val Gly Ile Thr Arg Ala Thr Gln Leu Pro Thr Arg Trp Leu Asp
          50           55           60
Gln Gly Ala Ser Gln Ala Leu Pro Ile Met Arg Val Ala Thr Arg Gln

```

```

65          70          75          80
Gln Ser Gly Phe Val Glu Asp Leu Phe Arg Ser Gln Val Ala Asp Lys
          85          90          95
Thr Asn Trp Arg Ala Leu Leu Lys Gly Asp Ala Gln Ser Val Asp Leu
          100          105          110
Lys Gln Val Arg Asp Gln Leu Phe Ala Ser Cys Ala Glu Gly Leu Leu
          115          120          125
Ser Leu Gln Glu Arg Phe Gly Leu Gln Ala Ile Gln Pro
          130          135          140

```

<210> 139  
 <211> 341  
 <212> DNA  
 <213> Homo sapiens

```

<400> 139
acgcgtcgtt tgaaggcttg atccgcacgt ccaattcgct ttgcgccaat gcgccgcagc
60
ttgtgaacag cagaatcaag ccgctggtta atcttctctg gagcttcata ggcgggggatg
120
ctacacgagc tggggagaca ctttgaaccc ggaattgtct gaataattct gtctcaaacc
180
tttgagcctt gtaacgactg aggggttcgga tggaaaaaca catgctccag gatgggaccg
240
acggccactt caccgatctc ttcatagccc tggcgtttgt agaaatccag gtagcgcgaa
300
tcgccagcgt cgagcacgac gcctgatgag tgcgggtcat t
341

```

<210> 140  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

```

<400> 140
Met Thr Arg Thr His Gln Ala Ser Cys Ser Thr Leu Ala Ile Arg Ala
1      5      10      15
Thr Trp Ile Ser Thr Asn Ala Arg Ala Met Lys Arg Ser Val Lys Trp
20     25     30
Pro Ser Val Pro Ser Trp Ser Met Cys Phe Ser Ile Arg Thr Leu Ser
35     40     45
Arg Tyr Arg Leu Gln Arg Phe Glu Thr Glu Leu Phe Arg Gln Phe Arg
50     55     60
Val Gln Ser Val Ser Pro Ala Arg Val Ala Ser Pro Pro Met Lys Leu
65     70     75     80
Pro Gly Arg Phe Thr Ser Gly Leu Ile Leu Phe Thr Ser Cys Gly
85     90     95
Ala Leu Ala Gln Ser Glu Leu Asp Val Arg Ile Lys Pro Ser Asn Asp
100    105    110
Ala

```

<210> 141  
 <211> 324

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 141

gaattcctct tggatagctt cgggtaaatg ggtacagcaa atatcaggag cgcaaccgca  
 60  
 acctttactt actggtacat gaacaccatt tacattacag ctatcgtagt caccaccagt  
 120  
 catgtgaaca gacacataac tgaaagggtt ataaaccaca gtctcacggt acgtatgacc  
 180  
 gtcaactgtg aacaccgcta agtaatagcc tgcgggggct tgcataaact cctttgacca  
 240  
 tgcgtaataa atacgtccgt cattagtcac acctgatggg gcgaaacaaa aagaacggca  
 300  
 gcagttatca ccgccatcac gcgt  
 324

&lt;210&gt; 142

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

Met	Gly	Gly	Asp	Asn	Cys	Cys	Arg	Ser	Phe	Cys	Phe	Ala	Pro	Ser	Gly
1				5					10					15	
Val	Thr	Asn	Asp	Gly	Arg	Ile	Tyr	Tyr	Ala	Trp	Ser	Lys	Glu	Phe	Met
		20					25						30		
Gln	Ala	Pro	Ala	Gly	Tyr	Tyr	Leu	Ala	Val	Phe	Thr	Val	Asp	Gly	His
		35				40					45				
Thr	Tyr	Arg	Glu	Thr	Val	Val	Tyr	Lys	Pro	Phe	Ser	Tyr	Val	Ser	Val
	50				55					60					
His	Met	Thr	Trp	Gly	Glu	Tyr	Asp	Ser	Cys	Asn	Val	Asn	Gly	Val	His
65				70					75					80	
Val	Pro	Val	Ser	Lys	Gly	Cys	Gly	Cys	Ala	Pro	Asp	Ile	Cys	Cys	Thr
			85				90						95		
His	Leu	Pro	Glu	Ala	Ile	Gln	Glu	Glu	Phe						
			100				105								

&lt;210&gt; 143

&lt;211&gt; 1325

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 143

nacgcgtgga tctgccagct gagcctggag ctgtgcaggc agctgccctg ctacgatgag  
 60  
 gcaccccagg agaagaactt cctgtacaaa tgcataaggca ccaccctggg tgctgcttca  
 120  
 agtaaggagg tggtagaggaa gcaccttcaa gagctgctgg agacggccag ataccaggag  
 180  
 gaggcagaac gcgagggcct cgcctgctgc ttcgggatct gtgccatctc ccacctcgag  
 240  
 gacacgctgg ccagctgga ggacttcgtg aggtcagagg tcttcagaaa atccattggc  
 300

attctcaaca tttttaagga tcgaagtga aacgaagtgg agaaggtgaa gagtgctctg  
 360  
 atcctgtgct atgggcacgt ggcgcccg ggcccccg agctgggtgct ggccaaggta  
 420  
 gagtcagaca tcctccggaa catcntgcca gcacttcagc acnncaagga cccagccctg  
 480  
 aagctgtgcc ttgtccagag tgtgtgcatg gtcagccgcg ccatctgcag cagcaccag  
 540  
 gctggctcct tccacttcac ccggaagca gagctgggtgg cacagatgat ggagtccatc  
 600  
 agggcagagc ccccggaactc cttgaggaca cctattcgga agaaagccat gctcacctgc  
 660  
 acttacttgg tctccgtgga gccagcgctg gacgagcagg cccgggcgga tgtgatccat  
 720  
 ggctgcctgc acagcatcat ggccctgctg cctgagccca aggaggagga cggaggctgc  
 780  
 cagaagtccc tgtatctgga gacactgcac gcccttgagg atctgctgac gagcctcctg  
 840  
 cagcggaaca tgacccccca aggctgcag atcatgattg agcacctgag cccatggatc  
 900  
 aagtccccaa gaggtcacgt agcggcgctg gccctaggcc tgagcgccct cctcgtgcgc  
 960  
 tacttcctgg agcacctgcg tgtcagtggc gcccaagtag ataccaggtt tccatctgag  
 1020  
 cccaggatcc tgtgcaatgg ccctggtgcc ctccacaac ctgggccttc tcacggcct  
 1080  
 ctttcccca cgggtgtgcgg acctgtggcc tgccaccgc caggaggccg tggactgtgt  
 1140  
 ctactccctg ctgtacctcc agctcggtta tgagggcttc tccgggact accgcgatga  
 1200  
 cgtggcggag cggctcctca gcctcaagga cggcctcgtg caccctgacc ccgccattct  
 1260  
 cttccacacc tgccacagt taggccagat tattgccaag cgcctcccc cagcccttca  
 1320  
 cgcgt  
 1325

<210> 144

<211> 390

<212> PRT

<213> Homo sapiens

<400> 144

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Cys	Tyr	Asp	Glu	Ala	Pro	Gln	Glu	Lys	Asn	Phe	Leu	Tyr	Lys	Cys	Ile
		20						25					30		
Gly	Thr	Thr	Leu	Gly	Ala	Ala	Ser	Lys	Glu	Val	Val	Arg	Lys	His	
		35					40				45				
Leu	Gln	Glu	Leu	Leu	Glu	Thr	Ala	Arg	Tyr	Gln	Glu	Glu	Ala	Glu	Arg
		50				55					60				
Glu	Gly	Leu	Ala	Cys	Cys	Phe	Gly	Ile	Cys	Ala	Ile	Ser	His	Leu	Glu
65				70					75					80	
Asp	Thr	Leu	Ala	Gln	Leu	Glu	Asp	Phe	Val	Arg	Ser	Glu	Val	Phe	Arg

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<210> 145
<211> 802
<212> DNA
<213> Homo sapiens
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120
acatcacccct ggtgaaggcc tgcaccacta gcgtcggcac catttccccg cgctggacaa
180
gacatcatgc cccatatctt gacagaatgt ctgacatgag tatgccacgc cgagcagcac
240
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cagaggacga caccgatctg gcggacgccg cccgttcatg gcgcagatac ctcacccctcg  
 300  
 tcatttggtg cgttatcgtc gctgtcctcg gactagggat ttccgggtat cttgcgtggt  
 360  
 ggtcattgtg cgatcaagct gccgggggtct gtcagcgtgg tgaacccgtt atgtactggt  
 420  
 gtccggtggt ctctctggcc attctcggac tcattatcgg ggtcttgacg cagatctggc  
 480  
 tggagaagcg ctggtggcac atgcttgcca tcgtcatccc ggctgttttc atcgtcgccg  
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 gtatcttttt ctggctcgcc gtctaagaag gggcgtcaca gattccacaa acgacacagg  
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 tattgatctc cgttttatcg gctcctagca gccgtggtca acgtatcgct atcaagcgat  
 660  
 acaggactcg tcgttcgcat cgttgtgtg ctgctgggaa acaatcccag cgatctactc  
 720  
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 780  
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<210> 146

<211> 151

<212> PRT

<213> Homo sapiens

<400> 146

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Thr	Ile	Ser	Pro	Arg	Arg	Thr	Arg	His	His	Ala	Pro	Tyr	Leu	Asp	Arg
			20					25					30		
Met	Ser	Asp	Met	Ser	Met	Pro	Arg	Arg	Ala	Ala	Pro	Glu	Asp	Asp	Thr
		35					40					45			
Asp	Leu	Ala	Asp	Ala	Ala	Arg	Ser	Trp	Arg	Arg	Tyr	Leu	Ile	Leu	Val
	50					55					60				
Ile	Cys	Gly	Val	Ile	Val	Ala	Val	Leu	Gly	Leu	Gly	Ile	Phe	Gly	Tyr
65				70					75					80	
Leu	Ala	Trp	Trp	Ser	Leu	Cys	Asp	Gln	Ala	Ala	Gly	Val	Cys	Gln	Arg
				85					90				95		
Gly	Glu	Pro	Val	Met	Tyr	Trp	Cys	Ser	Val	Val	Ser	Leu	Ala	Ile	Leu
			100					105				110			
Gly	Leu	Ile	Ile	Gly	Val	Leu	Thr	Gln	Ile	Trp	Leu	Glu	Lys	Arg	Trp
	115					120					125				
Trp	His	Met	Leu	Ala	Ile	Val	Ile	Pro	Ala	Val	Phe	Ile	Val	Ala	Gly
	130					135					140				
Ile	Phe	Phe	Trp	Leu	Ala	Val									
145					150										

<210> 147

<211> 368

<212> DNA

<213> Homo sapiens

<400> 147



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180  
gattactggg atctagcaac acctatgcca attgcgtggg gtacaacgga ccgaacagtt  
240  
attgctgatg cacgacgtac aatccccacc acggagtggg atatccttgc aagactacgt  
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360  
cccccccta  
368

<210> 148

<211> 117

<212> PRT

<213> Homo sapiens

<400> 148

Met	Thr	Leu	Leu	Ala	Leu	Val	Asp	Leu	Ser	Lys	Lys	Pro	Asp	Glu	Phe
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Thr	Gln	Trp	Ala	Leu	Val	Ala	Arg	Asp	Val	His	Asp	Ile	Pro	Gly	Leu
			20					25					30		
Arg	Lys	Val	Ile	Gly	Gln	Lys	Val	Pro	Cys	Val	Ala	Val	Thr	Gly	Ser
		35					40					45			
Glu	Lys	Val	Leu	His	Lys	Lys	Asp	Tyr	Trp	Asp	Leu	Ala	Thr	Pro	Met
	50					55					60				
Pro	Ile	Ala	Trp	Gly	Thr	Thr	Asp	Arg	Thr	Val	Ile	Ala	Asp	Ala	Arg
65					70					75				80	
Arg	Thr	Ile	Pro	Thr	Glu	Trp	Asp	Ile	Leu	Ala	Arg	Leu	Arg	Pro	
				85				90					95		
Arg	Leu	Glu	Glu	Val	Arg	Lys	Gln	Arg	Asn	Asp	Val	Leu	Leu	Leu	Asn
			100				105						110		
Glu	Glu	Asp	Pro	Pro											
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<210> 149

<211> 407

<212> DNA

<213> Homo sapiens

<400> 149

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120  
gcggtggatg gtatcgtgta ccgaagtgcg gatgaaggca agtcgtgggc cccaattaag  
180  
ggcctgaac agggtcaggc gcaccttttc gtgctccatc cctacgacaa gactcaagcg  
240  
tatattctga cgcgcagcac tcagcattgg cgcacgtcga accgtggcga gacgtggcag  
300

tcattctcaa cgctcatcc gcctacgacc ttgaaagcta tgcctctgga ctttcatccg  
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407

<210> 150  
<211> 135  
<212> PRT  
<213> Homo sapiens

<400> 150  
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Val Thr His Phe Pro Asn Met Ala Ala Gln Ile Gln Tyr Phe Glu Asp  
20 25 30  
Ser Ser Val Val Ile Trp His Asp Ala Val Asp Gly Ile Val Tyr Arg  
35 40 45  
Ser Ala Asp Glu Gly Lys Ser Trp Ala Pro Ile Lys Gly Pro Glu Gln  
50 55 60  
Gly Gln Ala His Leu Phe Val Leu His Pro Tyr Asp Lys Thr Gln Ala  
65 70 75 80  
Tyr Ile Leu Thr Arg Ser Thr Gln His Trp Arg Thr Ser Asn Arg Gly  
85 90 95  
Glu Thr Trp Gln Ser Phe Ser Thr Pro His Pro Pro Thr Thr Leu Lys  
100 105 110  
Ala Met Pro Leu Asp Phe His Pro Thr His His Asp Trp Ile Leu Phe  
115 120 125  
Thr Gly Gln Ala Cys Thr Val  
130 135

<210> 151  
<211> 448  
<212> DNA  
<213> Homo sapiens

<400> 151  
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120  
cagagcgggtg gtcggccggg ctctgcccc gtctcggtc ctccctcctc cccaccagaa  
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240  
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360  
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448

<210> 152

<211> 149  
 <212> PRT  
 <213> Homo sapiens

<400> 152  
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 35 40 45  
 Cys Pro Val Ser Ala Pro Pro Ser Ser Pro Pro Glu Gly Lys Thr Trp  
 50 55 60  
 Ala Leu Arg Glu Pro Cys Gly Met Phe Phe Val Ile Asn Cys Thr Ser  
 65 70 75 80  
 Ala Ser Thr Ala Arg Pro Arg Ala Lys Ser Arg Val Ser Gly Pro Trp  
 85 90 95  
 Ser Lys Leu Arg Leu Ser Ala Ala Thr Ser Gly Gly Gln Gly Glu Gly  
 100 105 110  
 Phe Ala Ala Glu Thr Ala Ala Ser Gln His Arg Ala Ile Leu Gly Cys  
 115 120 125  
 Ser Pro Pro Arg Gly Ala His Gly Lys Pro Ala Pro Gly Gly Arg Gly  
 130 135 140  
 Cys Met Asp Ile Arg  
 145

<210> 153  
 <211> 440  
 <212> DNA  
 <213> Homo sapiens

<400> 153  
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 120  
 tgcattgggtc cgtgtatatg cgtgtatatata tgcggggata tgtatatgtg tgtgtgtatg  
 180  
 aacaggtgta agtggggagc actcaggtgt gtctgtgtgt gtccgtgtac acgtgtgtaa  
 240  
 gtgggtgacc atgaaggggt gtgtgtgtcc gtgtgttaggt ttgcgtgcat gcacacatgc  
 300  
 atgtgtgtac tggggcatcc aagcccctgg tctccactcc attccacct acgcctacct  
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 420  
 acgtgggtgt ctgcacgcgt  
 440

<210> 154  
 <211> 69  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 154

Gly Arg His Ala Gly Val Cys Pro Ser Val Cys Pro Trp Val His Val  
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 Cys Val Cys Ile Cys Gly Gly Thr Gly Val Cys Pro Ser Val Cys Met  
 20 25 30  
 Gly Pro Cys Ile Cys Val Tyr Ile Cys Gly Asp Met Tyr Met Cys Val  
 35 40 45  
 Cys Met Asn Arg Cys Lys Trp Gly Ala Leu Arg Cys Val Cys Val Cys  
 50 55 60  
 Ser Cys Thr Arg Val  
 65

&lt;210&gt; 155

&lt;211&gt; 344

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 155

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 120  
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 180  
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 240  
 gaactgggca cctcgcaagc tacgccaccg cgatccatgc ccccgcccgt atcttcgcgc  
 300  
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 344

&lt;210&gt; 156

&lt;211&gt; 92

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 156

Met Ala Glu Leu Met Ala Asp Ala Ala Thr Gly Thr Lys Pro Ser Tyr  
 1 5 10 15  
 Leu Gln Arg Ser Ser Ser Ile Thr Ser Phe Glu Val Asp Arg Glu  
 20 25 30  
 Gln Arg His Ser Asp Asn Ala Pro Gln Glu Val Lys Ser Ser Leu Ser  
 35 40 45  
 Asp His Gly Arg Arg Ala Ser Ala Gln Gly Glu Leu Gly Thr Ser Gln  
 50 55 60  
 Ala Thr Pro Pro Arg Ser Met Pro Pro Pro Val Ser Ser Ala Ser Ser  
 65 70 75 80  
 Thr Ser Pro Leu Pro Ile Ser Ile Ile Ser Asp Leu  
 85 90

&lt;210&gt; 157

&lt;211&gt; 6816

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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120  
cttggcagca gacagtgaag tggaaatgga agaatggatc acaattctaa ataagatcct  
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ccagctcaac tttgaagctg caatgcaaga aaagcgaaat ggcgactctc acgaagatga  
240  
tgaacaaagc aaattggaag gttctgggtc cggttttagat agctacctgc cggaacttgc  
300  
caagagtgc agagaagcag aaatcaaact gaaaagtga agcagagtca aactttttta  
360  
tttgaccca gatgccaga agcttgactt ctcatcagct gagccagaag tgaagtcatt  
420  
tgaagagaag tttggaaaaa ggatccttgt caagtgaat gatttatctt tcaatttgca  
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540  
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600  
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660  
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720  
aagcagggaa tattttcagt cacttgctct catccagata tatttcttgt ggccagaatt  
780  
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840  
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960  
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1080  
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1560

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4800

cccaaactca caccgctgtc ggaaatttct cagagactcc ttaaactgta ctccgataaa  
4860  
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4920  
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4980  
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5040  
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5160  
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5280  
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5340  
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<210> 158

<211> 1572

<212> PRT

<213> Homo sapiens

<400> 158

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Asp	Phe	Arg	Lys	Pro	Glu	Lys	Met	Ala	Lys	Leu	Pro	Val	Ile	Leu	Gly
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Asn	Leu	Asp	Ile	Thr	Ile	Asp	Asn	Val	Ser	Ser	Asp	Phe	Pro	Asn	Tyr
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Val	Asn	Ser	Ser	Tyr	Ile	Pro	Thr	Lys	Gln	Phe	Glu	Thr	Cys	Ser	Lys
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Thr	Pro	Ile	Thr	Phe	Glu	Val	Glu	Glu	Phe	Val	Pro	Cys	Ile	Pro	Lys
			85						90					95	
His	Thr	Gln	Pro	Tyr	Thr	Ile	Tyr	Thr	Asn	His	Leu	Tyr	Val	Tyr	Pro
		100						105					110		
Lys	Tyr	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	Ser	Phe	Ala	Lys	Ala	Arg	Asn
		115					120					125			
Ile	Ala	Ile	Cys	Ile	Glu	Phe	Lys	Asp	Ser	Asp	Glu	Glu	Asp	Ser	Gln
	130					135					140				
Pro	Leu	Lys	Cys	Ile	Tyr	Gly	Arg	Pro	Gly	Gly	Pro	Val	Phe	Thr	Arg
	145				150					155				160	
Ser	Ala	Phe	Ala	Ala	Val	Leu	His	His	His	Gln	Asn	Pro	Glu	Phe	Tyr
			165						170					175	
Asp	Glu	Ile	Lys	Ile	Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	His
		180						185					190		
Leu	Leu	Leu	Thr	Phe	Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly
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Ser	Thr	Lys	Lys	Arg	Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp
	210					215					220				
Leu	Pro	Leu	Leu	Lys	Asp	Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile
	225				230					235				240	
Pro	Val	Ser	Ala	Asn	Leu	Pro	Ser	Gly	Tyr	Leu	Gly	Tyr	Gln	Glu	Leu
			245						250					255	
Gly	Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly

	260		265		270										
Lys	Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr
	275						280					285			
Gln	Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu
	290					295					300				
Ser	Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser
305				310						315					320
Leu	His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile
			325						330					335	
Leu	Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val
		340						345					350		
Ala	Val	Asn	Val	Thr	Arg	Val	Ile	His	Val	Val	Ala	Gln	Cys	His	
	355					360					365				
Glu	Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr
	370					375					380				
Lys	Ala	Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu
385				390						395					400
Leu	Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu
			405						410				415		
Thr	Ser	Asn	Lys	Leu	Leu	Lys	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu
		420						425					430		
Ile	Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu
	435					440						445			
Leu	Arg	Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Val	Glu	Thr
450						455					460				
Val	Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Arg	Asp	Asn
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Pro	Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys
			485						490					495	
Arg	Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn
		500						505					510		
Asn	Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu
	515						520					525			
Tyr	Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile
	530					535					540				
Pro	Leu	Asn	Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr
545				550						555					560
Gln	Asp	Leu	Gln	Leu	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn
			565						570					575	
His	Phe	Leu	Val	Gly	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln
		580						585					590		
Glu	Phe	Arg	Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu
	595						600					605			
Leu	Ile	Lys	His	Ser	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Glu
	610					615					620				
Ala	Arg	Ile	Ala	Thr	Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu
625				630						635					640
Asn	Val	Gln	Arg	Ile	Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn
			645						650					655	
Ala	Gly	Met	Thr	Val	Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn
		660						665					670		
Pro	Leu	Val	Thr	Pro	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His
	675						680					685			
Lys	Asp	Leu	Leu	Gly	Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr

690	695	700
Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser		
705	710	715
Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu		
	725	730
Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn		
	740	745
Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu		
	755	760
Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu		
	770	775
Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe		
785	790	795
Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg		
	805	810
Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly		
	820	825
Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp		
	835	840
Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu		
	850	855
Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe		
865	870	875
Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys		
	885	890
Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr		
	900	905
Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe		
	915	920
Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys		
	930	935
Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr		
945	950	955
Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr		
	965	970
Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser		
	980	985
Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe		
	995	1000
Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu		
	1010	1015
Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg		
1025	1030	1035
Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn		
	1045	1050
Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr		
	1060	1065
Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg		
	1075	1080
Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val		
	1090	1095
His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val		
1105	1110	1115
Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg		

1125 1130 1135  
 Arg Ser Arg Gly Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val  
 1140 1145 1150  
 Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly  
 1155 1160 1165  
 Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu  
 1170 1175 1180  
 Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala  
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 Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe  
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 Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys  
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 Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe  
 1235 1240 1245  
 Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser  
 1250 1255 1260  
 Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr  
 1265 1270 1275 1280  
 Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg  
 1285 1290 1295  
 Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met  
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 1330 1335 1340  
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 Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly  
 1365 1370 1375  
 Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys  
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 Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr  
 1395 1400 1405  
 Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val  
 1410 1415 1420  
 Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys  
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 Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg  
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 Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe  
 1475 1480 1485  
 Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys  
 1490 1495 1500  
 Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu  
 1505 1510 1515 1520  
 Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Ile Cys Pro Leu  
 1525 1530 1535  
 Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His Ile Phe Asn Ala  
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 Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly Met Thr Ser Ser

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Ser Ser Val Val  
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1560

1565

<210> 159  
<211> 540  
<212> DNA  
<213> Homo sapiens

<400> 159  
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120  
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180  
acagcccaga gatgcatgtg ccactctgtt gtgtgcttca accaaggggc gctctggcag  
240  
ggcttgggtg ggacttccca aagggtcatg aaaagttccc agtcaatgag atccatggag  
300  
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420  
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<210> 160  
<211> 110  
<212> PRT  
<213> Homo sapiens

<400> 160  
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Thr Pro Gly Thr Ala Gln Arg Cys Met Cys His Ser Val Val Cys Phe  
20 25 30  
Asn Gln Gly Ala Leu Trp Gln Gly Leu Gly Gly Thr Ser Gln Arg Ala  
35 40 45  
Trp Lys Ser Ser Gln Ser Met Arg Ser Met Glu Thr His Gly Ser Gly  
50 55 60  
Gly Gln Pro Gln Pro Lys Arg Thr Pro Ser Pro Ala Leu Cys Pro Arg  
65 70 75 80  
Thr His Gln Ala Leu Ser Leu Val Ala Phe Pro Asp Asn Leu Tyr Pro  
85 90 95  
Pro Gly His Gln Phe Ser Ser Met Thr Lys Lys Gly Ala Phe  
100 105 110

<210> 161  
<211> 351  
<212> DNA  
<213> Homo sapiens

&lt;400&gt; 161

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 120  
 gcccgggcga agcgcgaggg ccgcgtatgg tggagctttg agtacttccc gccgcgcacg  
 180  
 ccgcagggca tgcagaatct gtatgaccgt atcgagcgca tgagtcagct gggccccgag  
 240  
 tttgtggaca ttacgtggaa tgccgggggc cggacgtcgg atatgacgac gcagctggtc  
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 aagacggtgc atgcgtactt tgggtgctgag acgtgcatgc atctgacgtg c  
 351

&lt;210&gt; 162

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 162

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Phe	Ala	Gly	Arg	Arg	Ala	Trp	Leu	Ala	Ala	Thr	Met	Lys	Gly	Asp	Asp
			20				25						30		
Ser	Ser	Lys	Ile	Thr	His	Lys	Ile	Ala	Arg	Ala	Lys	Arg	Glu	Gly	Arg
		35				40						45			
Val	Trp	Trp	Ser	Phe	Glu	Tyr	Phe	Pro	Pro	Arg	Thr	Pro	Gln	Gly	Met
	50				55					60					
Gln	Asn	Leu	Tyr	Asp	Arg	Ile	Glu	Arg	Met	Ser	Gln	Leu	Gly	Pro	Glu
65				70				75					80		
Phe	Val	Asp	Ile	Thr	Trp	Asn	Ala	Gly	Gly	Arg	Thr	Ser	Asp	Met	Thr
			85					90					95		
Thr	Gln	Leu	Val	Lys	Thr	Val	His	Ala	Tyr	Phe	Gly	Val	Glu	Thr	Cys
			100					105					110		
Met	His	Leu	Thr	Cys											
			115												

&lt;210&gt; 163

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 163

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 gacacctaca ccctgcgtca gcccatcggc gtatgcgcag gcactactcc gttcaacttc  
 120  
 ccggcgatga ttccactgtg gatgttcccg atggcgattg cctgcggtaa cactttcgtg  
 180  
 ctcaaaccgt ccgaacaaga ccctctgtcg acgatgctgc tggtagaact ggcgctggaa  
 240  
 gccggtgtgc cggccggcgt gctcaacgtg gtgcacggcg gcaaggatgt ggtggatgcg  
 300

ctgtgcaccc ataaagatat caaggcagtt tctttcgtcg gttcgaccgc cgttggtacc  
360

<210> 164

<211> 120

<212> PRT

<213> Homo sapiens

<400> 164

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Ala	Gly	Gly	Val	Asp	Thr	Tyr	Thr	Leu	Arg	Gln	Pro	Ile	Gly	Val	Cys
			20					25					30		
Ala	Gly	Ile	Thr	Pro	Phe	Asn	Phe	Pro	Ala	Met	Ile	Pro	Leu	Trp	Met
		35				40					45				
Phe	Pro	Met	Ala	Ile	Ala	Cys	Gly	Asn	Thr	Phe	Val	Leu	Lys	Pro	Ser
	50					55					60				
Glu	Gln	Asp	Pro	Leu	Ser	Thr	Met	Leu	Leu	Val	Glu	Leu	Ala	Leu	Glu
65					70					75				80	
Ala	Gly	Val	Pro	Ala	Gly	Val	Leu	Asn	Val	Val	His	Gly	Gly	Lys	Asp
				85				90						95	
Val	Val	Asp	Ala	Leu	Cys	Thr	His	Lys	Asp	Ile	Lys	Ala	Val	Ser	Phe
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Val	Gly	Ser	Thr	Ala	Val	Gly	Thr								
			115				120								

<210> 165

<211> 728

<212> DNA

<213> Homo sapiens

<400> 165

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120  
aagtttgga accgcaacgt ctcatgaag gacaacagct cttcttcag cacagactcc  
180  
cgctcccgt cctcctccag gtccccgacg cgccacttcc gcagaagtga ctcccactca  
240  
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300  
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360  
gggaagaggc acgatctggc gccaccaag cgcagtcgaa agaagatggc ggcgctggag  
420  
tgtgaggacc cggagcgaga gctgaagaag cagaagcggg cagcccgtt ccagcacgga  
480  
cactcccccc gcttgcgcct cgagcccctg gtgctgcaga tgagcagcct ggagagcagt  
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600  
cactacctgc gcctcacctg tgccccgac ccgtccaccg tgcgcctgt ggcattccct  
660

gtggcaggtt ttgaaaaagt cgctgtgcat ggtcaagtgc cactggaaag agaagcagga  
 720  
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 728

<210> 166  
 <211> 242  
 <212> PRT  
 <213> Homo sapiens

<400> 166  
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 35 40 45  
 Met Lys Asp Asn Ser Ser Ser Ser Ser Thr Asp Ser Arg Ser Arg Ser  
 50 55 60  
 Ser Ser Arg Ser Pro Thr Arg His Phe Arg Arg Ser Asp Ser His Ser  
 65 70 75 80  
 Asp Ser Asp Ser Ser Tyr Ser Gly Asn Glu Cys His Pro Val Gly Arg  
 85 90 95  
 Arg Asn Pro Pro Pro Lys Gly Arg Gly Arg Gly Ala His Met Asp  
 100 105 110  
 Arg Gly Arg Gly Arg Ala Gln Arg Gly Lys Arg His Asp Leu Ala Pro  
 115 120 125  
 Thr Lys Arg Ser Arg Lys Lys Met Ala Ala Leu Glu Cys Glu Asp Pro  
 130 135 140  
 Glu Arg Glu Leu Lys Lys Gln Lys Arg Ala Ala Arg Phe Gln His Gly  
 145 150 155 160  
 His Ser Arg Arg Leu Arg Leu Glu Pro Leu Val Leu Gln Met Ser Ser  
 165 170 175  
 Leu Glu Ser Ser Gly Ala Asp Pro Asp Trp Gln Glu Leu Gln Ile Val  
 180 185 190  
 Gly Thr Cys Pro Asp Ile Thr Lys His Tyr Leu Arg Leu Thr Cys Ala  
 195 200 205  
 Pro Asp Pro Ser Thr Val Arg Pro Val Ala Phe Pro Val Ala Gly Phe  
 210 215 220  
 Glu Lys Val Ala Val His Gly Gln Val Pro Leu Glu Arg Glu Ala Gly  
 225 230 235 240  
 Leu Arg

<210> 167  
 <211> 510  
 <212> DNA  
 <213> Homo sapiens

<400> 167  
 nnacgcgtgg aaccagaact caggcccggtg tgaggagtct ggtttggaac acacggggcc  
 60  
 gcaacacaga attgtcaggt cctgtgccgt gaccaccaac cctcggggcca tgccaggtgc  
 120



tgggtgagggg caggtggctc ccgccaggcg cctgctggcc tgaccgcact ccgtccacag  
 180  
 gtcctcatgg gcgtcctccg gctgggcttc gtgtccgcct acctctcaca gccactgctc  
 240  
 gatggctttg ccatgggggc ctccgtgacc atcctgacct cgcagctcaa acacctgctg  
 300  
 ggcgtgcgga tcccgcggca ccaggggccc ggcatgggtg tcctcacatg gctgagcctg  
 360  
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Cys	Pro	Ser	Ser	Ser	Ile	Ser	Phe	Met	Leu	Glu	Trp	Thr	Val	Ala	Cys
			20					25					30		
Ser	Met	Tyr	Leu	Ala	Met	Pro	Val	Thr	Asn	Ala	Phe	Leu	Ser	Ser	Lys
			35				40					45			
Phe	Val	Ser	Lys	Leu	Ala	Trp	Tyr	Met	Met	Glu	Glu	Gly	Gly	Gly	Ser
			50				55				60				
Met	His	Gly	Cys	Trp	Ser	Gly	Arg	Gly	Ser	Ser	Ser	Ser	Arg	Ser	Thr
65					70				75					80	
Leu	Asp	Arg	Ala	Ser	Ser	Arg	Val	Thr	Cys	Val	Val	Met	Ala	Ala	Val
				85				90					95		
Ser	Val	Phe	Cys	Thr	Gly	Ser	Ala	Ala	Gly	Pro	Gly	Glu	Gly	Pro	Glu
			100				105					110			
Ala	Thr	Ala	Gly	Pro	Arg	Ala	Gly	Ala	Gln	Asp	Ala	Leu	Pro	Arg	Ser

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      115      120      125
Ala Ala Pro Pro Val Gln Asn Thr Glu Thr Ala Ala Met Thr Thr His
      130      135      140
Val Thr Leu Glu Asp Ala Leu Ser Asn Val Asp Leu Leu Glu Glu Leu
145      150      155      160
Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro Pro Pro Ser Ser Ile
      165      170      175
Met Tyr Gln Ala Asn Phe Asp Thr Asn Phe Glu Asp Arg Asn Ala Phe
      180      185      190
Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala Thr Val His Ser Ser
      195      200      205
Met Asn Glu Met Leu Glu Glu Gly His Glu Tyr Ala Val Met Leu Tyr
      210      215      220
Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln Val Lys Cys Asn Glu
225      230      235      240
Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr Val Glu Val Leu Glu
      245      250      255
Pro Glu Val Thr Lys Leu Met Asn Phe Met Tyr Phe Gln Arg Asn Ala
      260      265      270
Ile Glu Arg Phe Cys Gly Glu Val Arg Arg Leu Cys His Ala Glu Arg
      275      280      285
Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Ile Thr Leu Gly Lys Phe
      290      295      300
Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys Asn Met Lys Cys Ser
305      310      315      320
Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala Ala Gln Phe Leu Arg
      325      330      335
Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser Gln Asn Leu Ser Met
      340      345      350
Phe Leu Ala Asn His Asn Lys Ile Thr Gln Ser Leu Gln Gln Gln Leu
      355      360      365
Glu Val Ile Ser Gly Tyr Glu Glu Leu Leu Ala Asp Ile Val Asn Leu
      370      375      380
Cys Val Asp Tyr Tyr Glu Asn Arg Met Tyr Leu Thr Pro Ser Glu Lys
385      390      395      400
His Met Leu Leu Lys Val Met Gly Phe Gly Leu Tyr Leu Met Asp Gly
      405      410      415
Ser Val Ser Asn Ile Tyr Lys Leu Asp Ala Lys Lys Arg Ile Asn Leu
      420      425      430
Ser Lys Ile Asp Lys Tyr Phe Lys Gln Leu Gln Val Val Pro Leu Phe
      435      440      445
Gly Asp Met Gln Ile Glu Leu Ala Arg Tyr Ile Lys Thr Ser Ala His
      450      455      460
Tyr Glu Glu Asn Lys Ser Arg Trp Thr Cys Thr Ser Ser Gly Ser Ser
465      470      475      480
Pro Gln Tyr Asn Ile Cys Glu Gln Met Ile Gln Ile Arg Glu Asp His
      485      490      495
Met Arg Phe Ile Ser Glu Leu Ala Arg Tyr Ser Asn Ser Glu Val Val
      500      505      510
Thr Gly Ser Gly Arg Gln Glu Ala Gln Lys Thr Asp Ala Glu Tyr Arg
      515      520      525
Lys Leu Phe Asp Leu Ala Leu Gln Gly Leu Gln Leu Leu Ser Gln Trp
530      535      540
Ser Ala His Val Met Glu Val Tyr Ser Trp Lys Leu Val His Pro Thr

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545					550					555				560	
Asp	Lys	Tyr	Ser	Asn	Lys	Asp	Cys	Pro	Asp	Ser	Ala	Glu	Glu	Tyr	Glu
				565					570					575	
Arg	Ala	Thr	Arg	Tyr	Asn	Tyr	Thr	Ser	Glu	Glu	Lys	Phe	Ala	Leu	Val
				580					585					590	
Glu	Val	Ile	Ala	Met	Ile	Lys	Gly	Leu	Gln	Val	Leu	Met	Gly	Arg	Met
				595				600					605		
Glu	Ser	Val	Phe	Asn	His	Ala	Ile	Arg	His	Thr	Val	Tyr	Ala	Ala	Leu
						615					620				
Gln	Asp	Phe	Ser	Gln	Val	Thr	Leu	Arg	Glu	Pro	Leu	Arg	Gln	Ala	Ile
625						630					635				640
Lys	Lys	Lys	Lys	Asn	Val	Ile	Gln	Ser	Val	Leu	Gln	Ala	Ile	Arg	Lys
				645						650				655	
Thr	Val	Cys	Asp	Trp	Glu	Thr	Gly	His	Glu	Pro	Phe	Asn	Asp	Pro	Ala
				660					665					670	
Leu	Arg	Gly	Glu	Lys	Asp	Pro	Lys	Ser	Gly	Phe	Asp	Ile	Lys	Val	Pro
				675				680					685		
Arg	Arg	Ala	Val	Gly	Pro	Ser	Ser	Thr	Gln	Leu	Tyr	Met	Val	Arg	Thr
				690				695				700			
Met	Leu	Glu	Ser	Leu	Ile	Ala	Asp	Lys	Ser	Gly	Ser	Lys	Lys	Thr	Leu
705						710				715					720
Arg	Ser	Ser	Leu	Glu	Gly	Pro	Thr	Ile	Leu	Asp	Ile	Glu	Lys	Phe	His
					725					730					735
Arg	Glu	Ser	Phe	Tyr	Thr	His	Leu	Ile	Asn	Phe	Ser	Glu	Thr	Leu	
				740					745				750		
Gln	Gln	Cys	Cys	Asp	Leu	Ser	Gln	Leu	Trp	Phe	Arg	Glu	Phe	Phe	Leu
				755				760					765		
Glu	Leu	Thr	Met	Gly	Arg	Arg	Ile	Gln	Phe	Pro	Ile	Glu	Met	Ser	Met
				770				775				780			
Pro	Trp	Ile	Leu	Thr	Asp	His	Ile	Leu	Glu	Thr	Lys	Glu	Ala	Ser	Met
785						790					795				800
Met	Glu	Tyr	Val	Leu	Tyr	Ser	Leu	Asp	Leu	Tyr	Asn	Asp	Ser	Ala	His
				805						810					815
Tyr	Ala	Leu	Thr	Arg	Phe	Asn	Lys	Gln	Phe	Leu	Tyr	Asp	Glu	Ile	Glu
				820					825					830	
Ala	Glu	Val	Asn	Leu	Cys	Phe	Asp	Gln	Phe	Val	Tyr	Lys	Leu	Ala	Asp
				835				840					845		
Gln	Ile	Phe	Ala	Tyr	Tyr	Lys	Val	Met	Ala	Gly	Ser	Leu	Leu	Leu	Asp
				850				855				860			
Lys	Arg	Leu	Arg	Ser	Glu	Cys	Lys	Asn	Gln	Gly	Ala	Thr	Ile	His	Leu
865						870				875					880
Pro	Pro	Ser	Asn	Arg	Tyr	Glu	Thr	Leu	Leu	Lys	Gln	Arg	His	Val	Gln
				885						890					895
Leu	Leu	Gly	Arg	Ser	Ile	Asp	Leu	Asn	Arg	Leu	Ile	Thr	Gln	Arg	Val
				900					905				910		
Ser	Ala	Ala	Met	Tyr	Lys	Ser	Leu	Glu	Leu	Ala	Ile	Gly	Arg	Phe	Glu
				915					920				925		
Ser	Glu	Asp	Leu	Thr	Ser	Ile	Val	Glu	Leu	Asp	Gly	Leu	Leu	Glu	Ile
				930					935				940		
Asn	Arg	Met	Thr	His	Lys	Leu	Leu	Ser	Arg	Tyr	Leu	Thr	Leu	Asp	Gly
945						950					955				960
Phe	Asp	Ala	Met	Phe	Arg	Glu	Ala	Asn	His	Asn	Val	Ser	Ala	Pro	Tyr
				965						970					975
Gly	Arg	Ile	Thr	Leu	His	Val	Phe	Trp	Glu	Leu	Asn	Tyr	Asp	Phe	Leu

980	985	990
Pro Asn Tyr Cys Tyr Asn Gly Ser Thr Asn Arg Phe Val Arg Thr Val		
995	1000	1005
Leu Pro Phe Ser Gln Glu Phe Gln Arg Asp Lys Gln Pro Asn Ala Gln		
1010	1015	1020
Pro Gln Tyr Leu His Gly Ser Lys Ala Leu Asn Leu Ala Tyr Ser Ser		
1025	1030	1035
Ile Tyr Gly Ser Tyr Arg Asn Phe Val Gly Pro Pro His Phe Gln Val		
1045	1050	1055
Ile Cys Arg Leu Leu Gly Tyr Gln Gly Ile Ala Val Val Met Glu Glu		
1060	1065	1070
Leu Leu Lys Val Val Lys Ser Leu Leu Gln Gly Thr Ile Leu Gln Tyr		
1075	1080	1085
Val Lys Thr Leu Met Glu Val Met Pro Lys Ile Cys Arg Leu Pro Arg		
1090	1095	1100
His Glu Tyr Gly Ser Pro Gly Ile Leu Glu Phe His His Gln Leu		
1105	1110	1115
Lys Asp Ile Val Glu Tyr Ala Glu Leu Lys Thr Val Cys Phe Gln Asn		
1125	1130	1135
Leu Arg Glu Val Gly Asn Ala Ile Leu Phe Cys Leu Leu Ile Glu Gln		
1140	1145	1150
Ser Leu Ser Leu Glu Glu Val Cys Asp Leu Leu His Ala Ala Pro Phe		
1155	1160	1165
Gln Asn Ile Leu Pro Arg Val His Val Lys Glu Gly Glu Arg Leu Asp		
1170	1175	1180
Ala Lys Met Lys Arg Leu Glu Ser Lys Tyr Ala Pro Leu His Leu Val		
1185	1190	1195
Pro Leu Ile Glu Arg Leu Gly Thr Pro Gln Gln Ile Ala Ile Ala Arg		
1205	1210	1215
Glu Gly Asp Leu Leu Thr Lys Glu Arg Leu Cys Cys Gly Leu Ser Met		
1220	1225	1230
Phe Glu Val Ile Leu Thr Arg Ile Arg Ser Phe Leu Asp Asp Pro Ile		
1235	1240	1245
Trp Arg Gly Pro Leu Pro Ser Asn Gly Val Met His Val Asp Glu Cys		
1250	1255	1260
Val Glu Phe His Arg Leu Trp Ser Ala Met Gln Phe Val Tyr Cys Ile		
1265	1270	1275
Pro Val Gly Thr His Glu Phe Thr Val Glu Gln Cys Phe Gly Asp Gly		
1285	1290	1295
Leu His Trp Ala Gly Cys Met Ile Ile Val Leu Leu Gly Gln Gln Arg		
1300	1305	1310
Arg Phe Ala Val Leu Asp Phe Cys Tyr His Leu Leu Lys Val Gln Lys		
1315	1320	1325
His Asp Gly Lys Asp Glu Ile Ile Lys Asn Val Pro Leu Lys Lys Met		
1330	1335	1340
Val Glu Arg Ile Arg Lys Phe Gln Ile Leu Asn Asp Glu Ile Ile Thr		
1345	1350	1355
Ile Leu Asp Lys Tyr Leu Lys Ser Gly Asp Gly Glu Gly Thr Pro Val		
1365	1370	1375
Glu His Val Arg Cys Phe Gln Pro Pro Ile His Gln Ser Leu Ala Ser		
1380	1385	1390
Ser		

<210> 177  
 <211> 417  
 <212> DNA  
 <213> Homo sapiens

<400> 177  
 acgcgtgatg tcacactgcc tctgccgctg ggtcctaatt cgattgcacg caccatggct  
 60  
 gcagttcgtg gcgcgcatag tttctggcat gtttcgcgca tcctggagac cgatccccgc  
 120  
 gctgccgtga aaccgcctaa aaatgtgaag cgattgccca aagccgtgtc cgtggagcaa  
 180  
 atgcaaaagc tccttgccat acccagtctt aagactccta ccggcctgcg taatcgagcg  
 240  
 atacttgagt tcttatatgc taccggcgcg cgcgtgagcg agatgctggc aacagacctg  
 300  
 gacgatatac acctgggcga aaaacccgcg gatgaaaacg gggaatctat tgcacttccc  
 360  
 gggatgtgc gcctttttgg aaagggaggt aaagagcgtt tagtcccttt gggatcc  
 417

<210> 178  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens

<400> 178  
 Thr Arg Asp Val Thr Leu Pro Leu Pro Leu Gly Pro Asn Ser Ile Ala  
 1 5 10 15  
 Arg Thr Met Ala Val Arg Gly Ala His Ser Phe Trp His Ala Ser  
 20 25 30  
 Arg Ile Leu Glu Thr Asp Pro Ala Ala Val Lys Pro Pro Lys Asn  
 35 40 45  
 Val Lys Arg Leu Pro Lys Ala Val Ser Val Glu Gln Met Gln Lys Leu  
 50 55 60  
 Leu Ala Ile Pro Ser Leu Lys Thr Pro Thr Gly Leu Arg Asn Arg Ala  
 65 70 75 80  
 Ile Leu Glu Phe Leu Tyr Ala Thr Gly Ala Arg Val Ser Glu Met Leu  
 85 90 95  
 Ala Thr Asp Leu Asp Asp Ile His Leu Gly Glu Lys Pro Arg Asp Glu  
 100 105 110  
 Asn Gly Glu Ser Ile Ala Leu Pro Gly Tyr Val Arg Leu Phe Gly Lys  
 115 120 125  
 Gly Gly Lys Glu Arg Leu Val Pro Leu Gly Ser  
 130 135

<210> 179  
 <211> 362  
 <212> DNA  
 <213> Homo sapiens

<400> 179  
 acgcgtcgaa ggtgccggtg ggggcgatca ataacatcgc gcaatccctg gaagagcctc  
 60

aggtgattgc ccgtgggttg atggtggaag atcccgcatc cccaagaatc cgggaattcg  
 120  
 ccattgggcc gggcagcccg aatccaaaat gtcggggcac gcccagtggg agtatggtaa  
 180  
 ggggccggca ccgatgttgg nggcagcata cggatggaag tgctgggcga gcgcctgggt  
 240  
 ttgccggcag agcaactggg gcagctcaag gcgggcgggg tgatcgagca gttggattga  
 300  
 gcaatggcgg ccgcgaagcc cgccatttac cttgatgact gtttagcgcg cggattcttt  
 360  
 aa  
 362

<210> 180  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 180  
 Met Ala Gly Phe Ala Ala Ile Ala Gln Ser Asn Cys Ser Ile Thr  
 1 5 10 15  
 Pro Pro Ala Leu Ser Cys Pro Ser Cys Ser Ala Gly Lys Pro Arg Arg  
 20 25 30  
 Ser Pro Ser Thr Ser Ile Arg Met Leu Pro Pro Thr Ser Val Pro Ala  
 35 40 45  
 Pro Tyr His Thr Pro Thr Gly Arg Ala Pro Thr Phe Trp Ile Arg Ala  
 50 55 60  
 Ala Arg Pro Asn Gly Glu Phe Pro Asp Ser Trp Gly Cys Gly Ile Phe  
 65 70 75 80  
 His His Gln Pro Thr Gly Asn His Leu Arg Leu Phe Gln Gly Leu Arg  
 85 90 95  
 Asp Val Ile Asp Arg Pro His Arg His Leu Arg Arg  
 100 105

<210> 181  
 <211> 297  
 <212> DNA  
 <213> Homo sapiens

<400> 181  
 gcgttgatca tgtccgaccc aggcttgatc atgctgggtac gccgtcactt cccgtgcatg  
 60  
 ccgattcact tgtcggtaca ggccaatacg gtgaattggg ccagcgtcga gttctggcaa  
 120  
 cagcaaggta tctgccgggt aatcctgtcg cgggaattgt cactggaaga aatcggcgaa  
 180  
 atccgccaac aggtgccggc catggagctg gaagtgtttg tgcacgggtc cctgtacatg  
 240  
 gcctattccg ggcgctgttt gttgtccggc tatatgaaca agcgcgatgc caaccaa  
 297

<210> 182  
 <211> 99  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 182

Ala Leu Ile Met Ser Asp Pro Gly Leu Ile Met Leu Val Arg Arg His  
 1 5 10 15  
 Phe Pro Cys Met Pro Ile His Leu Ser Val Gln Ala Asn Thr Val Asn  
 20 25 30  
 Trp Ala Ser Val Glu Phe Trp Gln Gln Gln Gly Ile Cys Arg Val Ile  
 35 40 45  
 Leu Ser Arg Glu Leu Ser Leu Glu Glu Ile Gly Glu Ile Arg Gln Gln  
 50 55 60  
 Val Pro Ala Met Glu Leu Glu Val Phe Val His Gly Ala Leu Tyr Met  
 65 70 75 80  
 Ala Tyr Ser Gly Arg Cys Leu Leu Ser Gly Tyr Met Asn Lys Arg Asp  
 85 90 95  
 Ala Asn Gln

&lt;210&gt; 183

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 183

cgggacgtca ccatgaagcc gaccggctcg ggggatgtgg cgaacaaggt catcacccat  
 60  
 attccgttta acatcgtctc ccaggcgact catccattcc ttcgtacctt ggacgatgtc  
 120  
 aagcgcacat ctttggcgac cgacgggctc ggccaccagg tcctgctcaa gggctaccag  
 180  
 gccgagggcc acgactacgc acaccccgac tacggcggca acgtctccca ccgtgccggc  
 240  
 gggatgaagg atctcgagaa gtcaccgag tcgggcaggc agtggaacac cgatttcggc  
 300  
 attcacgtca acctggtgga gtcctatcct gaggcgaatc acttcggcga c  
 351

&lt;210&gt; 184

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 184

Arg Asp Val Thr Met Lys Pro Thr Gly Ser Gly Asp Val Ala Asn Lys  
 1 5 10 15  
 Val Ile Thr His Ile Pro Phe Asn Ile Val Ser Gln Ala Thr His Pro  
 20 25 30  
 Phe Leu Arg Thr Leu Asp Asp Val Lys Arg Ile Ser Leu Ala Thr Asp  
 35 40 45  
 Gly Leu Gly His Gln Val Leu Leu Lys Gly Tyr Gln Ala Glu Gly His  
 50 55 60  
 Asp Tyr Ala His Pro Asp Tyr Gly Gly Asn Val Ser His Arg Ala Gly  
 65 70 75 80  
 Gly Met Lys Asp Leu Glu Lys Leu Thr Glu Ser Gly Arg Gln Trp Asn

85 90 95  
 Thr Asp Phe Gly Ile His Val Asn Leu Val Glu Ser Tyr Pro Glu Ala  
 100 105 110  
 Asn His Phe Gly Asp  
 115

<210> 185  
 <211> 396  
 <212> DNA  
 <213> Homo sapiens

<400> 185  
 cgcggtgggtc tcagtaaaga aaatttggtg cttagaggat gcaccattag aaacacagag  
 60  
 gctgttggtg gcatgtggt ttatgcaggc catgaaacca aagcaatgct gaacaacagt  
 120  
 gggccacggt ataagcgcag caaattagaa agaagagcaa acacagatgt cctctggtgt  
 180  
 gtcattgcttc tggtcataat gtgcttaact ggcgcagtag gtcattggaat ctggctgagc  
 240  
 aggtatgaaa agatgcattt tttcaatgtt cccgagcctg atggacatat catatcacca  
 300  
 ctggtggcag gattttatat gtttggacc gtgatcattt tggtacaggt cttgattcct  
 360  
 atttctctct atgtttccat cgaaattgtg aagctt  
 396

<210> 186  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

<400> 186  
 Arg Val Gly Leu Ser Lys Glu Asn Leu Leu Arg Gly Cys Thr Ile  
 1 5 10 15  
 Arg Asn Thr Glu Ala Val Val Gly Ile Val Val Tyr Ala Gly His Glu  
 20 25 30  
 Thr Lys Ala Met Leu Asn Asn Ser Gly Pro Arg Tyr Lys Arg Ser Lys  
 35 40 45  
 Leu Glu Arg Arg Ala Asn Thr Asp Val Leu Trp Cys Val Met Leu Leu  
 50 55 60  
 Val Ile Met Cys Leu Thr Gly Ala Val Gly His Gly Ile Trp Leu Ser  
 65 70 75 80  
 Arg Tyr Glu Lys Met His Phe Phe Asn Val Pro Glu Pro Asp Gly His  
 85 90 95  
 Ile Ile Ser Pro Leu Leu Ala Gly Phe Tyr Met Phe Trp Thr Val Ile  
 100 105 110  
 Ile Leu Leu Gln Val Leu Ile Pro Ile Ser Leu Tyr Val Ser Ile Glu  
 115 120 125  
 Ile Val Lys Leu  
 130

<210> 187  
 <211> 423



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 187

cgagtgtctca ccgcgtcagc cgtcatgcgt cccactgagg ctgttgcttc tcggtcggca  
 60  
 gaacctcgac gagttcagcg gatcctggac cagcgcgagt gggtggcgt cttcgttgct  
 120  
 gatgagcatc gtcgtttgct tggcacggtc ggcatcaag aggtcatcga ggctgctcgc  
 180  
 cgcgagatc gcagtattgc tgacgcgggtg gaaactaacg gcacctcac ggcgcgagacc  
 240  
 gacactccgt tgtccgagct cttcgtccg accagcaacg ccagggtgcc gttggccggt  
 300  
 gtcgacgagg acttccacct catgggtgct atctctcggg tgacctgct cgacgcgatg  
 360  
 tcacgagctc gcgacgaggc aggagagggg tctgtcatgt ccttggagaa caccggaaag  
 420  
 ctt  
 423

&lt;210&gt; 188

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 188

Arg	Val	Leu	Thr	Ala	Ser	Ala	Val	Met	Arg	Pro	Thr	Glu	Ala	Val	Val
1				5					10					15	
Ser	Arg	Ser	Ala	Glu	Pro	Arg	Arg	Val	Gln	Arg	Ile	Leu	Asp	Gln	Arg
			20					25					30		
Glu	Trp	Ala	Gly	Val	Phe	Val	Val	Asp	Glu	His	Arg	Arg	Leu	Leu	Gly
		35				40					45				
Thr	Val	Gly	Asp	Gln	Glu	Val	Ile	Glu	Ala	Ala	Arg	Arg	Gly	Asp	Arg
	50				55					60					
Ser	Ile	Ala	Asp	Ala	Val	Glu	Thr	Asn	Gly	Ile	Leu	Thr	Ala	Arg	Thr
65					70				75					80	
Asp	Thr	Pro	Leu	Ser	Glu	Leu	Phe	Ala	Pro	Thr	Ser	Asn	Ala	Arg	Val
			85					90					95		
Pro	Leu	Ala	Val	Val	Asp	Glu	Asp	Phe	His	Leu	Met	Gly	Val	Ile	Ser
		100						105					110		
Arg	Val	Thr	Leu	Leu	Asp	Ala	Met	Ser	Arg	Ala	Arg	Asp	Glu	Ala	Gly
		115				120						125			
Glu	Gly	Ser	Val	Met	Ser	Leu	Glu	Asn	Thr	Gly	Lys	Leu			
	130					135						140			

&lt;210&gt; 189

&lt;211&gt; 429

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 189

ngatggttta ccaacatatg cacgggttcga gcggcaatag ctctcgggg gctggcagtg  
 60

aaatgtttga agatgccggc gtttccggcc tcaacttggt tcgatgccgt gggtccaccg  
 120  
 atttcgccga tgcggctcat cgcacgggta agaagtttcg tccagataac ccaggacaga  
 180  
 gcaagggtata tcaggctcag aaccaggaaa agcaggggctt taccacagtg ccccatatag  
 240  
 accgcgctag ctacggcaaa aggcgcgccc agtgggggtcc aggacagcac tttcatggct  
 300  
 gaaggggagcg catcccnagc ttcgcctagc cccagagcta acccagcgac cagtggacca  
 360  
 gcgccccatca tcagtaggaa ccctacgata atcagccctt gttttacccc tggaatggag  
 420  
 ctgatttcn  
 429

<210> 190  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 190  
 Met Met Gly Ala Gly Pro Leu Val Ala Gly Leu Ala Leu Gly Leu Gly  
 1 5 10 15  
 Glu Ala Xaa Asp Ala Leu Pro Ser Ala Met Lys Val Leu Ser Trp Thr  
 20 25 30  
 Pro Leu Gly Ala Pro Phe Ala Val Ala Ser Ala Val Tyr Met Gly His  
 35 40 45  
 Trp Gly Lys Ala Leu Leu Phe Leu Val Leu Ser Leu Ile Tyr Leu Ala  
 50 55 60  
 Leu Ser Trp Val Ile Trp Thr Lys Leu Leu Asn Arg Ala Met Ser Arg  
 65 70 75 80  
 Ile Gly Glu Ile Gly Gly Thr Thr Ala Ser Lys Gln Val Glu Ala Gly  
 85 90 95  
 Asn Ala Gly Ile Phe Lys His Phe Thr Ala Ser Pro Arg Gly Ala Ile  
 100 105 110  
 Ala Ala Arg Thr Val His Met Leu Val Asn His  
 115 120

<210> 191  
 <211> 4845  
 <212> DNA  
 <213> Homo sapiens

<400> 191  
 ccgccccggg ccatggcgac actcagcttc gtcttctcgc tgctgggggc agtgtcctgg  
 60  
 cctccgggctt ctgcctccgg ccaggagtcc tggcccggac aatcggcggc cgatattctg  
 120  
 tcggggggcgg cttcccgag acggtatctt ctgtatgacg tcaaccccc ggaaggcttc  
 180  
 aacctgcgca gggatgtcta tatccgaatc gcctctctcc tgaagactct gctgaagacg  
 240  
 gaggagtggg tgcttgctct gcctccatgg ggccgcctct atcaactggca gagtccctgac  
 300

atccaccagg tccggattcc ctggtctgag ttttttgatc ttccaagtct caataaaaaac  
360  
atcccegtca tcgagtatga gcagttcatc gcagaatctg gtgggccctt tattgaccag  
420  
gtttacgtcc tgcaaagtta cgcagagggg tggaaagaag ggacctggga agagaagggtg  
480  
gacgagcggc cgtgtattga tcagctcctg tactcccagg acaagcacga gtactacaga  
540  
ggatggtttt ggggttatga ggagaccagg ggtctaaacg tctcctgtct gtccgtccag  
600  
ggctcagcct ccacgtggc gccctgtctg ctgagaaaca catcagcccg gtccgtgatg  
660  
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 ctgtataaaa cattttggac tgtgaccatg taccttcctt ttaagaaaa ataaactgct  
 4800  
 ttatggaagt tggtaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa  
 4845

&lt;210&gt; 192

&lt;211&gt; 428

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 192

Pro Pro Gly Ala Met Ala Thr Leu Ser Phe Val Phe Leu Leu Leu Gly  
 1 5 10 15  
 Ala Val Ser Trp Pro Pro Ala Ser Ala Ser Gly Gln Glu Phe Trp Pro  
 20 25 30  
 Gly Gln Ser Ala Ala Asp Ile Leu Ser Gly Ala Ala Ser Arg Arg Arg

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      35              40              45
Tyr Leu Leu Tyr Asp Val Asn Pro Pro Glu Gly Phe Asn Leu Arg Arg
  50              55              60
Asp Val Tyr Ile Arg Ile Ala Ser Leu Leu Lys Thr Leu Leu Lys Thr
  65              70              75              80
Glu Glu Trp Val Leu Val Leu Pro Pro Trp Gly Arg Leu Tyr His Trp
      85              90              95
Gln Ser Pro Asp Ile His Gln Val Arg Ile Pro Trp Ser Glu Phe Phe
      100              105              110
Asp Leu Pro Ser Leu Asn Lys Asn Ile Pro Val Ile Glu Tyr Glu Gln
      115              120              125
Phe Ile Ala Glu Ser Gly Gly Pro Phe Ile Asp Gln Val Tyr Val Leu
      130              135              140
Gln Ser Tyr Ala Glu Gly Trp Lys Glu Gly Thr Trp Glu Glu Lys Val
      145              150              155              160
Asp Glu Arg Pro Cys Ile Asp Gln Leu Leu Tyr Ser Gln Asp Lys His
      165              170              175
Glu Tyr Tyr Arg Gly Trp Phe Trp Gly Tyr Glu Glu Thr Arg Gly Leu
      180              185              190
Asn Val Ser Cys Leu Ser Val Gln Gly Ser Ala Ser Ile Val Ala Pro
      195              200              205
Leu Leu Leu Arg Asn Thr Ser Ala Arg Ser Val Met Leu Asp Arg Ala
      210              215              220
Glu Asn Leu Leu His Asp His Tyr Gly Gly Lys Glu Tyr Trp Asp Thr
      225              230              235              240
Arg Arg Ser Met Val Phe Ala Arg His Leu Arg Glu Val Gly Asp Glu
      245              250              255
Phe Arg Ser Arg His Leu Asn Ser Thr Asp Asp Ala Asp Arg Ile Pro
      260              265              270
Phe Gln Glu Asp Trp Met Lys Met Lys Val Lys Leu Gly Ser Ala Leu
      275              280              285
Gly Gly Pro Tyr Leu Gly Val His Leu Arg Arg Lys Asp Phe Ile Trp
      290              295              300
Gly His Arg Gln Asp Val Pro Ser Leu Glu Gly Ala Val Arg Lys Ile
      305              310              315              320
Arg Ser Leu Met Lys Thr His Arg Leu Asp Lys Val Phe Val Ala Thr
      325              330              335
Asp Ala Val Arg Lys Glu Tyr Glu Glu Leu Lys Lys Leu Leu Pro Glu
      340              345              350
Met Val Arg Phe Glu Pro Thr Trp Glu Glu Leu Glu Leu Tyr Lys Asp
      355              360              365
Gly Gly Val Ala Ile Ile Asp Gln Trp Ile Cys Ala His Ala Arg Cys
      370              375              380
Leu Pro Thr Ser Leu Ser Ala Glu Ser Gly Ser Gly Gly Phe Gln Arg
      385              390              395              400
Phe Phe Cys Pro Lys Tyr Ser Val Ser Glu Gln Met Val Ala Cys Val
      405              410              415
His Ser Gly His Phe His Thr Val Cys Leu Leu Val
      420              425

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&lt;210&gt; 193

&lt;211&gt; 350

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 193

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 gcgcagctgt acgacgagcc cttcgtcgtc gcgctgcggg cgtcgcaccc gctggccgac  
 120  
 cgtgccagca tcagccccga ggaggtcaag ggcgagacca tgttgatgtt gggcacgggc  
 180  
 ccctggtttc cccgggcccc cggtgggggt ttggcccga tttggcgcgt ttctccagcg  
 240  
 ccgttaaggg catacgccgc agtttcgagg gctcgtcgtt ggagaccatc aagcacatcg  
 300  
 tgggttcggg catggcgtga cggtggtgcc gcagctgtcc gtgccgcgcg  
 350

&lt;210&gt; 194

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 194

Ala	Gly	Glu	Leu	Asp	Cys	Ala	Ile	Met	Ala	Glu	Pro	Phe	Pro	Asp	Thr
1				5					10					15	
Gly	Leu	Ala	Thr	Ala	Gln	Leu	Tyr	Asp	Glu	Pro	Phe	Val	Val	Ala	Leu
			20					25					30		
Arg	Ala	Ser	His	Pro	Leu	Ala	Asp	Arg	Ala	Ser	Ile	Ser	Pro	Glu	Glu
		35					40					45			
Val	Lys	Gly	Glu	Thr	Met	Leu	Met	Leu	Gly	Thr	Gly	Pro	Trp	Phe	Pro
	50				55					60					
Arg	Ala	Arg	Gly	Gly	Gly	Leu	Ala	Arg	Ile	Trp	Arg	Val	Ser	Pro	Ala
65					70				75					80	
Pro	Leu	Arg	Ala	Tyr	Ala	Ala	Val	Ser	Arg	Ala	Arg	Arg	Trp	Arg	Pro
			85					90					95		
Ser	Ser	Thr	Ser	Trp	Leu	Arg	Ala	Trp	Arg	Asp	Gly	Gly	Ala	Ala	Ala
			100					105					110		
Val	Arg	Ala	Ala												
			115												

&lt;210&gt; 195

&lt;211&gt; 495

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

acgcgtgaac ggcacggctt ggcgatcgga ggcgtcggcc ccgtcgttga gtgggcccgtt  
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 gaaatgggttc gcttcgacga aagcgagact ctgcaccgcc ttgcatcggg cgtccttgaa  
 120  
 ccagaacttg ggcacgattt ggccgccgtc ctgctcgatt ctcatcgggt tgctgtcatc  
 180  
 agcgagggat cgaactggct tgcctcgcta cccgtgatcg taggtcgcaa cacggaacag  
 240  
 tttcgcagca taccagacct tgcccgcgac cggatcgaca aactgcacca gttgagccat  
 300

cgcgaaatag cactgaaatcg cgagctcctg cgtgcccgcg ctgcgtcggg gcaggtgcgg  
 360  
 cactgccacg gcgacgcaca cctcggcaac atcgtcatga ttgacggcaa gccggtcctg  
 420  
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 ttccctctga tggat  
 495

<210> 196  
 <211> 165  
 <212> PRT  
 <213> Homo sapiens

<400> 196  
 Thr Arg Glu Arg Asp Gly Leu Ala Ile Gly Gly Val Gly Pro Val Val  
 1 5 10 15  
 Glu Trp Ala Val Glu Met Val Arg Phe Asp Glu Ser Glu Thr Leu Asp  
 20 25 30  
 Arg Leu Ala Ser Gly Val Leu Glu Pro Glu Leu Gly Asp Asp Leu Ala  
 35 40 45  
 Ala Val Leu Leu Asp Ser His Arg Val Ala Val Ile Ser Glu Gly Ser  
 50 55 60  
 Asn Trp Leu Ala Ser Leu Pro Val Ile Val Gly Arg Asn Thr Glu Gln  
 65 70 75 80  
 Phe Arg Ser Ile Pro Asp Leu Ala Arg Asp Arg Ile Asp Lys Leu His  
 85 90 95  
 Gln Leu Ser His Arg Glu Ile Ala Arg Asn Arg Glu Leu Leu Arg Ala  
 100 105 110  
 Arg Ala Ala Ser Gly Gln Val Arg His Cys His Gly Asp Ala His Leu  
 115 120 125  
 Gly Asn Ile Val Met Ile Asp Gly Lys Pro Val Leu Phe Asp Ala Ile  
 130 135 140  
 Glu Phe Asp Pro Asp Ile Ala Thr Thr Asp Val Leu Tyr Asp Phe Ala  
 145 150 155 160  
 Phe Pro Leu Met Asp  
 165

<210> 197  
 <211> 402  
 <212> DNA  
 <213> Homo sapiens

<400> 197  
 caagcaatgc ttgacgcagt tgttgaatac ttaccagcac cgactgatat tccagcaatc  
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 aaaggtatca atccagatga aactgaagggt gaacgtcacg caagcgatga tgagccattc  
 120  
 tcttcattag cattcaaaat tgcaactgac ccattcgtag gtaacttaac cttcttcggt  
 180  
 gtgtactcag gtgtaattaa ctctggtgat acagtattaa actctgtacg tcaaaaaagct  
 240  
 gaacgttttg gtcgtatcgt acagatgcac gctaataaac gtgaagaaat taaagaagtt  
 300



cgtagcgggag atatacgtgc agcaatcggc ttaaaagatg taactacggg tgaaccatta  
 360  
 tgtgctgtcg atgcaccaat cattcttgag cgtatggaat tc  
 402

<210> 198  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<400> 198  
 Gln Ala Met Leu Asp Ala Val Val Glu Tyr Leu Pro Ala Pro Thr Asp  
 1 5 10 15  
 Ile Pro Ala Ile Lys Gly Ile Asn Pro Asp Glu Thr Glu Gly Glu Arg  
 20 25 30  
 His Ala Ser Asp Asp Glu Pro Phe Ser Ser Leu Ala Phe Lys Ile Ala  
 35 40 45  
 Thr Asp Pro Phe Val Gly Asn Leu Thr Phe Phe Arg Val Tyr Ser Gly  
 50 55 60  
 Val Ile Asn Ser Gly Asp Thr Val Leu Asn Ser Val Arg Gln Lys Arg  
 65 70 75 80  
 Glu Arg Phe Gly Arg Ile Val Gln Met His Ala Asn Lys Arg Glu Glu  
 85 90 95  
 Ile Lys Glu Val Arg Ala Gly Asp Ile Ala Ala Ala Ile Gly Leu Lys  
 100 105 110  
 Asp Val Thr Thr Gly Glu Pro Leu Cys Ala Val Asp Ala Pro Ile Ile  
 115 120 125  
 Leu Glu Arg Met Glu Phe  
 130

<210> 199  
 <211> 507  
 <212> DNA  
 <213> Homo sapiens

<400> 199  
 acgcgtgaag tcgtgcatag atcgggtgtga catagagaag cctccgaccc aagctgcgta  
 60  
 tatcgacaaa agaccaagcg accctggacg ttctagacag aactctgcta cgaggcctga  
 120  
 caatagtga atccccgaga acccagctat ggaagggttt ccagatgctc gaaggcctgt  
 180  
 cataccagag gttagggttaa actgtatgga gactttcgag gtgaaagtgt actcgccggt  
 240  
 aaagcctgct cctaaagagg atttagatct gatagatcta tctcagatt caacctcggt  
 300  
 gcctgaaaaa cactctatac tctcaacctc cgacagcgac tctcttgat ttgagcctct  
 360  
 tccctctctc agaatagtcg agagtgcga agaagaggag acgatgaacc aaggcgatga  
 420  
 cggccctccc ggtaaaaatg ctgcctcttc tccctccatc cccagccatc cctccgtcct  
 480  
 cagcctgagc acagctccgc ttgtaca  
 507

<210> 200  
 <211> 153  
 <212> PRT  
 <213> Homo sapiens

<400> 200  
 Met Glu Gly Glu Glu Ala Ala Phe Leu Pro Glu Gly Pro Ser Ser Pro  
 1 5 10 15  
 Trp Phe Ile Val Ser Ser Ser Ser Ser Leu Ser Thr Ile Leu Arg Glu  
 20 25 30  
 Gly Arg Gly Ser Asn Thr Arg Glu Ser Leu Ser Glu Val Glu Ser Ile  
 35 40 45  
 Glu Cys Phe Ser Gly Pro Glu Val Glu Ser Glu Asp Arg Ser Ile Arg  
 50 55 60  
 Ser Lys Ser Ser Leu Gly Ala Gly Phe Thr Gly Glu Ser Thr Phe Thr  
 65 70 75 80  
 Ser Lys Val Ser Ile Gln Phe Asn Leu Thr Ser Gly Met Thr Gly Leu  
 85 90 95  
 Arg Ala Ser Gly Asn Pro Ser Ile Ala Gly Phe Ser Gly Ile Ser Leu  
 100 105 110  
 Leu Ser Gly Leu Val Ala Glu Phe Cys Leu Glu Arg Pro Gly Ser Leu  
 115 120 125  
 Gly Leu Cys Ala Ile Tyr Ala Ala Trp Val Gly Gly Phe Ser Met Ser  
 130 135 140  
 His Arg Ser Met His Asp Phe Thr Arg  
 145 150

<210> 201  
 <211> 527  
 <212> DNA  
 <213> Homo sapiens

<400> 201  
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 tgtgcctgca ggctcaccag ccagtcccct cctcaccaag gatgatgttc tccgtggtga  
 120  
 gctggtcctt ggtctcctgg aactcgtggc gcacctgggc cagctgcgcc tcgaaggcat  
 180  
 ccttctccat ctctttggct agctgcaagt tctggagctg ctcgttgagg tctgtgatct  
 240  
 catccacctg ctggttgagc gtgcgcttga ggaaggccac aatctccttc ttgttattgg  
 300  
 ccagctgctc aaactcctgg cggaacatct tctcctgcac agccagctca tcccacttcc  
 360  
 gctggtaccg ggctagccgg tctccaggt ctcggatctg gatgtggtag aactccttca  
 420  
 tctccttggc cagaggcggc tccacggcca ccaccggctc cttcttgccc cttttcttct  
 480  
 tgacttcaag ctccctgcct gccttgctca cactcttttt gggaggc  
 527

<210> 202

&lt;211&gt; 70

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 202

Gly Arg Pro Gln Ser Pro Ser Cys Tyr Trp Pro Ala Ala Gln Thr Pro  
 1 5 10 15  
 Gly Gly Thr Ser Ser Pro Ala Gln Pro Ala His Pro Thr Ser Ala Gly  
 20 25 30  
 Thr Gly Leu Ala Gly Pro Pro Gly Leu Gly Ser Gly Cys Gly Arg Thr  
 35 40 45  
 Pro Ser Ser Pro Trp Pro Glu Ala Ala Pro Arg Pro Pro Pro Ala Pro  
 50 55 60  
 Ser Cys Pro Leu Ser Ser  
 65 70

&lt;210&gt; 203

&lt;211&gt; 304

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 203

ngtgcaccgg tggatcatgga caacgccgcc tacgtggtct acacctcggg atccaccggc  
 60  
 cgacccaagg gagttgtcgt caccacacacc ggactcgaca gcttcgcact cgaccagcag  
 120  
 cgtcgattcc acgcagatca ccactctcga accctgcact tcgccacccc cagcttcgac  
 180  
 ggagccgtct tcgagtacct gcaggcattc ggtgtcggag ccaccatggt gatcgccccg  
 240  
 accgacatct acggcggcgc cgaactggca agtctcatcc gccgcgaaca cgtcactcac  
 300  
 gcgt  
 304

&lt;210&gt; 204

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 204

Xaa Ala Pro Val Val Met Asp Asn Ala Ala Tyr Val Val Tyr Thr Ser  
 1 5 10 15  
 Gly Ser Thr Gly Arg Pro Lys Gly Val Val Val Thr His Thr Gly Leu  
 20 25 30  
 Asp Ser Phe Ala Leu Asp Gln Gln Arg Arg Phe His Ala Asp His His  
 35 40 45  
 Ser Arg Thr Leu His Phe Ala Thr Pro Ser Phe Asp Gly Ala Val Phe  
 50 55 60  
 Glu Tyr Leu Gln Ala Phe Gly Val Gly Ala Thr Met Val Ile Val Pro  
 65 70 75 80  
 Thr Asp Ile Tyr Gly Gly Ala Glu Leu Ala Ser Leu Ile Arg Arg Glu  
 85 90 95  
 His Val Thr His Ala

100

&lt;210&gt; 205

&lt;211&gt; 356

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 205

nngaattcag caatgataac tggctcaatt gaaggtaaga caacaattga gggaattaat  
 60  
 gcacaattaa atacagtgtt aactttatctt tcaccacaat caaaagataa agatttaatt  
 120  
 atgcccagatc aacaagaaga aatagatatt ctgattgcaa ccgactgtat ttcagaagga  
 180  
 cagaacttac aagattgtga ttacttaata aactatgaca ttcattggaa tccagttcgt  
 240  
 atcattcaaa gatttggacg gattgatcga attgggtcga agaataaatg tgtacaatta  
 300  
 gttaactttt ggccagatat tacattagat gaatatattg atctaaaggg acgcgt  
 356

&lt;210&gt; 206

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 206

Xaa	Asn	Ser	Ala	Met	Ile	Thr	Gly	Ser	Ile	Glu	Gly	Lys	Thr	Thr	Ile
1				5					10					15	
Glu	Gly	Ile	Asn	Ala	Gln	Leu	Asn	Thr	Val	Leu	Thr	Leu	Phe	Ser	Pro
			20				25						30		
Gln	Ser	Lys	Asp	Lys	Asp	Leu	Ile	Met	Pro	Asp	Gln	Gln	Glu	Glu	Ile
		35				40					45				
Asp	Ile	Leu	Ile	Ala	Thr	Asp	Cys	Ile	Ser	Glu	Gly	Gln	Asn	Leu	Gln
	50					55					60				
Asp	Cys	Asp	Tyr	Leu	Ile	Asn	Tyr	Asp	Ile	His	Trp	Asn	Pro	Val	Arg
65				70					75					80	
Ile	Ile	Gln	Arg	Phe	Gly	Arg	Ile	Asp	Arg	Ile	Gly	Ser	Lys	Asn	Lys
			85				90						95		
Cys	Val	Gln	Leu	Val	Asn	Phe	Trp	Pro	Asp	Ile	Thr	Leu	Asp	Glu	Tyr
			100				105						110		
Ile	Asp	Leu	Lys	Gly	Arg										
			115												

&lt;210&gt; 207

&lt;211&gt; 324

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg  
 60  
 catgtgtgtg gcacgtgtng cactgtgtgt ggatgcatgg taatgtgcac gtgtgcactg  
 120

tgtgtggtgt gtatgcatgg tgtgtgcacg tgtgcactgt gtgtgtgtgt atgcatgtgt  
 180  
 gtgcacatgt gactgtgtg gtgtgtatgc atggtgtgtg cacgtgtgca ctgtgtatgc  
 240  
 atgngtgtgt gcatgtgtgc actgtgtatg catagtgtgc acgtgtgcac tgtgtggtgt  
 300  
 gtatgcatgg taatgtgcac gtgt  
 324

<210> 208  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 208  
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys  
 1 5 10 15  
 Val Val Cys Met His Gly Val Cys Thr Cys Xaa Thr Val Cys Gly Cys  
 20 25 30  
 Met Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val  
 35 40 45  
 Cys Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Met Cys  
 50 55 60  
 Thr Val Trp Cys Val Cys Met Val Cys Ala Arg Val His Cys Val Cys  
 65 70 75 80  
 Met Xaa Val Cys Met Cys Ala Leu Cys Met His Ser Val His Val Cys  
 85 90 95  
 Thr Val Trp Cys Val Cys Met Val Met Cys Thr Cys  
 100 105

<210> 209  
 <211> 168  
 <212> DNA  
 <213> Homo sapiens

<400> 209  
 nnctccagag gttatgaggt tggaagcccg gtttttttca ggtgcagaaa aggctaccat  
 60  
 attcaagggt ccacgactcg cacctgcctt gccaatata catggagtgg gatacagacc  
 120  
 gaatgtatac ctcatgcctg cagacagcca gaaaccccg cacacgcg  
 168

<210> 210  
 <211> 56  
 <212> PRT  
 <213> Homo sapiens

<400> 210  
 Xaa Ser Arg Gly Tyr Glu Val Gly Ser Pro Val Phe Phe Arg Cys Arg  
 1 5 10 15  
 Lys Gly Tyr His Ile Gln Gly Ser Thr Thr Arg Thr Cys Leu Ala Asn  
 20 25 30  
 Leu Thr Trp Ser Gly Ile Gln Thr Glu Cys Ile Pro His Ala Cys Arg

35 40 45  
 Gln Pro Glu Thr Pro Ala His Ala  
 50 55

<210> 211  
 <211> 354  
 <212> DNA  
 <213> Homo sapiens

<400> 211  
 tacatgggct ttgacacagt ggtggctgaa gctgcactaa ggggtgttgg aggcaatgtc  
 60  
 cagctggcag ctcagaccct tgcacaccat ggaggaagcc tcccacccga cctgcagttc  
 120  
 tcaggagagg actcctcccc cacaccgtcc acatccccat ctgactctgc agggacctct  
 180  
 agtgcctcga cagatgaaga catggagacg gaggctgtca acgaaatcct ggaggacatt  
 240  
 ccggagcacg aggaggacta cctggactcc acgctggagg atgaagaagt cattattgtc  
 300  
 gaatacttgt cctgcgttga aagtataagt tctgccngca aagaacaact gatac  
 354

<210> 212  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 212  
 Tyr Met Gly Phe Asp Thr Val Val Ala Glu Ala Ala Leu Arg Val Phe  
 1 5 10 15  
 Gly Gly Asn Val Gln Leu Ala Ala Gln Thr Leu Ala His His Gly Gly  
 20 25 30  
 Ser Leu Pro Pro Asp Leu Gln Phe Ser Gly Glu Asp Ser Ser Pro Thr  
 35 40 45  
 Pro Ser Thr Ser Pro Ser Asp Ser Ala Gly Thr Ser Ser Ala Ser Thr  
 50 55 60  
 Asp Glu Asp Met Glu Thr Glu Ala Val Asn Glu Ile Leu Glu Asp Ile  
 65 70 75 80  
 Pro Glu His Glu Glu Asp Tyr Leu Asp Ser Thr Leu Glu Asp Glu Glu  
 85 90 95  
 Val Ile Ile Ala Glu Tyr Leu Ser Cys Val Glu Ser Ile Ser Ser Ala  
 100 105 110  
 Xaa Lys Glu Gln Leu Ile  
 115

<210> 213  
 <211> 669  
 <212> DNA  
 <213> Homo sapiens

<400> 213  
 attgcccaat ctcagagtgt ccaggaaagc ctggagagcc tggtgcagtc tattggggaa  
 60

gttgaacaaa acctggaagg gaaacagggtg tcatcactct catcaggagt catccaggaa  
 120  
 gccttagcca caaatatgaa attgaagcag gacattgctc ggcaaaagag cagcttggag  
 180  
 gccaccctgt agatgggtgac cggattcatg gagacagcag acagtactac agcagcagt  
 240  
 ctgcagggca aactggcaga ggtgagccag cggttcgaac agctctgtct acagcagcaa  
 300  
 gaaaaggaga gtcacctaaa gaagcttcta ccccaggcag agatgtttga acacctctct  
 360  
 ggtaagctgc agcagttcat ggaaaacaaa agtcggatgc tggcctctgg aaatcagcca  
 420  
 gatcaagata ttacacattt cttccaacag atccaggagc tcaatttga aatggaagac  
 480  
 caacaggaga acctagatac tcttgagcac ctgggtcactg aactgagctc ttgtggcttt  
 540  
 gcgctggact tgtgccagca tcaggacagg gtacagaatc taagaaaaga cttcacagag  
 600  
 ctacagaaga cagttaaaga gagagagaaa gatgcatcat cttgccagga acagttggat  
 660  
 gaattccgg  
 669

<210> 214

<211> 223

<212> PRT

<213> Homo sapiens

<400> 214

Ile	Ala	Gln	Ser	Gln	Ser	Val	Gln	Glu	Ser	Leu	Glu	Ser	Leu	Leu	Gln
1				5				10						15	
Ser	Ile	Gly	Glu	Val	Glu	Gln	Asn	Leu	Glu	Gly	Lys	Gln	Val	Ser	Ser
		20					25						30		
Leu	Ser	Ser	Gly	Val	Ile	Gln	Glu	Ala	Leu	Ala	Thr	Asn	Met	Lys	Leu
		35				40						45			
Lys	Gln	Asp	Ile	Ala	Arg	Gln	Lys	Ser	Ser	Leu	Glu	Ala	Thr	Arg	Glu
		50				55					60				
Met	Val	Thr	Arg	Phe	Met	Glu	Thr	Ala	Asp	Ser	Thr	Thr	Ala	Ala	Val
65				70					75					80	
Leu	Gln	Gly	Lys	Leu	Ala	Glu	Val	Ser	Gln	Arg	Phe	Glu	Gln	Leu	Cys
			85					90					95		
Leu	Gln	Gln	Gln	Glu	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Leu	Leu	Pro	Gln
		100						105					110		
Ala	Glu	Met	Phe	Glu	His	Leu	Ser	Gly	Lys	Leu	Gln	Gln	Phe	Met	Glu
		115					120					125			
Asn	Lys	Ser	Arg	Met	Leu	Ala	Ser	Gly	Asn	Gln	Pro	Asp	Gln	Asp	Ile
	130				135						140				
Thr	His	Phe	Phe	Gln	Gln	Ile	Gln	Glu	Leu	Asn	Leu	Glu	Met	Glu	Asp
145				150					155					160	
Gln	Gln	Glu	Asn	Leu	Asp	Thr	Leu	Glu	His	Leu	Val	Thr	Glu	Leu	Ser
			165					170					175		
Ser	Cys	Gly	Phe	Ala	Leu	Asp	Leu	Cys	Gln	His	Gln	Asp	Arg	Val	Gln
		180					185					190			
Asn	Leu	Arg	Lys	Asp	Phe	Thr	Glu	Leu	Gln	Lys	Thr	Val	Lys	Glu	Arg

195                      200                      205  
 Glu Lys Asp Ala Ser Ser Cys Gln Glu Gln Leu Asp Glu Phe Arg  
 210                      215                      220

<210> 215

<211> 814

<212> DNA

<213> Homo sapiens

<400> 215

aaatttcgta cccgctccgg cacagtacga gcccttgacg atgtgagcct ggctattaag  
 60  
 agagggttcca tctcagccgt tatcggggcac tccggagccg gcaaattccac cctgggttcgc  
 120  
 ctcatcaacg gattagagac tcccacgcgt ggccgcgtct tggtagacgg caccgacgtc  
 180  
 tcgcagctct cggacaaaagc gatgcgcccgc ctacgcgcag acatcgggat gatcttccaa  
 240  
 cagttcaacc tattcggctc aaggaccatc tacgacaacg ttgcctatcc actcaagctg  
 300  
 gctcattgga agaaagcaga cgagaagaag cgcgtcaccg aattgctgag cttcgtcggg  
 360  
 ttgacgagca aagcctggga ccatccagac cagctctcgg gcggacagaa acagcgggtt  
 420  
 ggtattgccc gagcgctagc aactaaacca tcgattttgt tggctgacga gtccacctcg  
 480  
 gcgctggatc cagaaacgac agctgatgtc ctatccctgc tcaagcgggt caatgcggaa  
 540  
 ctagggggtga cggtcgtcgt catcacccac gagatggagg tcgtccgctc gattgccag  
 600  
 caggtctcgg tactagcagc tggccatctc gtcgagctcg gaagcgcgcg ccaggtcttc  
 660  
 gctcatccac agtcagagac caccacgcgt ttcttggcga cgattatcgg ccagcaccgg  
 720  
 agtgggggagg aacaggcacg gttgcagtcg gaaaaccag atgcacgact cgtcgacgtc  
 780  
 agttcgggtg ccagtcactc gttcgggtgac gcgt  
 814

<210> 216

<211> 271

<212> PRT

<213> Homo sapiens

<400> 216

Lys Phe Arg Thr Arg Ser Gly Thr Val Arg Ala Leu Asp Asp Val Ser  
 1                      5                      10                      15  
 Leu Ala Ile Lys Arg Gly Ser Ile Ser Ala Val Ile Gly His Ser Gly  
 20                      25                      30  
 Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Glu Thr Pro  
 35                      40                      45  
 Thr Arg Gly Arg Val Leu Val Asp Gly Thr Asp Val Ser Gln Leu Ser  
 50                      55                      60  
 Asp Lys Ala Met Arg Pro Leu Arg Ala Asp Ile Gly Met Ile Phe Gln



```

65          70          75          80
Gln Phe Asn Leu Phe Gly Ser Arg Thr Ile Tyr Asp Asn Val Ala Tyr
      85          90          95
Pro Leu Lys Leu Ala His Trp Lys Lys Ala Asp Glu Lys Lys Arg Val
      100        105        110
Thr Glu Leu Leu Ser Phe Val Gly Leu Thr Ser Lys Ala Trp Asp His
      115        120        125
Pro Asp Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg
      130        135        140
Ala Leu Ala Thr Lys Pro Ser Ile Leu Leu Ala Asp Glu Ser Thr Ser
145          150          155          160
Ala Leu Asp Pro Glu Thr Thr Ala Asp Val Leu Ser Leu Leu Lys Arg
      165        170        175
Val Asn Ala Glu Leu Gly Val Thr Val Val Val Ile Thr His Glu Met
      180        185        190
Glu Val Val Arg Ser Ile Ala Gln Gln Val Ser Val Leu Ala Ala Gly
      195        200        205
His Leu Val Glu Ser Gly Ser Ala Arg Gln Val Phe Ala His Pro Gln
      210        215        220
Ser Glu Thr Thr Gln Arg Phe Leu Ala Thr Ile Ile Gly Gln His Pro
225          230          235          240
Ser Gly Glu Glu Gln Ala Arg Leu Gln Ser Glu Asn Pro Asp Ala Arg
      245        250        255
Leu Val Asp Val Ser Ser Val Ala Ser His Ser Phe Gly Asp Ala
      260        265        270

```

&lt;210&gt; 217

&lt;211&gt; 500

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 217

```

nnacgcgtcg cgatgaaaga ggcgctgaaa ggtgccatcc agattccaac agtgactttt
60
agctctgaga agtccaatac tacagccctg gctgagttcg gaaaatacat tcataaagtc
120
tttcttacag tggtcagcac cagctttatc cagcatgaag tcgtggaaga gtatagccac
180
ctgttcacta tccaaggctc ggaccccagc ttgcagccct acctgctgat ggctcacttt
240
gatgtggtgc ctgccctga agaaggctgg gaggtgcccc cattctctgg gttggagcgt
300
gatggcgtea tctatggttg gggcacactg gacgacaaga actctgtgat ggcattactg
360
caggccttgg agctcctgct gatcaggaag tacatcccc gaagatcttt cttcatttct
420
ctgggccatg atgaggagtc atcagggaca ggggctcaga ggatctcagc cctgctacag
480
tcaaggggcg tccagctagc
500

```

&lt;210&gt; 218

&lt;211&gt; 166

&lt;212&gt; PRT

<213> Homo sapiens

<400> 218

```

Xaa Arg Val Ala Met Lys Glu Ala Leu Lys Gly Ala Ile Gln Ile Pro
 1           5           10           15
Thr Val Thr Phe Ser Ser Glu Lys Ser Asn Thr Thr Ala Leu Ala Glu
 20           25           30
Phe Gly Lys Tyr Ile His Lys Val Phe Pro Thr Val Val Ser Thr Ser
 35           40           45
Phe Ile Gln His Glu Val Val Glu Glu Tyr Ser His Leu Phe Thr Ile
 50           55           60
Gln Gly Ser Asp Pro Ser Leu Gln Pro Tyr Leu Leu Met Ala His Phe
 65           70           75           80
Asp Val Val Pro Ala Pro Glu Glu Gly Trp Glu Val Pro Pro Phe Ser
 85           90           95
Gly Leu Glu Arg Asp Gly Val Ile Tyr Gly Trp Gly Thr Leu Asp Asp
100           105           110
Lys Asn Ser Val Met Ala Leu Leu Gln Ala Leu Glu Leu Leu Leu Ile
115           120           125
Arg Lys Tyr Ile Pro Arg Arg Ser Phe Phe Ile Ser Leu Gly His Asp
130           135           140
Glu Glu Ser Ser Gly Thr Gly Ala Gln Arg Ile Ser Ala Leu Leu Gln
145           150           155           160
Ser Arg Gly Val Gln Leu
165

```

<210> 219

<211> 361

<212> DNA

<213> Homo sapiens

<400> 219

```

acgcggttgaa acgggtatat tggggatgac gccgctgtgc aatatgcgca aggccataca
60
caaggctccgc acgctcccat gtccctcggt ttcgacagtt cttttgcgcc gcattatggc
120
gaagccgtcg agattgcgcc tgatatcaag cgcatacagg tcaacaaccc cagccccctc
180
acttttttgc gcaccaacag ttatctgata ggccgcgata cgctggcatt gatcgatccc
240
ggtcgcgttg acgaggecca tcacgcggcg ctgctgcgtg ccattgccgg ccggccggtc
300
agccatatct ttgtcagcca cacacaccgg gaccactcgc cagtcgcgac ggttttgaaa
360
g
361

```

<210> 220

<211> 102

<212> PRT

<213> Homo sapiens

<400> 220

```

Met Ala Asp Arg Pro Ala Gly Asn Gly Thr Gln Gln Arg Arg Val Met

```

```

      1           5           10           15
Gly Leu Val Lys Arg Thr Gly Ile Asp Gln Cys Gln Arg Ile Ala Ala
      20           25           30
Asp Gln Ile Thr Val Gly Ala Glu Lys Ser Glu Gly Ala Gly Val Val
      35           40           45
Asp Arg Asp Ala Leu Asp Ile Arg Arg Asn Leu Asp Gly Phe Ala Ile
      50           55           60
Met Arg Arg Lys Arg Thr Val Glu Asn Glu Gly His Gly Ser Val Arg
      65           70           75           80
Thr Leu Cys Met Ala Leu Arg Ile Leu His Ser Gly Val Ile Pro Asn
      85           90           95
Ile Pro Val Ser Thr Arg
      100

```

&lt;210&gt; 221

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 221

```

agatctctgt gtcgtcggct gcaaagagga tgagcccaga tgcatatcag gggctccctc
60
ccacatccca cctgctcggg cagcccacgg cagccccaca ctgctgcagc acacctcgct
120
gcagctctgg ttctctctca gaaatatccc tgccaccctg ctaagccttg gccaacactg
180
caccctgtcc caatgcggct ccagtgaacca cacccccagg gcataccctc ctacagagca
240
ttcccaaaaa aggctagagt agacaccagc ctgctccgta gggggcctcc accccattct
300
ccaaggcctc caccagggga cgctctggtga accagcatcc aggctgggcc cacctccctg
360
ctcagagtcc atgttctgtg acaaggggtg caactgggat t
401

```

&lt;210&gt; 222

&lt;211&gt; 124

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 222

```

Met Asp Ser Glu Gln Gly Gly Gly Pro Gly Leu Asp Ala Gly Ser Pro
 1           5           10           15
Gly Val Pro Gly Trp Arg Pro Trp Arg Met Gly Trp Arg Pro Pro Thr
      20           25           30
Glu Gln Ala Gly Val Tyr Ser Ser Leu Phe Trp Glu Cys Ser Val Gly
      35           40           45
Gly Tyr Ala Leu Gly Val Trp Ser Leu Glu Pro His Trp Asp Arg Val
      50           55           60
Gln Cys Trp Pro Arg Leu Ser Arg Val Ala Gly Ile Phe Leu Arg Arg
      65           70           75           80
Asn Gln Ser Cys Ser Glu Val Cys Cys Ser Ser Val Gly Leu Pro Trp
      85           90           95
Ala Ala Arg Ala Gly Gly Met Trp Glu Gly Ala Pro Asp Met His Leu

```

100 105 110  
 Gly Ser Ser Ser Leu Gln Pro Thr Thr Gln Arg Ser  
 115 120

<210> 223  
 <211> 331  
 <212> DNA  
 <213> Homo sapiens

<400> 223  
 tcatgaaatc tgtgggcagt gacccaggag ggtatgggca ggcccaacca ggttggtgtg  
 60  
 cccttgaagc cccacagacc tgccagggca gcagggcagt tgggagccgg agaacctgag  
 120  
 aaccaagcca ggctgcatgc aggaggctgg cacgtgaacg ctgcagggtg tgccggcagc  
 180  
 cgtggtgcct ggcagatagt gttcgacccc cnaggacctt cttgctgggc agcccagtcc  
 240  
 aaaagctgtt cccgcttaag ccacccccac cgccttggcc acacctggca catgggtgaa  
 300  
 gcaagggcac ttcccggggc ttcctgttcc c  
 331

<210> 224  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 224  
 Met Pro Leu Leu His Pro Cys Ala Arg Cys Gly Gln Gly Gly Gly Gly  
 1 5 10 15  
 Gly Leu Ser Gly Asn Ser Phe Trp Thr Gly Leu Pro Ser Lys Lys Val  
 20 25 30  
 Leu Gly Gly Arg Thr Leu Ser Ala Arg His His Gly Cys Arg Gln His  
 35 40 45  
 Leu Gln Arg Ser Arg Ala Ser Leu Leu His Ala Ala Trp Leu Gly Ser  
 50 55 60  
 Gln Val Leu Arg Leu Pro Thr Ala Leu Leu Pro Trp Gln Val Cys Gly  
 65 70 75 80  
 Ala Ser Arg Ala His Gln Pro Gly Trp Ala Cys Pro Tyr Pro Pro Gly  
 85 90 95  
 Ser Leu Pro Thr Asp Phe Met  
 100

<210> 225  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

<400> 225  
 tgatcacggg cgtgagccac cagcccagca tcccttgccct ttcattcgca cctccacctc  
 60  
 cagaatgacc ctcattccct cctgcacaga cggtgacagc agtaactcct acaaacacca  
 120

ccagactgat cttcaagagc agaggaactc ccaatcacga ttccaccccc gccgggctct  
 180  
 caaatcctcc agggctgcct gctatggggg agggaggcac actttgcttg gctctcaagg  
 240  
 cctcagccag ccgggtccaa accaactccc agcctggcct caccatccca ccgccaaacc  
 300  
 tttgctcaca ctggccccctc ttcctggaac atgggcctn  
 339

<210> 226

<211> 91

<212> PRT

<213> Homo sapiens

<400> 226

Met	Thr	Leu	Ile	Pro	Ser	Cys	Thr	Asp	Gly	Asp	Ser	Ser	Asn	Ser	Tyr
1				5				10					15		
Lys	His	His	Gln	Thr	Asp	Leu	Gln	Glu	Gln	Arg	Asn	Ser	Gln	Ser	Arg
			20				25						30		
Phe	His	Pro	Arg	Arg	Ala	Leu	Lys	Ser	Ser	Arg	Ala	Ala	Cys	Tyr	Gly
		35				40					45				
Gly	Gly	Arg	His	Thr	Leu	Leu	Gly	Ser	Gln	Gly	Leu	Ser	Gln	Pro	Gly
	50				55					60					
Pro	Asn	Gln	Leu	Pro	Ala	Trp	Pro	His	His	Pro	Thr	Ala	Lys	Pro	Leu
65			70					75						80	
Leu	Thr	Leu	Ala	Pro	Leu	Pro	Gly	Thr	Trp	Ala					
			85					90							

<210> 227

<211> 353

<212> DNA

<213> Homo sapiens

<400> 227

gtcgaccctc tcgattgtgg cgaactccat ggctgctgcg ggcctgcgta ggctctcgag  
 60  
 tagctcgacg tcgggttcgc gagggctcgc agcgtggcca tgctgcttct tggatggttc  
 120  
 gggcaactcc tcgggggatt cgagcagttc ttggcgcacc tgctctggcg tcatcccgga  
 180  
 ggccaggccg acaagtgtcg cctcctgcca cccgctgagc gacgctgcca tgttgagtac  
 240  
 ggcgtcttca ctggtcaggg cgagcgcggt atcgaccagg ttggcgtcca ggccgagaga  
 300  
 cagcatgtct gctcagtcgc ggtgatgact ggagtggcgg tctcctgcac ggg  
 353

<210> 228

<211> 102

<212> PRT

<213> Homo sapiens

<400> 228

Met Leu Ser Leu Gly Leu Asp Ala Asn Leu Val Asp Thr Ala Leu Ala

```

      1           5           10           15
Leu Thr Ser Glu Asp Ala Val Leu Asn Met Ala Ala Ser Leu Ser Gly
      20           25           30
Trp Gln Glu Ala Ala Leu Val Gly Leu Ala Ser Gly Met Thr Pro Glu
      35           40           45
Gln Val Arg Gln Glu Leu Leu Glu Ser Pro Glu Glu Leu Pro Glu Pro
      50           55           60
Ser Lys Lys Gln His Gly His Ala Ala Ser Pro Arg Glu Pro Asp Val
      65           70           75           80
Glu Leu Leu Glu Ser Leu Arg Arg Pro Ala Ala Ala Met Glu Phe Ala
      85           90           95
Thr Ile Glu Gly Val Asp
      100

```

&lt;210&gt; 229

&lt;211&gt; 743

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 229

```

nnngctaggg acacggcctc ctccctcaaca ggcagtgcct gtgcaggctc aggggcatca
60
tcaaagataa cacagggtctg gtcaggggct gctggctgct cctgccccag gactggctcc
120
aggatgggca aggctgcctc cctggtagcc agggggagag gggaaggag caccaggag
180
tgggccagca ggtgtggcat cggccaggag gagatggagg ccagcagcag ccaagaccag
240
agtaaagtgt ctgccccagg ggtgtctaca gcccaggacc gggtagttgg aaagccagcc
300
cagcttgga ctcagcggag ccaggaggca gatgttcagg actgggagtt cagaaagagg
360
gattcccagg gcacttactc cagccgggat gcagaactcc aggaccagga attcggaaag
420
agagattcac tgggtaccta cagtagtcga gatgtaagcc ttggggactg ggaatttggg
480
aagagagatt ctctgggtgc ttatgccagc caagatgcc aagagcagg ccaagatttg
540
gggaagaggg accaccatgg taggtacagc agccaggatg ccgatgagca ggactgggag
600
tttcagaaga gagatgtgtc actcggcacc tatggcagcc gggctgcgga gccacaggaa
660
caggagtttg ggaagagcgc ttggataagg gactacagca gtggtggcag ctccaggacc
720
cttgacgccc aggacagaag ctt
743

```

&lt;210&gt; 230

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 230

```

Xaa Ala Arg Asp Thr Ala Ser Ser Ser Thr Gly Ser Ala Cys Ala Gly

```

1                      5                      10                      15  
 Ser Gly Ala Ser Ser Lys Ile Thr Gln Gly Trp Ser Gly Ala Ala Gly  
                     20                      25                      30  
 Cys Ser Cys Pro Arg Thr Gly Ser Arg Met Gly Lys Ala Ala Ser Leu  
                     35                      40                      45  
 Val Ala Arg Gly Arg Gly Glu Gly Ser Thr Arg Glu Trp Ala Ser Arg  
                     50                      55                      60  
 Cys Gly Ile Gly Gln Glu Glu Met Glu Ala Ser Ser Ser Gln Asp Gln  
 65                      70                      75                      80  
 Ser Lys Val Ser Ala Pro Gly Val Leu Thr Ala Gln Asp Arg Val Val  
                     85                      90                      95  
 Gly Lys Pro Ala Gln Leu Gly Thr Gln Arg Ser Gln Glu Ala Asp Val  
                     100                      105                      110  
 Gln Asp Trp Glu Phe Arg Lys Arg Asp Ser Gln Gly Thr Tyr Ser Ser  
                     115                      120                      125  
 Arg Asp Ala Glu Leu Gln Asp Gln Glu Phe Gly Lys Arg Asp Ser Leu  
 130                      135                      140  
 Gly Thr Tyr Ser Ser Arg Asp Val Ser Leu Gly Asp Trp Glu Phe Gly  
 145                      150                      155                      160  
 Lys Arg Asp Ser Leu Gly Ala Tyr Ala Ser Gln Asp Ala Asn Glu Gln  
                     165                      170                      175  
 Gly Gln Asp Leu Gly Lys Arg Asp His His Gly Arg Tyr Ser Ser Gln  
                     180                      185                      190  
 Asp Ala Asp Glu Gln Asp Trp Glu Phe Gln Lys Arg Asp Val Ser Leu  
                     195                      200                      205  
 Gly Thr Tyr Gly Ser Arg Ala Ala Glu Pro Gln Glu Gln Glu Phe Gly  
                     210                      215                      220  
 Lys Ser Ala Trp Ile Arg Asp Tyr Ser Ser Gly Gly Ser Ser Arg Thr  
 225                      230                      235                      240  
 Leu Asp Ala Gln Asp Arg Ser  
                     245

&lt;210&gt; 231

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 231

acgcgttgcc caccgagagg ctggcgaggg tgtgcagcac ggcgcagtgt ggcaggggtcc

60

cagggtgcag cctgcgcagc agctcctcca tcaccttgct gatgaactgt cttcccacgg

120

ccaccaggac gccactcgcc gcctgctgcc agtcccagac caggtccttc gtcttggtca

180

tctcgctgga ggccaggagg atgatggtgc tggtgtgtc cttgtccagc tcaactggcg

240

gactgctcag gaccctctcc atggcctca ggaccgctgc tcggtatggg tgtgccagct

300

tgtcatgctg ccgcagatac tcctgcgagg caggagcgt ctccaccctg ctggacgcc

360

tcaccgataa ggacccccctg gtgcaggagc aggtctgcag tgccctgtgc tccctcgggg

420

aggtgcggcc g

431

<210> 232  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 232  
 Met Ala Ser Ser Arg Val Glu Thr Leu Arg Ala Cys Glu Glu Tyr Leu  
 1 5 10 15  
 Arg Gln His Asp Lys Leu Ala His Pro Tyr Arg Ala Ala Val Leu Arg  
 20 25 30  
 Ala Met Glu Arg Val Leu Ser Ser Arg Ala Ser Glu Leu Asp Lys Asp  
 35 40 45  
 Thr Ala Ser Thr Ile Ile Leu Leu Ala Ser Ser Glu Met Thr Lys Thr  
 50 55 60  
 Lys Asp Leu Val Trp Asp Trp Gln Gln Ala Ala Ser Gly Val Leu Val  
 65 70 75 80  
 Ala Val Gly Arg Gln Phe Ile Ser Lys Val Met Glu Glu Leu Leu Arg  
 85 90 95  
 Arg Leu His Pro Gly Thr Leu Pro His Cys Ala Val Leu His Thr Leu  
 100 105 110  
 Ala Ser Leu Ser Val Ala Asn Ala  
 115 120

<210> 233  
 <211> 606  
 <212> DNA  
 <213> Homo sapiens

<400> 233  
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 aagggtgggca cccttagcat tcccaaaaag caccagccct cctcatcctt ccagcttct  
 120  
 gtgctggaat gcaccccat cggaaggct cgaaaactca ggacacatta ggatcacctg  
 180  
 gaaagcat tgcacaaacgc atctccctgc gggtcagggt ccaagttaa atcaaaacttc  
 240  
 aggtgatgct gactcagggt gctccagaaa cacctgggga agcagcactt tggaggctgc  
 300  
 ctctcacatc caccacacag caagtgggca gggagctagg taaatctcct tccagttga  
 360  
 gaaggggctc ggagcaggca cagagaagag atacccttag aatgcaagtt gttcagctgc  
 420  
 gaaagtccag cctgcaggct tcctgggcaa gctagtgggc tgaagtatgc cacagcaaca  
 480  
 ggcttctaga gccggctgcc cagctcctac tctgcctctg ccactcactg actgtgtggt  
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 cttgagcagg tcacctgtct gacttggtga gagctgacag gcatcacctg ttagaggctt  
 600  
 acgcgt  
 606

<210> 234



<211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 234  
 Met His Pro His Arg Lys Gly Ser Lys Thr Gln Asp Thr Leu Gly Ser  
 1 5 10 15  
 Pro Gly Lys His Leu Ser Lys Arg Ile Ser Leu Arg Val Arg Val Gln  
 20 25 30  
 Val Lys Ile Lys Leu Gln Val Met Leu Thr Gln Val Ala Pro Glu Thr  
 35 40 45  
 Pro Gly Glu Ala Ala Leu Trp Arg Leu Pro Leu Thr Ser Thr Pro Gln  
 50 55 60  
 Gln Val Gly Arg Glu Leu Gly Lys Ser Pro Ser Gln Leu Arg Arg Gly  
 65 70 75 80  
 Ser Glu Gln Ala Gln Arg Arg Asp Thr Leu Arg Met Gln Val Val Gln  
 85 90 95  
 Leu Arg Lys Ser Ser Leu Gln Ala Ser Trp Ala Ser  
 100 105

<210> 235  
 <211> 328  
 <212> DNA  
 <213> Homo sapiens

<400> 235  
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 atagcaaaca cttaaaacag cagcagtaca gagctgaaaa ccagattctt ttgaaagaga  
 120  
 ttgaaagtct agaggaagaa cgacttgatc tgaaaaaaaa aattcgccaa atgggtcaag  
 180  
 aaagaggaaa aagaagggca acttcaggat taaccactgg ggacctgaac ctaactgaaa  
 240  
 acatttctca aggagataga ataagtgaaa gaaaattgga tttattgagc ctcaaaaata  
 300  
 tgagtgaagc acaatcaaag aatgaatt  
 328

<210> 236  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
 Met Ile Asp Leu Thr Glu Phe Arg Asn Ser Lys His Leu Lys Gln Gln  
 1 5 10 15  
 Gln Tyr Arg Ala Glu Asn Gln Ile Leu Lys Glu Ile Glu Ser Leu  
 20 25 30  
 Glu Glu Glu Arg Leu Asp Leu Lys Lys Lys Ile Arg Gln Met Ala Gln  
 35 40 45  
 Glu Arg Gly Lys Arg Arg Ala Thr Ser Gly Leu Thr Thr Gly Asp Leu  
 50 55 60  
 Asn Leu Thr Glu Asn Ile Ser Gln Gly Asp Arg Ile Ser Glu Arg Lys

65                                      70                                      75                                      80  
 Leu Asp Leu Leu Ser Leu Lys Asn Met Ser Glu Ala Gln Ser Lys Asn  
                                     85                                      90                                      95  
 Glu

<210> 237

<211> 2059

<212> DNA

<213> Homo sapiens

<400> 237

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 gagcaggaag ccggcggtcca tagctacggc ccatacgggc atgtctgccca tggctccggt  
 120  
 gatgtcagac tgcacatgaa atcgggttacg gtaccccagg atcatcgcta ccgagtacac  
 180  
 cccgaacagc acccgctggg cggcgatcag cgtgaggagg tgccccacca gtggcacttt  
 240  
 tcttagatag cggaacccat ccaccacatc cccagtcacc gttctcatcg tccgggaacg  
 300  
 atccaccagt ggcgcccaa gctcccgacg tgaaaactgc agcccctagg cgaccgagac  
 360  
 tgcaagagg gctgaggaga tgcagaaaat gatcgtgtcg gcgtggtgca caggaatatg  
 420  
 gcgtccggca atcatgcgca ctgctgcagc aacaaccgca ccgatcatga gccctagcgg  
 480  
 ccaatcggtg gcatgattga cgatgccgc aggtagtcgc gcttgctgat ggtgtattcc  
 540  
 aaccagcga ccaaggcggg gagcaaaaac cggttcaggc tcatcgcgat gagcaacca  
 600  
 atgagcaagg ccagggtgga gggcttatcg cgcgcaccac ccagaccaa gatccccagc  
 660  
 ccgacccagg tgacggcacg cattcatctg cgtattgtcc cgactacacc gtgagggcgc  
 720  
 tctctgatct gcagctcatc aagggttacg gactgcagta cctcaatgca ctctggcta  
 780  
 cccgagccca gaacctgcca cagtcacctg agaacaccga cctgcagggt attccaggca  
 840  
 gccagaccag gtccttggt gagaagacca ccacagcggc agctttccca gtagcccttt  
 900  
 ccctctttgg cacagtggga acctccagtt gataaatgac tgtggactag cgcgcgtttt  
 960  
 ttgttttcag agcacacgta agggccagc cacagcaggc ccggcgctccc ggtggaaggc  
 1020  
 agccctgggc ggaacccagg cgtttaacgg ctactaggc agccccagat ctggggaagc  
 1080  
 agatgagcac gtggggagct ggagtgaact gacgagaagt tttgtgccc cctgccccca  
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 1200  
 ctagacatca atgcctggat ccttcagccg gccctgccct cctttaggag acaggagtca  
 1260

ccagggcaca gccctccagg cccgcctcag gaaggaatga aaggaatgcc atcatctcta  
 1320  
 gttcccgagg cccagccttc cccttctccc ccggggcagg gacagtgcgg catattcaga  
 1380  
 ttcagacctc tttgggctga gccaccttgt gaggcagtt actgcctttg tgtggcctg  
 1440  
 acctctatctt gtttgccttt aatttgccaa cctatcgctg ctggcagcac tttttgagca  
 1500  
 agccgagagc acccattttg gctggggatt cagatcgatg gccttggtcca tgttgctcct  
 1560  
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 1620  
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 1740  
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 1800  
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 1860  
 agtagctgcc tgttgacact gctccacacc tccccacagc ctccctgcag gtgctgtgtg  
 1920  
 gccgtgatgt gcagagagca gtgagggagg gttcatgaac caggtggatc ctctttaaaa  
 1980  
 aaaaaaaaaag tttttgttat atctctaaaa tcccatagct aggaacagaa aaaaaggaaa  
 2040  
 agacttgaaa tgttctaga  
 2059

<210> 238

<211> 129

<212> PRT

<213> Homo sapiens

<400> 238

Ala	Glu	Gln	Lys	Phe	Cys	Ala	Arg	Leu	Pro	Pro	Ser	Pro	Pro	Gly	His
1				5					10					15	
Val	Leu	Asp	Gly	Pro	Cys	Ser	Cys	Gly	Ser	Trp	Val	Ser	Ser	Glu	Leu
			20					25					30		
Asp	Ile	Asn	Ala	Trp	Ile	Leu	Gln	Pro	Ala	Leu	Pro	Ser	Phe	Arg	Arg
		35				40					45				
Gln	Glu	Ser	Pro	Gly	His	Ser	Pro	Pro	Gly	Pro	Pro	Gln	Glu	Gly	Met
	50				55				60						
Lys	Gly	Met	Pro	Ser	Ser	Leu	Val	Pro	Arg	Ala	Gln	Pro	Ser	Pro	Ser
65					70				75					80	
Pro	Pro	Gly	Gln	Gly	Gln	Cys	Gly	Ile	Phe	Arg	Phe	Arg	Pro	Leu	Trp
			85				90						95		
Ala	Glu	Pro	Pro	Cys	Glu	Cys	Ser	Tyr	Cys	Leu	Cys	Val	Ala	Val	Thr
		100					105					110			
Ser	Ile	Cys	Leu	Leu	Leu	Ile	Cys	Gln	Pro	Ile	Ala	Ala	Gly	Ser	Thr
		115				120					125				
Phe															

<210> 239  
 <211> 388  
 <212> DNA  
 <213> Homo sapiens

<400> 239  
 ntctagatca ctctgtagcg catgggttaa tgctgacaca atagaaaagt gcgaggacat  
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 cctcgaatta atgagatggg ggactggatg agtcaagttc tcgtcgttgc ggcggctgtc  
 120  
 ggtagctgc cctcctcca cttctgcttc tcggcggtac cccataccgt attggccgcg  
 180  
 tgttcacctt tgaatgcagc catgtcgtcg tctccgtatc gaaatgatgt gccatcgaag  
 240  
 atgccgacct cagcatcggc atctgcagtg atgagtgcgt atcgcgccac acgaaacgcc  
 300  
 cagcgcaacc gtgtcctcgc acgatacgaa gtgcttgggt atctcagctc tggtagctat  
 360  
 ggtcgtgtat ataaagcaaa ggaacttn  
 388

<210> 240  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<400> 240  
 Met Val Asp Trp Met Ser Gln Val Leu Val Val Ala Ala Ala Val Gly  
 1 5 10 15  
 Gln Leu Pro Leu Leu His Phe Cys Phe Ser Ala Leu Pro His Thr Val  
 20 25 30  
 Leu Ala Ala Cys Ser Pro Leu Asn Ala Ala Met Ser Ser Ser Pro Tyr  
 35 40 45  
 Arg Asn Asp Val Pro Ser Lys Met Pro Thr Ser Ala Ser Ala Ser Ala  
 50 55 60  
 Val Met Ser Ala Tyr Arg Ala Thr Arg Asn Ala Gln Arg Asn Arg Val  
 65 70 75 80  
 Leu Ala Arg Tyr Glu Val Leu Gly Tyr Leu Ser Ser Gly Thr Tyr Gly  
 85 90 95  
 Arg Val Tyr Lys Ala Lys Glu Leu  
 100

<210> 241  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

<400> 241  
 ncggggggcc gagttgaaag ctgccggcac actggctgtg ctgcttgctt cacttctcgg  
 60  
 gatgctgctt ccagggcggg cctgggggaa acatcggcct tcccaggcac ccttagcccc  
 120  
 tcccactctg gggcccttag cacagtcctt gggacccac atgctgcctt tcaggctgat  
 180

gtgggcaaac tcggcagccc agcctactcc cgggccatgg gccaccatct cagcttccct  
 240  
 ggggctaagc cgtgtgctct gaatcaaaag cagtagtggc atcggcggca ctggcgccat  
 300  
 gggaaacggg ttgacttgca caaccagcac  
 330

<210> 242  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 242  
 Met Ala Pro Val Pro Pro Met Pro Leu Leu Leu Leu Ile Gln Ser Thr  
 1 5 10 15  
 Arg Leu Ser Pro Arg Glu Ala Glu Met Val Ala His Gly Pro Gly Val  
 20 25 30  
 Gly Trp Ala Ala Glu Phe Ala His Ile Ser Leu Lys Gly Ser Met Trp  
 35 40 45  
 Gly Pro Arg Asp Cys Ala Lys Gly Pro Gln Met Gly Arg Ala Lys Gly  
 50 55 60  
 Ala Trp Glu Gly Arg Cys Phe Pro Gln Ala Arg Pro Gly Ser Ser Ile  
 65 70 75 80  
 Pro Arg Ser Glu Ala Ser Ser Thr Ala Ser Val Pro Ala Ala Phe Asn  
 85 90 95  
 Ser Ala Pro Arg  
 100

<210> 243  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

<400> 243  
 nnaccttctc tccgcgttat taccaaagat gctatgcacg taactgcgga ggaaattctt  
 60  
 cacacaggcc accccgcccc cactgcgctc gtcgctaate ttccctataa cgttgcggtg  
 120  
 cccgtactgc tacacatgct agatattctc ccctccttgc ggactacagt ggtgatggtg  
 180  
 caggcagaag tagccgatcg attggetgcc acaccaggca gccgcattta cgggtgtcccc  
 240  
 agcgtcaaag tcaactttta cgggactgtc tcgcgtgcgg gagcaattgg acgcaatgtc  
 300  
 ttctggccgg ctcccaatgt tgattctggn  
 330

<210> 244  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 244  
 Xaa Pro Ser Leu Arg Val Ile Thr Lys Asp Ala Met His Val Thr Ala

```

      1           5           10           15
Glu Glu Ile Leu His Thr Gly His Pro Ala Pro Thr Ala Leu Val Ala
      20           25           30
Asn Leu Pro Tyr Asn Val Ala Val Pro Val Leu Leu His Met Leu Asp
      35           40           45
Ile Leu Pro Ser Leu Arg Thr Thr Val Val Met Val Gln Ala Glu Val
      50           55           60
Ala Asp Arg Leu Ala Ala Thr Pro Gly Ser Arg Ile Tyr Gly Val Pro
      65           70           75           80
Ser Val Lys Val Asn Phe Tyr Gly Thr Val Ser Arg Ala Gly Ala Ile
      85           90           95
Gly Arg Asn Val Phe Trp Pro Ala Pro Asn Val Asp Ser Gly
      100           105           110

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&lt;210&gt; 245

&lt;211&gt; 355

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 245

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tctagatcct gaatcaccca cctcctagtt tcggattcac ctccgccggc gtcacctgaa
60
aacaatgtcg agcccgaatg gatgatggta gccacaccca tctcggaaag gtggaatgca
120
gcgtgttgca gaaacagaag ttgaccgtcg gaggtaggcg gcattcgctt cggatcgaag
180
cgtcccgagg catccatctc gagttgacga cgaaaatctt tccagtccac gccgtagggg
240
ganttggcaa ccacagcatc gaatttgtcc agaaggaagt ggtcgttggt gagggatttg
300
ccccattcaa tacgcgcac ttcccggaag cgcgcctcta ttgcggccaa cgcgt
355

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&lt;210&gt; 246

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 246

```

Met Arg Val Leu Asn Gly Ala Ile Pro Ser Pro Thr Thr Thr Ser Phe
1           5           10           15
Trp Thr Asn Ser Met Leu Trp Leu Pro Xaa Pro Pro Thr Ala Trp Thr
      20           25           30
Gly Lys Ile Phe Val Val Asn Ser Arg Trp Met Pro Arg Asp Ala Ser
      35           40           45
Ile Arg Ser Glu Cys Arg Leu Pro Pro Thr Val Asn Phe Cys Phe Cys
      50           55           60
Asn Thr Leu His Ser Thr Phe Pro Arg Trp Val Trp Leu Pro Ser Ser
      65           70           75           80
Ile Arg Ala Arg His Cys Phe Gln Val Thr Pro Ala Glu Val Asn Pro
      85           90           95
Lys Leu Gly Gly Gly
      100

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<210> 247  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<400> 247  
 atggccgcga atgggcaccg tgcacgggc gtctctcccc gctacgacca gtacaaggac  
 60  
 gcctgggaca ccagcgtcgt gtccgagatc aagatgggag acaggtacga gacggtcagg  
 120  
 ttcttccact gctacaagcg cggagtggac cgcgtgttcg ttgaccaccc actgttctcg  
 180  
 gagagggttt ggggaaagac cgaggagaag atctacgggc ctgacgctgg aacggactac  
 240  
 agggacaacc agctgcggtt cagcctgcta tgccaggcag cacttgaagc tccaaggatc  
 300  
 ctgagcctca acaacaaccc atacttctcc gga  
 333

<210> 248  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 248  
 Met Ala Ala Asn Gly His Arg Val Met Val Val Ser Pro Arg Tyr Asp  
 1 5 10 15  
 Gln Tyr Lys Asp Ala Trp Asp Thr Ser Val Val Ser Glu Ile Lys Met  
 20 25 30  
 Gly Asp Arg Tyr Glu Thr Val Arg Phe Phe His Cys Tyr Lys Arg Gly  
 35 40 45  
 Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg Val Trp  
 50 55 60  
 Gly Lys Thr Glu Glu Lys Ile Tyr Gly Pro Asp Ala Gly Thr Asp Tyr  
 65 70 75 80  
 Arg Asp Asn Gln Leu Arg Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu  
 85 90 95  
 Ala Pro Arg Ile Leu Ser Leu Asn Asn Asn Pro Tyr Phe Ser Gly  
 100 105 110

<210> 249  
 <211> 5503  
 <212> DNA  
 <213> Homo sapiens

<400> 249  
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 120  
 tcgccacgca ccgcatgccca cctgaacccc agccccgatg gtgaggccta cacactggct  
 180  
 tcgagaccac ccgtccgcct caatgatgtc atgctcaggc tgggtgacgga gctgcgctgg  
 240

cagaagttcg tcatgttcta cgacagcgag tatgatatcc gtgggcttca aagctttctg  
300  
gaccaggcct cgcggctggg ccttgacgtc tctttacaaa aggtggacaa gaacattagc  
360  
cacgtattca ccagcctgtt caccacgatg aagacagagg agctgaatcg ctaccgggac  
420  
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480  
gccgtggaga ccaacctggc ttccaaggac agccactggg tctttgtgaa tgaggaaatc  
540  
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600  
caaatctttc cgtctgcaaa ggacaatcag aaatgcacga ggaacaacca ccgcatctcc  
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720  
ctgtatgaca gtgttctgat gctggccaac gcctttcaca ggaagctgga ggaccggaag  
780  
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960  
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1140  
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1380  
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1800  
cgggattctg ctgtatatga gtacttccga gccaaaggca ccaacccctt ggagcaggac  
1860



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1920  
tccagtcctt cagaaggcat caggaaggca aagaagggga actacgcctt cctgtgggat  
1980  
gtggccgtgg tggaatacgc agccctgacg gatgacgact gctcggtgac tgtcatcggc  
2040  
aacagcatca gcagcaaggg ttacgggatt gccttcgacg atggcagccc ctacagggac  
2100  
ctcttctccc agaggatcct ggagctgcag gacacagggg acctggatgt gctgaagcag  
2160  
aagtgggtgg cgcacatggg ccgctgtgac ctcaccagcc atgccagcgc ccaggccgac  
2220  
ggcaaatccc tcaagctgca cagcttcgcc ggggtcttct gcatcctggc cattggcctg  
2280  
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2340  
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2400  
ctcatggatg aagacattgc tcacaagcag atttccccag cgtcgattga gctctcggcc  
2460  
ctggagatgg ggggcctggc tcccaccag accttgagc cgacacggga gtaccagaac  
2520  
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2580  
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2640  
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2760  
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2820  
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2880  
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2940  
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caaaaactgt atgaatgact ttgtaaattt tgttctatat gaataaaaag gcaaattact  
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3120  
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3180  
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3420  
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3480

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4560  
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4620  
aaagtcctta gtgacatgat tgagcagtaa agaacggcca aatcacacag tcagctaaaa  
4680  
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4740  
ctgatattcg tgctacctag gcaatccatt gacatttctc caatcagagc atgtggacct  
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<210> 250
<211> 927
<212> PRT
<213> Homo sapiens
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Ala	Asn	Ala	Leu	Gln	Ser	Leu	Thr	Asp	Ala	Met	His	Ile	Pro	His	Leu
		20						25					30		
Phe	Val	Gln	Arg	Asn	Pro	Gly	Gly	Ser	Pro	Arg	Thr	Ala	Cys	His	Leu
		35					40					45			
Asn	Pro	Ser	Pro	Asp	Gly	Glu	Ala	Tyr	Thr	Leu	Ala	Ser	Arg	Pro	Pro
	50					55					60				
Val	Arg	Leu	Asn	Asp	Val	Met	Leu	Arg	Leu	Val	Thr	Glu	Leu	Arg	Trp
65					70					75					80
Gln	Lys	Phe	Val	Met	Phe	Tyr	Asp	Ser	Glu	Tyr	Asp	Ile	Arg	Gly	Leu
			85						90					95	
Gln	Ser	Phe	Leu	Asp	Gln	Ala	Ser	Arg	Leu	Gly	Leu	Asp	Val	Ser	Leu
			100					105					110		
Gln	Lys	Val	Asp	Lys	Asn	Ile	Ser	His	Val	Phe	Thr	Ser	Leu	Phe	Thr
		115					120					125			
Thr	Met	Lys	Thr	Glu	Glu	Leu	Asn	Arg	Tyr	Arg	Asp	Thr	Leu	Arg	Arg
	130					135					140				
Ala	Ile	Leu	Leu	Leu	Ser	Pro	Gln	Gly	Ala	His	Ser	Phe	Ile	Asn	Glu
145					150					155					160
Ala	Val	Glu	Thr	Asn	Leu	Ala	Ser	Lys	Asp	Ser	His	Trp	Val	Phe	Val
				165					170					175	
Asn	Glu	Glu	Ile	Ser	Asp	Pro	Glu	Ile	Leu	Asp	Leu	Val	His	Ser	Ala
			180					185					190		
Leu	Gly	Arg	Met	Thr	Val	Val	Arg	Gln	Ile	Phe	Pro	Ser	Ala	Lys	Asp
		195					200					205			
Asn	Gln	Lys	Cys	Thr	Arg	Asn	Asn	His	Arg	Ile	Ser	Ser	Leu	Leu	Cys
	210					215					220				
Asp	Pro	Gln	Glu	Gly	Tyr	Leu	Gln	Met	Leu	Gln	Ile	Ser	Asn	Leu	Tyr
225					230					235					240
Leu	Tyr	Asp	Ser	Val	Leu	Met	Leu	Ala	Asn	Ala	Phe	His	Arg	Lys	Leu
				245					250					255	
Glu	Asp	Arg	Lys	Trp	His	Ser	Met	Ala	Ser	Leu	Asn	Cys	Ile	Arg	Lys

[illegible]

```

      690              695              700
Arg Ile Leu Glu Leu Gln Asp Thr Gly Asp Leu Asp Val Leu Lys Gln
705              710              715              720
Lys Trp Trp Pro His Met Gly Arg Cys Asp Leu Thr Ser His Ala Ser
      725              730              735
Ala Gln Ala Asp Gly Lys Ser Leu Lys Leu His Ser Phe Ala Gly Val
      740              745              750
Phe Cys Ile Leu Ala Ile Gly Leu Leu Leu Ala Cys Leu Val Ala Ala
      755              760              765
Leu Glu Leu Trp Trp Asn Ser Asn Arg Cys His Gln Glu Thr Pro Lys
      770              775              780
Glu Asp Lys Glu Val Asn Leu Glu Gln Val His Arg Arg Met Asn Ser
785              790              795              800
Leu Met Asp Glu Asp Ile Ala His Lys Gln Ile Ser Pro Ala Ser Ile
      805              810              815
Glu Leu Ser Ala Leu Glu Met Gly Gly Leu Ala Pro Thr Gln Thr Leu
      820              825              830
Glu Pro Thr Arg Glu Tyr Gln Asn Thr Gln Leu Ser Val Ser Thr Phe
      835              840              845
Leu Pro Glu Gln Ser Ser His Gly Thr Ser Arg Thr Leu Ser Ser Gly
      850              855              860
Pro Ser Ser Asn Leu Pro Leu Pro Leu Ser Ser Ala Thr Met Pro
865              870              875              880
Ser Met Gln Cys Lys His Arg Ser Pro Asn Gly Gly Leu Phe Arg Gln
      885              890              895
Ser Pro Val Lys Thr Pro Ile Pro Met Ser Phe Gln Pro Val Pro Gly
      900              905              910
Gly Val Leu Pro Glu Ala Leu Asp Thr Ser His Gly Thr Ser Ile
      915              920              925

```

&lt;210&gt; 251

&lt;211&gt; 291

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 251

```

nngatcagcc gcggggtccg cgccctcgat tcggcggttg agaccgagag tctgcgtgag
60
gacgtcaacg cgctcgaacg gctgcggttg gccgtgcgcg ccagcgtggt catectcatc
120
gagtaccacc attcggtgac cctgctgctg cgggtgcgcg ggaactcacc tctggaacga
180
gaggccctcg aggccgcg cgtatcgat gcgaaggttc ccgtctcgt cgagagcgcc
240
atcgccgagg gtggtctgcg ctcgatttc actccgggc tcatcacgcg t
291

```

&lt;210&gt; 252

&lt;211&gt; 97

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 252

```

Xaa Ile Ser Arg Gly Val Arg Ala Leu Asp Ser Ala Val Glu Thr Glu

```

```

1           5           10           15
Ser Leu Arg Glu Asp Val Asn Ala Leu Glu Arg Leu Arg Leu Ala Val
20           25           30
Arg Ala Ser Val Val Ile Leu Ile Glu Tyr His His Ser Val Thr Leu
35           40           45
Leu Leu Arg Val Arg Gly Asn Ser Pro Leu Glu Arg Glu Ala Leu Glu
50           55           60
Ala Arg Arg Arg Ile Asp Ala Lys Val Pro Ala Leu Val Glu Ser Ala
65           70           75           80
Ile Ala Glu Gly Gly Leu Arg Ser Asp Phe Thr Pro Gly Leu Ile Thr
85           90           95
Arg

```

<210> 253  
 <211> 327  
 <212> DNA  
 <213> Homo sapiens

```

<400> 253
gtgcacggat gggagcgcctc gcgcgcgtgc tggcgccttc acagcccggc gagcggcgtg
60
cgctcacggc cctgtaccga ccgatctcgc aaccttcgcg agaccgatcc accaaccgcg
120
cccacatgtc ggcagtgatg gcgggcacct tgcgggagaa ggccgggaag gtcgagcgag
180
ccaatgaccg tcgcacggtc ggcacgctcc acgagcggga cgagaagctc gcggcaggac
240
gctcactcgt cgcgggtgtcc tccgcggtct ccatcacgtt ccctgcgaca tggaacgccc
300
acgacttcgg acggcgactc gacgcgt
327

```

<210> 254  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

```

<400> 254
Met Gly Ala Leu Ala Arg Val Leu Val Pro Ser Gln Pro Gly Glu Arg
1           5           10           15
Arg Ala Leu Thr Val Leu Tyr Arg Pro Ile Ser Gln Pro Ser Ala Asp
20           25           30
Arg Ser Thr Asn Arg Ala His Met Ser Ala Val Met Ala Gly Thr Leu
35           40           45
Arg Glu Lys Ala Gly Lys Val Glu Arg Ala Asn Asp Arg Arg Thr Val
50           55           60
Gly Thr Leu His Glu Arg Asp Glu Lys Leu Ala Ala Gly Arg Ser Leu
65           70           75           80
Val Ala Val Ser Ser Ala Val Ser Ile Thr Val Pro Ala Thr Trp Asn
85           90           95
Ala His Asp Phe Gly Arg Arg Leu Asp Ala
100          105

```

<210> 255  
 <211> 372  
 <212> DNA  
 <213> Homo sapiens

<400> 255  
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 atcgtggacc atagacctga cttaatctta tgtgattgga tgatgccagg agggagtggc  
 120  
 atcgagctaa ctcgtcgctt aaagaaagac agcacgacag cagaaatccc tgttatttta  
 180  
 ctaacggcca aaagtgaaga agacaataaa attcaaggct tagaagtcgg tgcagatgac  
 240  
 tacatcacta aacctttctc tcctcgtgaa ctagtagcac gcctcaaggc ggtattacgc  
 300  
 cgagcgactc cacaaggat tgatgatcct attgaaattg atggtttaac gcttgatccc  
 360  
 attagccaac gc  
 372

<210> 256  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 256  
 Leu Glu Met Ala Gly Tyr Glu Tyr Met Glu Ala Glu Asn Ser Gln Gln  
 1 5 10 15  
 Ala His Glu Ile Ile Val Asp His Arg Pro Asp Leu Ile Leu Cys Asp  
 20 25 30  
 Trp Met Met Pro Gly Gly Ser Gly Ile Glu Leu Thr Arg Arg Leu Lys  
 35 40 45  
 Lys Asp Ser Thr Thr Ala Glu Ile Pro Val Ile Leu Leu Thr Ala Lys  
 50 55 60  
 Ser Glu Glu Asp Asn Lys Ile Gln Gly Leu Glu Val Gly Ala Asp Asp  
 65 70 75 80  
 Tyr Ile Thr Lys Pro Phe Ser Pro Arg Glu Leu Val Ala Arg Leu Lys  
 85 90 95  
 Ala Val Leu Arg Arg Ala Thr Pro Gln Gly Ile Asp Asp Pro Ile Glu  
 100 105 110  
 Ile Asp Gly Leu Thr Leu Asp Pro Ile Ser Gln Arg  
 115 120

<210> 257  
 <211> 639  
 <212> DNA  
 <213> Homo sapiens

<400> 257  
 nnacgcgtag cggtcgaggt tgcggacacc atgccgaac ccggcctgct cgccatcgag  
 60  
 gcacccatgg gacacggcaa gaccgaggcc gccctcatgt gcgcacaggt gctcgccgaa  
 120

cggttcgggc tcggcgccat cttcttcggt ctaccgacga tggccacgtc caatcccatg  
 180  
 ttcggtcgag ttcgggaatg gctggacgct gtgccagcca aggacccgtc aagcatttcc  
 240  
 ctggctcact cgaaagctgg actcaacgag gagtaccagc agctcatgcc gtggaacgcc  
 300  
 accatggccg tctacgacga aggtgccggc acgcagcgtg aagcttcggc gatcgtccat  
 360  
 gagtgggttct tgggccgcaa gcgcgcgac tcggccgacc acgtcgtcgg gaccatcgac  
 420  
 caggcactgt tcaccggtct caaagccaag catgtggtgt tacgccacct cggctctggcg  
 480  
 agcaaggctc tcatcattga tgaggtccac gccgccgacg tctatatgcg cgaatacctc  
 540  
 aaggctgtcc tcgaatggct cggcgcctac cgcacgccag tcatcctcat gtccgcgacg  
 600  
 ctgccaccgg cccaacgtca tgaactcgcg ctagcgtag  
 639

<210> 258

<211> 213

<212> PRT

<213> Homo sapiens

<400> 258

Xaa	Arg	Val	Ala	Val	Glu	Val	Ala	Asp	Thr	Met	Pro	Glu	Pro	Gly	Leu
1				5					10					15	
Leu	Ala	Ile	Glu	Ala	Pro	Met	Gly	His	Gly	Lys	Thr	Glu	Ala	Ala	Leu
			20					25						30	
Met	Cys	Ala	Gln	Val	Leu	Ala	Glu	Arg	Phe	Gly	Leu	Gly	Gly	Ile	Phe
		35					40					45			
Phe	Gly	Leu	Pro	Thr	Met	Ala	Thr	Ser	Asn	Pro	Met	Phe	Gly	Arg	Val
		50				55					60				
Arg	Glu	Trp	Leu	Asp	Ala	Val	Pro	Ala	Lys	Asp	Pro	Ser	Ser	Ile	Ser
65					70					75				80	
Leu	Ala	His	Ser	Lys	Ala	Gly	Leu	Asn	Glu	Glu	Tyr	Gln	Gln	Leu	Met
				85					90					95	
Pro	Trp	Asn	Ala	Thr	Met	Ala	Val	Tyr	Asp	Glu	Gly	Ala	Gly	Thr	Gln
			100					105						110	
Arg	Glu	Ala	Ser	Ala	Ile	Val	His	Glu	Trp	Phe	Leu	Gly	Arg	Lys	Arg
		115				120						125			
Ala	Ile	Leu	Ala	Asp	His	Val	Gly	Thr	Ile	Asp	Gln	Ala	Leu	Phe	
		130				135					140				
Thr	Gly	Leu	Lys	Ala	Lys	His	Val	Val	Leu	Arg	His	Leu	Gly	Leu	Ala
145					150					155					160
Ser	Lys	Val	Val	Ile	Ile	Asp	Glu	Val	His	Ala	Ala	Asp	Val	Tyr	Met
			165						170					175	
Arg	Glu	Tyr	Leu	Lys	Val	Val	Leu	Glu	Trp	Leu	Gly	Ala	Tyr	Arg	Thr
			180						185					190	
Pro	Val	Ile	Leu	Met	Ser	Ala	Thr	Leu	Pro	Pro	Ala	Gln	Arg	His	Glu
			195				200					205			
Leu	Ala	Leu	Ala	Tyr											
															210



<210> 259  
 <211> 252  
 <212> DNA  
 <213> Homo sapiens

<400> 259  
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 60  
 ncatgggtgtg tgcacgtgtg cnaactgtgta tgcattggtaa tgtgcacgtg tgcancgtgtg  
 120  
 tgtnggtgtg tatgcatgng tgtgtgcacg tgtgcactgn agtgtggggg gtatgcatgg  
 180  
 tgtgtgcaca tgagcactgt gtggtgtgta tgcattggtgn ggtgcacgtg tgcactgtgt  
 240  
 atgcaatggt gt  
 252

<210> 260  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens

<400> 260  
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys  
 1 5 10 15  
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met  
 20 25 30  
 Val Met Cys Thr Cys Ala Xaa Val Cys Xaa Cys Val Cys Met Xaa Val  
 35 40 45  
 Cys Thr Cys Ala Leu Xaa Cys Gly Val Tyr Ala Trp Cys Val His Met  
 50 55 60  
 Ser Thr Val Trp Cys Val Cys Met Val Xaa Cys Thr Cys Ala Leu Cys  
 65 70 75 80  
 Met Gln Trp Cys

<210> 261  
 <211> 1202  
 <212> DNA  
 <213> Homo sapiens

<400> 261  
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 60  
 ctgtggggcg gcacgtcttt cggatcgctg ggaatcatca acggttacgc gggggcctta  
 120  
 ttcaaagcgc tcggctggat tccgatcttt tccgaagatc cgtcgtgggc ctcggctact  
 180  
 ggcaagggtt accttgccag tctcgtcctg gccatcatga tcttgccaat tatcactgct  
 240  
 gttagcccggt acgtcatgcc ccgaacgccc catgatcaag tcgaggccgc gctcgccttc  
 300  
 ggatcgacgc gctgggaggt catcaagctt gcagtgttcc cccactcgcg gtccggcatc  
 360

atttccggat ccatgttggg tctaggacgc gccctcggcg agacctggc tgtcaccctc  
 420  
 atcctgcaga cgatgagccc catggcgctc aaacagaacc tcaacctgtc gatcttcgtc  
 480  
 ggtggtgaga cattcgcgtc gaagattgcc ggtaacttct ccgaggccat tagcgatccc  
 540  
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 600  
 aacgcgactg cccggttgat tgcggcgaag ggggttaagc gatgagcgcc accaccctg  
 660  
 accacatcac ccaccatggc gacaacacgc ccggacagct agatctctcc cgcccgtctg  
 720  
 gtaaacggac tatcaagagc ggctgcgcct caacattcat gatcgtggcc accgtactgg  
 780  
 ctgttatccc actggcctgg ctgctcttcg cggcgcctcg gcgcggcacc ggatcactat  
 840  
 tccacgcgtc gtggtggacc cactcgatgg atccctcctt cgacttggcc gagcagggcg  
 900  
 ccatccacgc tatcgtcgga acccttgaaa ttggccttat tacatcgatt atctcggtac  
 960  
 cgatcgctct gatgaccgcg atcttcctag tcgagtacgc ccgcggaact aagatcgcca  
 1020  
 aggtcattag ctctgcgcgtc gacgtgctaa ccggtgtacc ttcaatcgtc gcggccctct  
 1080  
 tcgtcttcgc cgtagtcggt accaccttcg gtggcaccca atccgcgtgg gcctcctcgt  
 1140  
 tggccctcat gatcctcatg gtcccgacgg tgctgcgac aaccgaggaa atgctcaagc  
 1200  
 tt  
 1202

<210> 262

<211> 214

<212> PRT

<213> Homo sapiens

<400> 262

Ala	Ser	Pro	Val	Ala	Phe	Val	Val	Asp	Leu	Leu	Ala	Ala	Val	Pro	Ser
1				5				10					15		
Ile	Val	Phe	Gly	Leu	Trp	Gly	Gly	Ile	Val	Phe	Gly	Ser	Ser	Gly	Ile
			20					25					30		
Ile	Asn	Gly	Tyr	Ala	Gly	Ala	Leu	Phe	Lys	Ala	Leu	Gly	Trp	Ile	Pro
		35					40					45			
Ile	Phe	Ser	Glu	Asp	Pro	Ser	Trp	Ser	Ser	Ala	Thr	Gly	Thr	Val	Tyr
	50					55				60					
Leu	Ala	Ser	Leu	Val	Leu	Ala	Ile	Met	Ile	Leu	Pro	Ile	Ile	Thr	Ala
65				70						75				80	
Val	Ser	Arg	Asp	Val	Met	Pro	Arg	Thr	Pro	His	Asp	Gln	Val	Glu	Ala
			85					90					95		
Ala	Leu	Ala	Leu	Gly	Ser	Thr	Arg	Trp	Glu	Val	Ile	Lys	Leu	Ala	Val
			100				105					110			
Phe	Pro	His	Ser	Arg	Ser	Gly	Ile	Ile	Ser	Gly	Ser	Met	Leu	Gly	Leu
		115				120						125			
Gly	Arg	Ala	Leu	Gly	Glu	Thr	Leu	Ala	Val	Thr	Leu	Ile	Leu	Gln	Thr

```

      130              135              140
Met Ser Pro Met Ala Leu Lys Gln Asn Leu Asn Leu Ser Ile Phe Val
145              150              155              160
Gly Gly Glu Thr Phe Ala Ser Lys Ile Ala Gly Asn Phe Ser Glu Ala
      165              170              175
Ile Ser Asp Pro Thr Ser Leu Gly Ala Leu Val Ala Ser Ala Leu Ala
      180              185              190
Leu Phe Val Ile Thr Phe Val Val Asn Ala Thr Ala Arg Leu Ile Ala
      195              200              205
Ala Lys Gly Val Lys Arg
      210

```

```

<210> 263
<211> 424
<212> DNA
<213> Homo sapiens

```

```

<400> 263
acgcgtgagt gctctgcgct ggaaacaacg gtgatagagc ccatccgccg tgaactttcc
60
gacgtggtgc tcgtgaacaa gctcgaaaag tatgtacgcy aacgtacctc ggaagacgtt
120
gcgcacatgg aagaggatgc ggaccagacg ggcaacgaca tcctcacgac gatcctgctg
180
tcgaactggg atccactatt ggatatgacg acgcaggatc atgtgctggc catgcaaaaag
240
gcttatatgg cctcgccatt ccgtgccaat ttggacctgg catacccatc ttcgacgcca
300
caggcccagt cccagccggc gatgccgccg tgggagacag ggacctcagc cagtagcatg
360
gcggatgctc gtgaatttgc gctgctgaag ctgtacctgc gtagcttgct gcagaagcac
420
gann
424

```

```

<210> 264
<211> 99
<212> PRT
<213> Homo sapiens

```

```

<400> 264
Met Glu Glu Asp Ala Asp Gln Thr Gly Asn Asp Ile Leu Thr Thr Ile
1      5      10      15
Leu Leu Ser Asn Trp Asp Pro Leu Leu Asp Met Thr Thr Gln Asp His
      20      25      30
Val Leu Ala Met Gln Lys Ala Tyr Met Ala Ser Pro Phe Arg Ala Asn
      35      40      45
Leu Asp Leu Ala Tyr Pro Ser Ser Thr Pro Gln Ala Gln Ser Gln Pro
      50      55      60
Ala Met Pro Pro Trp Glu Thr Gly Thr Ser Ala Ser Ser Met Ala Asp
65      70      75      80
Ala Arg Glu Phe Ala Leu Leu Lys Leu Tyr Leu Arg Ser Leu Leu Gln
      85      90      95
Lys His Xaa

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<210> 265  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 265  
 ncgtacggcc ctggcggtccg catggacgag ggataccatt ccggcatgac ggtgccgggt  
 60  
 gccttcgact ccctcatcgg caagctcatc atcactgggtg atagccgtga gcaagccctg  
 120  
 gctcgagctg cccgcgccct cgacgaaatc gtcacgacg gcatgcccac ggtcattccc  
 180  
 tttcaccagg cgggtggttca cgacccggct ttcactgccg ccgacggctg cttcggcgctc  
 240  
 tttaccgact ggatcgaaac cgagttcgac aacaagatcg agccatacac cgggtctctg  
 300  
 ggcgagtctg ccaattccga gcctcctcgt gaggtcgctg tcgagggtcaa cggtaaaccgc  
 360

<210> 266  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 266  
 Xaa Tyr Gly Pro Gly Val Arg Met Asp Glu Gly Tyr His Ser Gly Met  
 1 5 10 15  
 Thr Val Pro Gly Ala Phe Asp Ser Leu Ile Gly Lys Leu Ile Ile Thr  
 20 25 30  
 Gly Asp Ser Arg Glu Gln Ala Leu Ala Arg Ala Ala Arg Ala Leu Asp  
 35 40 45  
 Glu Ile Val Ile Asp Gly Met Pro Thr Val Ile Pro Phe His Gln Ala  
 50 55 60  
 Val Val His Asp Pro Ala Phe Thr Ala Ala Asp Gly Cys Phe Gly Val  
 65 70 75 80  
 Phe Thr Asp Trp Ile Glu Thr Glu Phe Asp Asn Lys Ile Glu Pro Tyr  
 85 90 95  
 Thr Gly Ser Leu Gly Glu Ser Ala Asn Ser Glu Pro Pro Arg Glu Val  
 100 105 110  
 Val Val Glu Val Asn Gly Lys Arg  
 115 120

<210> 267  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

<400> 267  
 natcctcaac gtgtgttcag ttccacgcga aagatcatgt tcgtcatcgg atcgatgccg  
 60  
 ttaacgcac ctagtcaatc caccgatggc gaccctggca aaaaatacga ggtgacttgg  
 120

ctagatctcg ggcaccttca ccctagtcgg ccgggactcg tcactatcac cacaactgtc  
 180  
 gatgatgacg tcatcacctc ttcccaggta aatgtcggca acctccaccg cggggatgaa  
 240  
 aaacttttcg aagctcgcga ttaccgccag attccgatgc ttgcatcacg tcatggctgg  
 300  
 acagctccat tcattggtga gaccggcgca gcccatgcc a tcgaggatgc gatgggcatt  
 360  
 accatcccaa ctgcggtggc atggatacga accctgctcg ctgagttcag cagaatcacc  
 420  
 tcacacttca cttttttgtc atgggtaggc catcactgtg atgatgccgg c  
 471

<210> 268

<211> 157

<212> PRT

<213> Homo sapiens

<400> 268

Xaa	Pro	Gln	Arg	Val	Phe	Ser	Ser	Thr	Arg	Lys	Ile	Met	Phe	Val	Ile
1				5					10					15	
Gly	Ser	Met	Pro	Leu	Thr	His	Pro	Ser	Gln	Ser	Thr	Asp	Gly	Asp	Pro
			20					25					30		
Gly	Lys	Lys	Tyr	Glu	Val	Thr	Trp	Leu	Asp	Leu	Gly	His	Leu	His	Pro
		35					40					45			
Ser	Arg	Pro	Gly	Leu	Val	Thr	Ile	Thr	Thr	Thr	Val	Asp	Asp	Asp	Val
	50					55					60				
Ile	Thr	Ser	Ser	Gln	Val	Asn	Val	Gly	Asn	Leu	His	Arg	Gly	Asp	Glu
65				70					75					80	
Lys	Leu	Phe	Glu	Ala	Arg	Asp	Tyr	Arg	Gln	Ile	Pro	Met	Leu	Ala	Ser
			85					90					95		
Arg	His	Gly	Trp	Thr	Ala	Pro	Phe	Ile	Gly	Glu	Thr	Gly	Ala	Ala	His
		100						105					110		
Ala	Ile	Glu	Asp	Ala	Met	Gly	Ile	Thr	Ile	Pro	Thr	Arg	Val	Ala	Trp
		115				120						125			
Ile	Arg	Thr	Leu	Leu	Ala	Glu	Phe	Ser	Arg	Ile	Thr	Ser	His	Phe	Thr
	130					135					140				
Phe	Leu	Ser	Trp	Val	Gly	His	His	Cys	Asp	Asp	Ala	Gly			
145				150						155					

<210> 269

<211> 387

<212> DNA

<213> Homo sapiens

<400> 269

acgcgtgtcg tgtttccaga aaaaaccaat aaattagagt ttatggtaga agtgattgct  
 60  
 gatatgacgg taatcaatcc atttgatttc tttgtggaaa gctacgcaga agactaccca  
 120  
 tttgcttatg acaaagctct taaaaaagag ttagaacctt atttacaggt ttctgaacct  
 180  
 tggttcgttac tcgacaaatg gctgtctggt gttgatcggt aaaaaacacc gatcaatgat  
 240

tttctagtcg caataaacag tcgccttgcc ggtgatattg gctatggat tcgcttagaa  
 300  
 ccgggcgttc agtcacctga agaaacgctc acattaatga aaggctcttg tcgcgatacc  
 360  
 tcgggggttat tggttcaaat actacgc  
 387

<210> 270  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

<400> 270  
 Thr Arg Val Val Phe Pro Glu Lys Thr Asn Lys Leu Glu Phe Met Val  
 1 5 10 15  
 Glu Val Ile Ala Asp Met Thr Val Ile Asn Pro Phe Asp Phe Phe Val  
 20 25 30  
 Glu Ser Tyr Ala Glu Asp Tyr Pro Phe Ala Tyr Asp Lys Ala Leu Lys  
 35 40 45  
 Lys Glu Leu Glu Pro Tyr Leu Gln Val Ser Glu Pro Cys Ser Leu Leu  
 50 55 60  
 Asp Lys Trp Leu Ser Gly Val Asp Arg Glu Lys Thr Pro Ile Asn Asp  
 65 70 75 80  
 Phe Leu Val Ala Ile Asn Ser Arg Leu Ala Gly Asp Ile Gly Tyr Gly  
 85 90 95  
 Ile Arg Leu Glu Pro Gly Val Gln Ser Pro Glu Glu Thr Leu Thr Leu  
 100 105 110  
 Met Lys Gly Ser Cys Arg Asp Thr Ser Gly Leu Leu Val Gln Ile Leu  
 115 120 125  
 Arg

<210> 271  
 <211> 443  
 <212> DNA  
 <213> Homo sapiens

<400> 271  
 gccggcacca acggaagtc ctctaccgcg cgcattggctg attcgctttt gcgtgccttc  
 60  
 caccgccgag tgggttttgg aaccagccca cacctgcagc gcgttactga gcgcacggc  
 120  
 attgatggcc agcccattca cccgcgcgat tatgtacgca tctggcacga gattaagcca  
 180  
 tttgtggaaa tggtcgatgc cgaatcggac gtgcctatgt ctaagtccga ggtcttcgtg  
 240  
 ggctgtcct atgctgcgtt tgccgacgcc cccggggacg tcgctgtcgt cgaagtcggc  
 300  
 cttggcggac gttgggacgc taccaatgtg gtcaacgcgg atgtctctgt cattaccccg  
 360  
 gtgggcatgg accacacgga ttacctgggg gagacgatca ctgaaatcgc aggcgagaaa  
 420  
 gctggcatta ttaagccacg cgt  
 443

<210> 272  
 <211> 147  
 <212> PRT  
 <213> Homo sapiens

<400> 272  
 Ala Gly Thr Asn Gly Lys Ser Ser Thr Ala Arg Met Val Asp Ser Leu  
 1 5 10 15  
 Leu Arg Ala Phe His Arg Arg Val Gly Leu Val Thr Ser Pro His Leu  
 20 25 30  
 Gln Arg Val Thr Glu Arg Ile Gly Ile Asp Gly Gln Pro Ile His Pro  
 35 40 45  
 Arg Asp Tyr Val Arg Ile Trp His Glu Ile Lys Pro Phe Val Glu Met  
 50 55 60  
 Val Asp Ala Glu Ser Asp Val Pro Met Ser Lys Phe Glu Val Phe Val  
 65 70 75 80  
 Gly Leu Ser Tyr Ala Ala Phe Ala Asp Ala Pro Gly Asp Val Ala Val  
 85 90 95  
 Val Glu Val Gly Leu Gly Gly Arg Trp Asp Ala Thr Asn Val Val Asn  
 100 105 110  
 Ala Asp Val Ser Val Ile Thr Pro Val Gly Met Asp His Thr Asp Tyr  
 115 120 125  
 Leu Gly Glu Thr Ile Thr Glu Ile Ala Gly Glu Lys Ala Gly Ile Ile  
 130 135 140  
 Lys Pro Arg  
 145

<210> 273  
 <211> 864  
 <212> DNA  
 <213> Homo sapiens

<400> 273  
 caaagtaaga ctgcttcaaa ttttgtgttc tgetctgcag ctgctcccc cctgctgtcg  
 60  
 aagagaagcc aaagcccccc cccccacct caaaggctcg gaagtctggc atccctactt  
 120  
 ccgagcctgg atcccagtaa ggatcttgcc ctccctgcaa caccgagtgc cttagacagc  
 180  
 tgctgcctga gaactggcct ccagccggtg tcttcattcc atggggctcc ctgctgactg  
 240  
 catttcctga tctgggatga tgtttaccag cccaaaacca gtcatgttct tccaaaagct  
 300  
 tctctttgat agaattttga ggccatgcca cctcccttcc agtccacatg gaattccaga  
 360  
 atcagtcaca gcctctgatt ttttccaaga agagattgcc ttcaccattg ttaaattgtc  
 420  
 gcctgtacgg cagagacatg gtgggtctgca caagcctgga caagttcttc catattgatg  
 480  
 gtgggagcaa ccctgtaat ctactccttg gaaggatttt ttgctttgct tatgaaaagc  
 540  
 tgtgcttgag acttaggtac ttttctcacg tggacacact gatcccatcc catattgcat  
 600

ctttgaagag atggatatca agtacacttt ggtagctgaa ataatcatat ctttctgatg  
 660  
 tctattgtat ctcctttgag gaaaagaaca cacattttta atggagattg gctgctttca  
 720  
 ggtatgtgtg tctatcattg aaagagcatg gactcaaaca tcagccctga gttcttgagt  
 780  
 ccacccaact cccatcttct tgtggcacag gaaagctgcc ctctccctct cccaccacac  
 840  
 tcctgactaa tgcccttcac gcgt  
 864

<210> 274  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 274  
 Met Trp Thr Gly Arg Glu Val Ala Trp Pro Gln Asn Ser Ile Lys Glu  
 1 5 10 15  
 Lys Leu Leu Glu His Asp Trp Phe Trp Ala Gly Lys His His Pro  
 20 25 30  
 Arg Ser Gly Asn Ala Val Ser Arg Glu Pro His Gly Met Arg Thr Pro  
 35 40 45  
 Ala Gly Gly Gln Phe Ser Gly Ser Ser Cys Leu Arg His Ser Val Leu  
 50 55 60  
 Gln Gly Gly Gln Asp Pro Tyr Trp Asp Pro Gly Ser Glu Val Gly Met  
 65 70 75 80  
 Pro Asp Phe Arg Ala Phe Glu Val Gly Gly Gly Gly Phe Gly Phe Ser  
 85 90 95  
 Ser Thr Ala Gly Gly Ser Glu Leu Gln Ser Arg Thr Gln Asn Leu Lys  
 100 105 110  
 Gln Ser Tyr Phe  
 115

<210> 275  
 <211> 911  
 <212> DNA  
 <213> Homo sapiens

<400> 275  
 naaattttaa ggaacctccc ttctataacg gagagtattt attgcagctt tcctttctgt  
 60  
 ttattttcag gaatgaaagg aattaccag ccttctgctt ttatacctac agctgaaagt  
 120  
 aattcctttc agcctcaggt gaagactttg ccattctcaa ttgatgctaa acagcagttg  
 180  
 caacggaaaa tccagaagaa gcagcaagaa cagaaactac aatccccctt gccaggagaa  
 240  
 tctgcagcaa aaaagtcaga aagtgtaca agcaatggag tgactaatct tcctaattgga  
 300  
 aatccttcaa tcctttctcc tcaacctatt ggtatcggtg tggcagctgt ccctagtccc  
 360  
 attccgggcc agcgggactag gcaattggtg acttcaccga gtccaatgag ttcttctnga  
 420



cggcaagtt cttccctca atgtacaggt ggtcactcag cacatgcagt ctgtgaaaca  
 480  
 ggcaccaaag actccccaga acgttccagc agtcctgggtg ggaatcggtc tgccccgcac  
 540  
 cgttaccctc agatcttacc caaaccagcg aacaccagtg cactcaccat tcgctctcca  
 600  
 actactgtcc tctttactag tagtcccatc aaaactgctg ttgtaccgcg ttcacacatg  
 660  
 agttctctaa atgtggtgaa aatgacaaca atatccctca caccagcaa cagtaacacc  
 720  
 cctcttaaac attctgcctc agtcagcagt gctacaggaa caacagaaga atcaaggagt  
 780  
 gttccacaga tcaagaatgg ttctgtcgtg tcgcttcagt ctctggggtc caggagcagc  
 840  
 agtgcggggg gaacatctgc tgtggaagtc aaagtggaac ccgaaacatc atcagatgag  
 900  
 catcctgtac a  
 911

<210> 276

<211> 279

<212> PRT

<213> Homo sapiens

<400> 276

Met	Lys	Gly	Ile	Thr	Gln	Pro	Ser	Ala	Phe	Ile	Pro	Thr	Ala	Glu	Ser
1				5						10				15	
Asn	Ser	Phe	Gln	Pro	Gln	Val	Lys	Thr	Leu	Pro	Ser	Pro	Ile	Asp	Ala
			20					25					30		
Lys	Gln	Gln	Leu	Gln	Arg	Lys	Ile	Gln	Lys	Lys	Gln	Gln	Glu	Gln	Lys
		35					40					45			
Leu	Gln	Ser	Pro	Leu	Pro	Gly	Glu	Ser	Ala	Ala	Lys	Lys	Ser	Glu	Ser
	50					55					60				
Ala	Thr	Ser	Asn	Gly	Val	Thr	Asn	Leu	Pro	Asn	Gly	Asn	Pro	Ser	Ile
65					70					75					80
Leu	Ser	Pro	Gln	Pro	Ile	Gly	Ile	Val	Val	Ala	Ala	Val	Pro	Ser	Pro
			85					90					95		
Ile	Pro	Val	Gln	Arg	Thr	Arg	Gln	Leu	Val	Thr	Ser	Pro	Ser	Pro	Met
		100					105					110			
Ser	Ser	Ser	Xaa	Arg	Gln	Ser	Ser	Ser	Pro	Gln	Cys	Thr	Gly	Gly	His
		115				120					125				
Ser	Ala	His	Ala	Val	Cys	Glu	Thr	Gly	Thr	Lys	Asp	Ser	Pro	Glu	Arg
	130					135					140				
Ser	Ser	Ser	Pro	Gly	Gly	Asn	Arg	Ser	Ala	Arg	His	Arg	Tyr	Pro	Gln
145					150					155				160	
Ile	Leu	Pro	Lys	Pro	Ala	Asn	Thr	Ser	Ala	Leu	Thr	Ile	Arg	Ser	Pro
			165						170				175		
Thr	Thr	Val	Leu	Phe	Thr	Ser	Ser	Pro	Ile	Lys	Thr	Ala	Val	Val	Pro
		180						185					190		
Ala	Ser	His	Met	Ser	Ser	Leu	Asn	Val	Val	Lys	Met	Thr	Thr	Ile	Ser
		195				200						205			
Leu	Thr	Pro	Ser	Asn	Ser	Asn	Thr	Pro	Leu	Lys	His	Ser	Ala	Ser	Val
	210					215					220				
Ser	Ser	Ala	Thr	Gly	Thr	Thr	Glu	Glu	Ser	Arg	Ser	Val	Pro	Gln	Ile

225                      230                      235                      240  
 Lys Asn Gly Ser Val Val Ser Leu Gln Ser Pro Gly Ser Arg Ser Ser  
                                  245                      250                      255  
 Ser Ala Gly Gly Thr Ser Ala Val Glu Val Lys Val Glu Pro Glu Thr  
                                  260                      265                      270  
 Ser Ser Asp Glu His Pro Val  
                                  275

<210> 277  
 <211> 652  
 <212> DNA  
 <213> Homo sapiens

<400> 277  
 nnaccggtgg ggactctcgc tgaggtcctt aatggccctt ctcgtgtccc ggacggcacc  
 60  
 atgaaccttg ttggtgggct gcgtcaggca atggccacca ctggttactc ggaggtcaaa  
 120  
 gagttccagc gcatcgagct gacgattcgc taaccgttcc accacgcaga atggtgttcc  
 180  
 ggtgagcggg tggatagcta gccttcggcc atgagtgaag tgcccgatga attggtcgtg  
 240  
 ttgcgtggcg cgattgacaa catggacgcc gccctcatcc atctgcttgc cgaaaggttc  
 300  
 cggattactc gcgaggtagg ccgcctcaag gcggagtgcg gtttacctcc ggccgacccc  
 360  
 gcccgtaggg ctgagcagat cgcgcggttg cggcagttag cggtcgagtc gaacctcgac  
 420  
 cccgaattcg cgcagaaggt catcacgttc atcgtggccg aggtggtgcg tcaccacgaa  
 480  
 gctattgctg acgattctgg cgacgactct ggagtggcgg atacggggga ggcggatgtc  
 540  
 cctgggtcgg gcagctgagt tacagatcag gcgatgacgt cgccctggtg caccctcgac  
 600  
 gggattccga cgacgactgt gccgggggcg acatccttga cgaccaacgc gt  
 652

<210> 278  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 278  
 Met Ser Glu Val Pro Asp Glu Leu Val Val Leu Arg Gly Ala Ile Asp  
 1                      5                      10                      15  
 Asn Met Asp Ala Ala Leu Ile His Leu Leu Ala Glu Arg Phe Arg Ile  
                                  20                      25                      30  
 Thr Arg Glu Val Gly Arg Leu Lys Ala Glu Cys Gly Leu Pro Pro Ala  
                                  35                      40                      45  
 Asp Pro Ala Arg Glu Ala Glu Gln Ile Ala Arg Leu Arg Gln Leu Ala  
                                  50                      55                      60  
 Val Glu Ser Asn Leu Asp Pro Glu Phe Ala Gln Lys Val Ile Thr Phe  
 65                      70                      75                      80  
 Ile Val Ala Glu Val Val Arg His His Glu Ala Ile Ala Asp Asp Ser

85 90 95  
 Gly Asp Asp Ser Gly Val Ala Asp Thr Gly Glu Ala Asp Val Pro Gly  
 100 105 110  
 Ser Gly Ser  
 115

<210> 279  
 <211> 348  
 <212> DNA  
 <213> Homo sapiens

<400> 279  
 cgggagggtca cacaagcatt caaaccatag cagatggtaa atgttatgtt atgtgtattt  
 60  
 taccacaatc cttaaaaaga aaagaaagaa aggcataatg aaccctagt tacctctcat  
 120  
 ccagcttcaa aattgtcagt gcatgggtcaa tcttgtctta tctgcccctc acccaccctt  
 180  
 ttccagaaaag aagaccaga ggattccaca tctgcctgga aaccacgacc agtctcgact  
 240  
 ggaagttgtt gttaatgttg catgtattca taaaacctct aggcatttct agtgtccctc  
 300  
 agaatttttc caaattcagg caaacacaga aattacttcc aaaaattt  
 348

<210> 280  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 280  
 Met Cys Ile Leu Pro Gln Ser Leu Lys Arg Lys Glu Arg Lys Ala Tyr  
 1 5 10 15  
 Gly Thr Pro Ser Tyr Leu Ser Ser Ser Phe Lys Ile Val Ser Ala Trp  
 20 25 30  
 Ser Ile Leu Ser Tyr Leu Pro Leu Thr His Pro Phe Pro Glu Arg Arg  
 35 40 45  
 Pro Arg Gly Phe His Ile Cys Leu Glu Thr Thr Thr Ser Leu Asp Trp  
 50 55 60  
 Lys Leu Leu Leu Met Leu His Val Phe Ile Lys Pro Leu Gly Ile Ser  
 65 70 75 80  
 Ser Val Pro Gln Asn Phe Ser Lys Phe Arg Gln Thr Gln Lys Leu Leu  
 85 90 95  
 Pro Lys Ile

<210> 281  
 <211> 384  
 <212> DNA  
 <213> Homo sapiens

<400> 281  
 agatctgcgc agatcgataa tggattaaag actcttgacg ctggagtcac cgagatgaac  
 60

aacaaggtgt tgggggcaac gaaggctgtc ggtgattcca ccactaccgt caaccaggtg  
 120  
 aattctgcgt taggaantgc cgactcagcg gcagagaaga cgtcgagcgc cgttactcag  
 180  
 acgcgcgtgg gtgcccaggg gattaccggc gctgctcaaa atgtcatggc tgattcccaa  
 240  
 gctgtcaact cagccatggt tccgcttatt aataacgtga caaagaatct tcctaccttg  
 300  
 caaaaacagg ccaggaatct cgtgtcagtg aacggtagcc tgacagaacc caacggtagt  
 360  
 tctgtcatta agattcaaca gacc  
 384

<210> 282

<211> 110

<212> PRT

<213> Homo sapiens

<400> 282

Met	Asn	Asn	Lys	Val	Leu	Gly	Ala	Thr	Lys	Ala	Val	Gly	Asp	Ser	Thr
1			5						10				15		
Thr	Thr	Val	Asn	Gln	Val	Asn	Ser	Ala	Leu	Gly	Xaa	Ala	Asp	Ser	Ala
		20					25					30			
Ala	Glu	Lys	Thr	Ser	Ser	Ala	Val	Thr	Gln	Thr	Arg	Val	Gly	Ala	Gln
	35					40					45				
Ala	Ile	Thr	Gly	Ala	Ala	Gln	Asn	Val	Met	Ala	Asp	Ser	Gln	Ala	Val
	50					55				60					
Asn	Ser	Ala	Met	Val	Pro	Leu	Ile	Asn	Asn	Val	Thr	Lys	Asn	Leu	Pro
65				70					75					80	
Thr	Leu	Gln	Lys	Gln	Ala	Arg	Asn	Leu	Val	Ser	Val	Asn	Gly	Thr	Leu
			85					90					95		
Gln	Asn	Pro	Asn	Gly	Asp	Ser	Val	Ile	Lys	Ile	Gln	Gln	Thr		
			100					105					110		

<210> 283

<211> 426

<212> DNA

<213> Homo sapiens

<400> 283

cgcgtagacc aatgtgagac ggccgtcacc aagggcatgc gcgacaagtc ggttggtagc  
 60  
 ggaccggata ttgtgcgtcg cgagctgcgc catgtcgtga cgagcggcac gattgtcgat  
 120  
 ggaagcgtac tggctgacga attgagcagc tactgcatga gtatcaagga gcacgtccgc  
 180  
 tctgatggcc tatccgagtt tggcatctgc accctcgacg ccgccaccgc cgagttccga  
 240  
 tacatgacat tcgtcgacga tgccgtgctg tcacaactcg agacattgct gcgttctcta  
 300  
 cgcacaaagg aagtcttgca tgaaaaaggg gtcattgttc ctccacgct gcgcttgatc  
 360  
 cgcaacgcgg tgcccaccac ctgccaatt accatgctca agcctgatac cgaattgtcg  
 420

gagaga  
426

<210> 284  
<211> 142  
<212> PRT  
<213> Homo sapiens

<400> 284  
Arg Val Asp Gln Cys Glu Thr Ala Val Thr Lys Gly Met Arg Asp Lys  
1 5 10 15  
Ser Val Gly Ser Gly Pro Asp Ile Val Arg Arg Glu Leu Arg His Val  
20 25 30  
Val Thr Ser Gly Thr Ile Val Asp Gly Ser Val Leu Ala Asp Glu Leu  
35 40 45  
Ser Ser Tyr Cys Met Ser Ile Lys Glu His Val Arg Ser Asp Gly Leu  
50 55 60  
Ser Glu Phe Gly Ile Cys Thr Leu Asp Ala Ala Thr Ala Glu Phe Arg  
65 70 75 80  
Tyr Met Thr Phe Val Asp Asp Ala Val Leu Ser Gln Leu Glu Thr Leu  
85 90 95  
Leu Arg Ser Leu Arg Ile Lys Glu Val Leu His Glu Lys Gly Val Met  
100 105 110  
Leu Pro Ser Thr Leu Arg Leu Ile Arg Asn Ala Val Pro Thr Thr Cys  
115 120 125  
Gln Ile Thr Met Leu Lys Pro Asp Thr Glu Leu Ser Glu Arg  
130 135 140

<210> 285  
<211> 345  
<212> DNA  
<213> Homo sapiens

<400> 285  
acgcgtgcag tcccttaccg acatgctggc agatgagctc gacggcagcc gcttcaccgg  
60  
cgatttctca gaaatctaca aacgtcagaa ctcgatcttc gccgatgtaa ggaataactt  
120  
ttacaaaaaa ggataccgca tcatcaacgt agcgaatggt gtattgcgca agatttcact  
180  
ggtaagcgca ggcaatgcag acaatgtgaa aggtcaggcc ctgttcttcc gcggtgtggc  
240  
gcatttcgaa ctcgtgcgtt tgtttgcaca accctgggggt tatacttcgg acaattcaca  
300  
ctacggcatc ccgctccgca atgaaatcgt aattggttct attcn  
345

<210> 286  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 286  
Met Leu Ala Asp Glu Leu Asp Gly Ser Arg Phe Thr Gly Asp Phe Ser

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      1           5           10           15
Glu Ile Tyr Lys Arg Gln Asn Ser Ile Phe Gly Asp Val Arg Asn Asn
      20           25           30
Phe Tyr Lys Lys Gly Tyr Arg Ile Ile Asn Val Ala Asn Gly Val Leu
      35           40           45
Arg Lys Ile Ser Leu Val Ser Ala Gly Asn Ala Asp Asn Val Lys Gly
      50           55           60
Gln Ala Leu Phe Phe Arg Gly Val Ala His Phe Glu Leu Val Arg Leu
      65           70           75           80
Phe Ala Gln Pro Trp Gly Tyr Thr Ser Asp Asn Ser His Tyr Gly Ile
      85           90           95
Pro Leu Arg Asn Glu Ile Val Ile Gly Ser Ile
      100           105

```

&lt;210&gt; 287

&lt;211&gt; 1379

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 287

```

nnttaactgc ccctttgcag tctttattct gggacattag cactgtcttg ttatcttgct
60
tcagttgagg gattcgggac aatagcagtg ctgatggtaa tggtggcgat ttccctgttt
120
gttttgcagg tcacggccag gggctttggg ccgctgttac agtttgccta cactgccaag
180
ctgttactca gcagagaaaa catccgcgag gtcacccgct gtgctgagtt cctgcgcatg
240
cacaacctgg aggactcctg cttcagcttc ctgcagaccc agctcctgaa cagtgaggat
300
ggcctgtttg tgtgccggaa ggatgctgctg tgccagcgcc cacacgagga ctgcgagaac
360
tctgcaggag aggaggagga tgaagaggag gagacgatgg attcagagac ggccaagatg
420
gcttgcccca gggaccagat gcttccagag cccatcagct ttgaggccgc cgccatcccc
480
gtagcagaga aggaagaagc cctgctgccc gagcctgacg tgcccacaga caccaaggag
540
agctcagaaa aggacgcgtt aacgcagtac cccagataca agaaatacca gcttgcatgt
600
accaagaatg tctataatgc atcatcacac agtacctcag gttttgcaag cacattccgg
660
gaagataact ctagcaacag cctcaagccg gggcttgcca gggggcagat taaaagtgag
720
ccgcccagtg aagagaatga ggaagagagc atcacgctct gcctgtcttg agatgagcct
780
gacgccaagg acagagcggg ggatgtcgag atggaccgga aacagcccag ccctgcccct
840
acccccacgg cccagctgg ggcgcctgc ctggagagat ccaggagcgt ggctcgcgcc
900
tcctgcttaa ggtctctgtt cagcataacg aaaagtgtgg agctgtcttg cctgcccagt
960
acatctcagc agcactttgc caggagtcca gcctgccctt ttgacaaggg gatcactcag
1020

```

ggtgacctta aaactgacta cacccttttc acaggggaatt atggacagcc ccacgtgggc  
 1080  
 cagaaggagg tgtccaactt caccatgggg tcgcccctca gggggcctgg gttggaggct  
 1140  
 ctctgtaaac aggagggaga gctggaccgg aggagcgtga tcttctcctc cagcgcttgt  
 1200  
 gaccaagtga gcacctcggt gcattcttat tctgggggtga gcagtttgga caaagacctc  
 1260  
 tctgagccgg tgccaaaggg tctgtgggtg ggagccggcc agtccctccc cagctcgag  
 1320  
 gcctactccc acggtgggct gatggccgac cacttgccag gaaggatgcg gcccaacac  
 1379

<210> 288

<211> 428

<212> PRT

<213> Homo sapiens

<400> 288

Met	Val	Met	Leu	Ala	Ile	Ser	Leu	Phe	Val	Leu	Gln	Val	Thr	Ala	Arg
1				5					10					15	
Gly	Phe	Gly	Pro	Leu	Leu	Gln	Phe	Ala	Tyr	Thr	Ala	Lys	Leu	Leu	Leu
			20					25					30		
Ser	Arg	Glu	Asn	Ile	Arg	Glu	Val	Ile	Arg	Cys	Ala	Glu	Phe	Leu	Arg
		35				40						45			
Met	His	Asn	Leu	Glu	Asp	Ser	Cys	Phe	Ser	Phe	Leu	Gln	Thr	Gln	Leu
	50					55					60				
Leu	Asn	Ser	Glu	Asp	Gly	Leu	Phe	Val	Cys	Arg	Lys	Asp	Ala	Ala	Cys
65					70					75				80	
Gln	Arg	Pro	His	Glu	Asp	Cys	Glu	Asn	Ser	Ala	Gly	Glu	Glu	Glu	Asp
			85						90					95	
Glu	Glu	Glu	Glu	Thr	Met	Asp	Ser	Glu	Thr	Ala	Lys	Met	Ala	Cys	Pro
			100					105					110		
Arg	Asp	Gln	Met	Leu	Pro	Glu	Pro	Ile	Ser	Phe	Glu	Ala	Ala	Ala	Ile
		115				120						125			
Pro	Val	Ala	Glu	Lys	Glu	Glu	Ala	Leu	Leu	Pro	Glu	Pro	Asp	Val	Pro
	130					135					140				
Thr	Asp	Thr	Lys	Glu	Ser	Glu	Lys	Asp	Ala	Leu	Thr	Gln	Tyr	Pro	
145				150					155					160	
Arg	Tyr	Lys	Lys	Tyr	Gln	Leu	Ala	Cys	Thr	Lys	Asn	Val	Tyr	Asn	Ala
			165						170					175	
Ser	Ser	His	Ser	Thr	Ser	Gly	Phe	Ala	Ser	Thr	Phe	Arg	Glu	Asp	Asn
		180					185					190			
Ser	Ser	Asn	Ser	Leu	Lys	Pro	Gly	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Ser
	195					200						205			
Glu	Pro	Pro	Ser	Glu	Glu	Asn	Glu	Glu	Glu	Ser	Ile	Thr	Leu	Cys	Leu
	210					215					220				
Ser	Gly	Asp	Glu	Pro	Asp	Ala	Lys	Asp	Arg	Ala	Gly	Asp	Val	Glu	Met
225				230						235				240	
Asp	Arg	Lys	Gln	Pro	Ser	Pro	Ala	Pro	Thr	Pro	Thr	Ala	Pro	Ala	Gly
			245						250					255	
Ala	Ala	Cys	Leu	Glu	Arg	Ser	Arg	Ser	Val	Ala	Ser	Pro	Ser	Cys	Leu
		260					265							270	
Arg	Ser	Leu	Phe	Ser	Ile	Thr	Lys	Ser	Val	Glu	Leu	Ser	Gly	Leu	Pro

```

      275              280              285
Ser Thr Ser Gln Gln His Phe Ala Arg Ser Pro Ala Cys Pro Phe Asp
      290              295              300
Lys Gly Ile Thr Gln Gly Asp Leu Lys Thr Asp Tyr Thr Pro Phe Thr
      305              310              315              320
Gly Asn Tyr Gly Gln Pro His Val Gly Gln Lys Glu Val Ser Asn Phe
      325              330              335
Thr Met Gly Ser Pro Leu Arg Gly Pro Gly Leu Glu Ala Leu Cys Lys
      340              345              350
Gln Glu Gly Glu Leu Asp Arg Arg Ser Val Ile Phe Ser Ser Ser Ala
      355              360              365
Cys Asp Gln Val Ser Thr Ser Val His Ser Tyr Ser Gly Val Ser Ser
      370              375              380
Leu Asp Lys Asp Leu Ser Glu Pro Val Pro Lys Gly Leu Trp Val Gly
      385              390              395              400
Ala Gly Gln Ser Leu Pro Ser Ser Gln Ala Tyr Ser His Gly Gly Leu
      405              410              415
Met Ala Asp His Leu Pro Gly Arg Met Arg Pro Asn
      420              425

```

<210> 289  
 <211> 822  
 <212> DNA  
 <213> Homo sapiens

```

<400> 289
ngcattaccg ggctgaagac ggggtgctcat gacctcaacg atataggcta ttgctagaac
60
cacgccggcc cacgccgcgc aaagcgcaga cacggcacca ggaggggtca catggctgat
120
agcaagtcca aggcgaagga cgagcgcact gccgatgaga tcaggcggga tattgcagcg
180
acccgtgctt gcctggcagc cgggggtggag aacctcgtgg aggaggtgca tccggcaacc
240
ctcaagcgtg aagcatctga tcgtgcccggt gattttgtgc agggtagagt tgatcaggtc
300
aagagccagg tcaaagatga gaaatggtgg cgcgtgcagc ggatcgcgat ggccgcagga
360
gtgctcgctg ccggcgtcgt cagcattatt gtgctgcgcg cgatagtcgg tcgcgcaacg
420
ggcgtaccg ctctgcgcaa gcttgagaag ctgcagcttt ctcaggcgaa gcgggttcga
480
aaagatgcca agcagcgtag taaggaagat gaaaaggcag ccaagaaaaa tgccaagctc
540
ggcaagaaga acgctaagaa gtacggcaag ctcgataccg atgactcgtc ggtaagcaac
600
cttgccgaga aaatgctcaa acaggccgcc gtgctgcgtg cacaggcggc tgccggggcg
660
tgagaacagt gccgcctagc aaacagcggg cacagcgcaa aacaggtttg gctccgaccc
720
atgggtggacc ggagccaaac tgtgttaccg catcatttga taccgcagc agccaggcct
780
gcgacaatgc gacgctggaa taccagcacc atgatgacta gt
822

```



<210> 290  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 290  
 Met Ala Asp Ser Lys Ser Lys Ala Lys Asp Glu Arg Thr Ala Asp Glu  
 1 5 10 15  
 Ile Arg Arg Asp Ile Ala Ala Thr Arg Ala Cys Leu Ala Ala Gly Val  
 20 25 30  
 Glu Asn Leu Val Glu Glu Val His Pro Ala Thr Leu Lys Arg Glu Ala  
 35 40 45  
 Ser Asp Arg Ala Arg Asp Phe Val Gln Gly Glu Phe Asp Gln Val Lys  
 50 55 60  
 Ser Gln Val Lys Asp Glu Lys Trp Trp Arg Val Gln Arg Ile Ala Met  
 65 70 75 80  
 Ala Ala Gly Val Leu Ala Ala Gly Val Val Ser Ile Ile Val Leu Arg  
 85 90 95  
 Ala Ile Val Gly Arg Ala Thr Gly Ala Thr Ala Arg Arg Lys Leu Glu  
 100 105 110  
 Lys Leu Gln Leu Ser Gln Ala Lys Arg Val Arg Lys Asp Ala Lys Gln  
 115 120 125  
 Arg Ser Lys Glu Asp Glu Lys Ala Ala Lys Lys Asn Ala Lys Leu Gly  
 130 135 140  
 Lys Lys Asn Ala Lys Lys Tyr Gly Lys Leu Asp Thr Asp Asp Ser Ser  
 145 150 155 160  
 Val Ser Asn Leu Ala Glu Lys Met Leu Lys Gln Ala Ala Val Leu Arg  
 165 170 175  
 Ala Gln Ala Ala Ala Gly Ala  
 180

<210> 291  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
 ctccacgccg acaagactta cgacgggcgt cgctgccggg ctgagtgccg ggcccgtcc  
 60  
 atcacccccc gcatcgctcg ccgcggcgtg gagaccagcg agcgcttggg ccggtatcgc  
 120  
 tgggtcgtcg agcgcacctt cgctggctc aaccgcttcc ggcgcctcgc catccgctac  
 180  
 gagcggcgtg ctgacatcca cgaagccttc gtgacccctg gctgcgccct catctgcctc  
 240  
 aaccagatca gacggttttg ttaggtgctg taaagggaga atggctgcag ctgggctatc  
 300  
 tgctccctcg tcaaccagaa acaggctgct catcctcact caacaacgcg t  
 351

<210> 292  
 <211> 87  
 <212> PRT

<213> Homo sapiens

<400> 292

```

Leu His Ala Asp Lys Thr Tyr Asp Gly Arg Arg Cys Arg Ala Glu Cys
 1           5           10           15
Arg Ala Arg Ser Ile Thr Pro Arg Ile Ala Arg Arg Gly Val Glu Thr
 20           25           30
Ser Glu Arg Leu Gly Arg Tyr Arg Trp Val Val Glu Arg Thr Phe Ala
 35           40           45
Trp Leu Asn Arg Phe Arg Arg Leu Ala Ile Arg Tyr Glu Arg Arg Ala
 50           55           60
Asp Ile His Glu Ala Phe Val Ile Leu Gly Cys Ala Leu Ile Cys Leu
 65           70           75           80
Asn Gln Ile Arg Arg Phe Cys
                85

```

<210> 293

<211> 716

<212> DNA

<213> Homo sapiens

<400> 293

```

nncttcacca caccggccat caacgcacct cctcgtgata acttgacctt ctgccgaacc
60
ggttaatcag tttagtggcg aggcattgaca cgttgacgag tcagctgtgg tacatgtgcg
120
gaacactcac aatgccacgg cgcatgttg ctgtcgggtca cgacccttat ggtgatcgct
180
gtgagaaccc gaacggcaga tgcgattctg gcggcactgg atctgaacag gtttaagggt
240
gcgaagactt tcgatgttcc agtgtgcgtc atagctgggt cggggacagg taaaactcgt
300
gctgtcactc atcgattgca ctacgggtgca gcgacaggca agcttgatcc gcgtcgtacc
360
ctcgcgggtca cttttacgac taaggcagct ggcacgatga gaggtcgact cgccgatctg
420
ggggttgttg gtgtgcaggc tcgcactatt cattctgcgg cgttgcggca gatcaagttt
480
ttctggcctc gtgcatataa ctgtgagttg ccaccgggtga gtgattctcg tttctcgatg
540
gtggcggaga cgacccatcg cattgggtctg ggcaatgaca aggcgctgct gcgcgacttg
600
tccgccgaga tctcgtgggc gaaggtctca aatgtgccga ctgatcaata cgcacccctg
660
gctagggcgg aaggtcgggt ggtggcggga gtttcggcaa ctgacgtagg acgcgt
716

```

<210> 294

<211> 190

<212> PRT

<213> Homo sapiens

<400> 294

```

Met Leu Leu Ser Val Thr Thr Leu Met Val Ile Ala Val Arg Thr Arg

```

```

1           5           10           15
Thr Ala Asp Ala Ile Leu Ala Ala Leu Asp Leu Asn Arg Phe Lys Val
20           25           30
Ala Lys Thr Phe Asp Val Pro Val Cys Val Ile Ala Gly Ala Gly Thr
35           40           45
Gly Lys Thr Arg Ala Val Thr His Arg Ile Ala Tyr Gly Ala Ala Thr
50           55           60
Gly Lys Leu Asp Pro Arg Arg Thr Leu Ala Val Thr Phe Thr Thr Lys
65           70           75           80
Ala Ala Gly Thr Met Arg Gly Arg Leu Ala Asp Leu Gly Val Val Gly
85           90           95
Val Gln Ala Arg Thr Ile His Ser Ala Ala Leu Arg Gln Ile Lys Phe
100          105          110
Phe Trp Pro Arg Ala Tyr Asn Cys Glu Leu Pro Pro Val Ser Asp Ser
115          120          125
Arg Phe Ser Met Val Ala Glu Thr Thr His Arg Ile Gly Leu Gly Asn
130          135          140
Asp Lys Ala Leu Leu Arg Asp Leu Ser Ala Glu Ile Ser Trp Ala Lys
145          150          155          160
Val Ser Asn Val Pro Thr Asp Gln Tyr Ala Ser Leu Ala Arg Ala Glu
165          170          175
Gly Arg Val Val Ala Gly Val Ser Ala Thr Asp Val Gly Arg
180          185          190

```

&lt;210&gt; 295

&lt;211&gt; 417

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 295

```

ttcatatcag gcagtacccg agtccatgcg atcaacaacg tcagcgtatc tttcacccat
60
tctggagtgc accttctcat gggagaaagc ggatcaggaa aaagcaccct catcaatctc
120
ctagctggtc tggatacccc agattcgggg tccgtctacg cagaaggcgt caccgtatct
180
gatcagagcg aggcgagcag agcccaattt cgattacgcc acatcgccgt catcttcag
240
gacgacaacc tcatcgctga gttgaccaat accgagaata ttgcgctacc cctgtgggcg
300
cagggcacat cgaagtccga tgccactgaa atcgcccacg aagccatgcg aaaactagga
360
atcgagtcac tgggcagacg ctaccccggc gaggtctcgg gtggccaacg gcaacgc
417

```

&lt;210&gt; 296

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 296

```

Phe Ile Ser Gly Ser Thr Arg Val His Ala Ile Asn Asn Val Ser Val
1           5           10           15
Ser Phe Thr His Ser Gly Val His Leu Leu Met Gly Glu Ser Gly Ser

```

```

      20      25      30
Gly Lys Ser Thr Leu Ile Asn Leu Leu Ala Gly Leu Asp Thr Pro Asp
      35      40      45
Ser Gly Ser Val Tyr Ala Glu Gly Val Thr Val Ser Asp Gln Ser Glu
      50      55      60
Ala Ser Arg Ala Gln Phe Arg Leu Arg His Ile Ala Val Ile Phe Gln
      65      70      75      80
Asp Asp Asn Leu Ile Ala Glu Leu Thr Asn Thr Glu Asn Ile Ala Leu
      85      90      95
Pro Leu Trp Ala Gln Gly Thr Ser Lys Ser Asp Ala Thr Glu Ile Ala
      100      105      110
His Glu Ala Met Arg Lys Leu Gly Ile Glu Ser Leu Gly Arg Arg Tyr
      115      120      125
Pro Gly Glu Val Ser Gly Gly Gln Arg Gln Arg
      130      135

```

<210> 297  
 <211> 378  
 <212> DNA  
 <213> Homo sapiens

```

<400> 297
tacaccatcg gtgaccagat tgtcgaagct ctgcaggtgc actcgaagat gtccgacaag
60
gacgcttggg cgcgtgccat cgagctgctc gacttggtgg ggattccgaa tcccagagtg
120
cgtgccaaag cttttccgca cgagttttcc ggtggcatga ggcaacgagt cgtcatcgcc
180
atggccatcg cgaacgaccc tgacctcatc atcgccgacg agccgacgac ggccctcgac
240
gtgaccatcc aggcccagat tctcgatttg ctgcgcgtag cccagcgtga aacccatgcg
300
ggcgtcgtaa tgatcaccca cgacctcggt gtggtagctg gtctggctga cagggttgcc
360
gtgatgtatg ccggacgc
378

```

<210> 298  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

```

<400> 298
Tyr Thr Ile Gly Asp Gln Ile Val Glu Ala Leu Gln Val His Ser Lys
1      5      10      15
Met Ser Asp Lys Asp Ala Trp Ala Arg Ala Ile Glu Leu Leu Asp Leu
20      25      30
Val Gly Ile Pro Asn Pro Glu Val Arg Ala Lys Ala Phe Pro His Glu
35      40      45
Phe Ser Gly Gly Met Arg Gln Arg Val Val Ile Ala Met Ala Ile Ala
50      55      60
Asn Asp Pro Asp Leu Ile Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp
65      70      75      80
Val Thr Ile Gln Ala Gln Ile Leu Asp Leu Arg Val Ala Gln Arg

```

```

      85          90          95
Glu Thr His Ala Gly Val Val Met Ile Thr His Asp Leu Gly Val Val
      100          105          110
Ala Gly Leu Ala Asp Arg Val Ala Val Met Tyr Ala Gly Arg
      115          120          125

```

&lt;210&gt; 299

&lt;211&gt; 368

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 299

```

gtgcacggtt tcgtggcat gcgcaatgac cgggagaact tgcgttttga tccgagactt
60
ccagcccaat ggacgtcgat caaacaccac atgtctcattg gcgactctca catgctcggt
120
ttcctggaac gtgacgccat tacgttccag attctgtcgg gccatgaccg cgacgtgaca
180
gtgcgcggtg agctctacca cattgggggtt gagccggtga gggtgccgtt gtccgatcag
240
gggcccgttg gtcttagcct gcgcgttacc catccgatct cggggttgctg tcgagctgac
300
ggttctctta tcaactgcaga agttcccggc agcattgctg agacgattgg gtcttctccg
360
atctcgac
368

```

&lt;210&gt; 300

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 300

```

Val His Gly Phe Val Gly Met Arg Asn Asp Arg Glu Asn Leu Arg Phe
  1          5          10          15
Asp Pro Arg Leu Pro Ala Gln Trp Thr Ser Ile Lys His His Met Leu
      20          25          30
Ile Gly Asp Ser His Met Leu Val Phe Leu Glu Arg Asp Ala Ile Thr
      35          40          45
Phe Gln Ile Leu Ser Gly His Asp Arg Asp Val Thr Val Arg Gly Glu
      50          55          60
Leu Tyr His Ile Gly Val Glu Pro Val Arg Val Pro Leu Ser Asp Gln
      65          70          75          80
Gly Pro Leu Arg Pro Ser Leu Arg Val Thr His Pro Ile Ser Gly Leu
      85          90          95
Arg Arg Ala Asp Gly Ser Leu Ile Thr Ala Glu Val Pro Gly Ser Ile
      100          105          110
Ala Glu Thr Ile Gly Ser Ser Pro Ile Ser
      115          120

```

&lt;210&gt; 301

&lt;211&gt; 456

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 301

ggccggggtta ttgcccgcgc gtttgtcggg gaaacccggc agaccttcga gcgcaccggc  
60  
aaccggcgcg actattecgt accgccgcgc gaaccgacct tgctcgacag gcttacggac  
120  
gcggggccgga cggatgatcg aatcggaag attggtgata tctacgcgca caaaggcgtg  
180  
tctcaggtgc gtaaggcaat ggcaatattg gccttggtcg atgaaacct cattgccatg  
240  
gacgacgcgc aggacggcga tctggtcttc accaacttcg tggatttcga catgctctac  
300  
gggcatcgca gggatgtgcc cggctatgcc gccgcgctcg aggttttcga ccggaggctg  
360  
ccggaagcca tggcgaaatt gcggacgggc gatcttctga tcctgacagc cgatcatggc  
420  
tgcgaccgga ccctcaaggg aaccgaccac acgcgt  
456

&lt;210&gt; 302

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 302

Gly Arg Val Ile Ala Arg Pro Phe Val Gly Glu Thr Arg Gln Thr Phe  
1 5 10 15  
Glu Arg Thr Gly Asn Arg Arg Asp Tyr Ser Val Pro Pro Pro Glu Pro  
20 25 30  
Thr Leu Leu Asp Arg Leu Thr Asp Ala Gly Arg Thr Val Ile Ala Ile  
35 40 45  
Gly Lys Ile Gly Asp Ile Tyr Ala His Lys Gly Val Ser Gln Val Arg  
50 55 60  
Lys Ala Met Ala Ile Leu Ala Leu Phe Asp Glu Thr Leu Ile Ala Met  
65 70 75 80  
Asp Asp Ala Gln Asp Gly Asp Leu Val Phe Thr Asn Phe Val Asp Phe  
85 90 95  
Asp Met Leu Tyr Gly His Arg Arg Asp Val Pro Gly Tyr Ala Ala Ala  
100 105 110  
Leu Glu Ala Phe Asp Arg Arg Leu Pro Glu Ala Met Ala Lys Leu Arg  
115 120 125  
Thr Gly Asp Leu Leu Ile Leu Thr Ala Asp His Gly Cys Asp Pro Thr  
130 135 140  
Leu Lys Gly Thr Asp His Thr Arg  
145 150

&lt;210&gt; 303

&lt;211&gt; 402

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 303

nncgtgggca tcgaggagtt cctcgacatg aagtatcacg cgacgccgat tcctcgctgc  
60

tgacagcggg tttccggaac acatcagcgt tcagacagga gcgaggagac catgtacctg  
 120  
 ggtgctcagc tgttcagtga cagcgagtac gagcagcgcc tgagacgtgt ccgtgagctc  
 180  
 atggaccgtc aggggtctgtc ggcgatcatc gtcaccgatc cggccaacat cttctatctg  
 240  
 atcggttaca acgcctggtc gttctacacc ccgcagatgc tgttcgtgcc gatcgacgga  
 300  
 gagatgggtcc tctacgctcg cgagatggat cgcatggcgc acatcngcac gacgtcgttg  
 360  
 cccgccgac agatcgtcgg ttaccggag agttatgtgc ac  
 402

<210> 304

<211> 97

<212> PRT

<213> Homo sapiens

<400> 304

Met	Tyr	Leu	Gly	Ala	Gln	Leu	Phe	Ser	Asp	Ser	Glu	Tyr	Glu	Gln	Arg
1				5					10					15	
Leu	Arg	Arg	Val	Arg	Glu	Leu	Met	Asp	Arg	Gln	Gly	Leu	Ser	Ala	Ile
			20					25					30		
Ile	Val	Thr	Asp	Pro	Ala	Asn	Ile	Phe	Tyr	Leu	Ile	Gly	Tyr	Asn	Ala
		35				40					45				
Trp	Ser	Phe	Tyr	Thr	Pro	Gln	Met	Leu	Phe	Val	Pro	Ile	Asp	Gly	Glu
	50					55				60					
Met	Val	Leu	Tyr	Ala	Arg	Glu	Met	Asp	Arg	Met	Ala	His	Ile	Xaa	Thr
65					70				75					80	
Thr	Ser	Leu	Pro	Ala	Asp	Gln	Ile	Val	Gly	Tyr	Pro	Glu	Ser	Tyr	Val
			85					90						95	

His

<210> 305

<211> 375

<212> DNA

<213> Homo sapiens

<400> 305

nnacgcgtcg gttccgcatc gagcgaccgg atcgcatcga cgagcacgct gcaccagtgc  
 60  
 gtgtcgtcct ggccaatatg ggcgatcagc cggtagagtt cgggatcgtc gtcacactcg  
 120  
 gccgccattt cggatgcgac acgcgcgcct gcgcgctcgg cctccagcaa ctcgtcgagc  
 180  
 gtcgccacca gcgcggcgcg atcttcatgc ggagtcagat cggcgcgggc gtcaggccccg  
 240  
 tcgccatcgc tcggaatcga catgcagcac cctcctgccca ggatcgatgg cgtaatacgt  
 300  
 gcgacggtag acggcgcggtg ttgcacgaac gtgcaaatca gcgcgtgcct cgtgccatat  
 360  
 acgtcacatc atatg  
 375

<210> 306  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 306  
 Xaa Arg Val Gly Ser Ala Ser Ser Asp Arg Ile Ala Ser Thr Ser Thr  
 1 5 10 15  
 Leu His Gln Cys Val Ser Ser Trp Arg Ile Trp Ala Ile Ser Arg Tyr  
 20 25 30  
 Ser Ser Gly Ser Ser Leu Thr Ser Ala Ala Ile Ser Asp Ala Thr Arg  
 35 40 45  
 Ala Pro Ala Arg Ser Ala Ser Ser Asn Ser Ser Val Ala Thr Ser  
 50 55 60  
 Ala Ala Arg Ser Ser Cys Gly Val Arg Ser Ala Arg Ala Ser Gly Pro  
 65 70 75 80  
 Ser Pro Cys Val Gly Ile Asp Met Gln His Pro Pro Ala Arg Ile Asp  
 85 90 95  
 Gly Val Ile Arg Ala Thr Val His Gly Ala Cys Cys Thr Asn Val Gln  
 100 105 110  
 Ile Ser Ala Cys Leu Val Pro Tyr Thr Ser His His Met  
 115 120 125

<210> 307  
 <211> 685  
 <212> DNA  
 <213> Homo sapiens

<400> 307  
 actagttctg gccgctcccc tggggctttg ggtaacaatt gtcagcccca cccatcctag  
 60  
 ggtaggaag gctattctct ttggccactc tcatacctaag acctatttgg agaacctctg  
 120  
 ggggtttgagt ctttttttca gcagaatgag gcttgatccc gcattatagc acctcgacaca  
 180  
 tttgatgtct cttcttttca cccactcacc ccaccctggg gggtggggca aaaaagtggc  
 240  
 tcaaagctgc ggttcagagt tccttgtaaa caaggctcct ccctcactgt cctcaccctg  
 300  
 ctccagcaga gggagcagcg gaaggaccac tctgctgcag ccatgcttgt ttctaaccaca  
 360  
 gcagaactgg acataatggg aacagggtct gaagacaatc aatccagggc tgcagtgggt  
 420  
 gctgagtctg gggaagcctc cacctggagg ggcagctggg cagtggcagc tcccttgga  
 480  
 tggctcagcc tctggacatc accccaccca accagagccc tggctcttgc tggatgtcca  
 540  
 cagatgagtg cctgggattg gtctcagcca ctatgggggg gatgtgcagg gagaggtgat  
 600  
 gagggagtga gcaggactgt ctatgtgcct ctgtcctcat cctgaggctt gggctctgaaa  
 660  
 ttggtgctgc agcactggca cgcgt  
 685



<210> 308  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 308  
 Met Leu Val Ser Asn Pro Ala Glu Leu Asp Ile Met Gly Thr Gly Ser  
 1 5 10 15  
 Glu Asp Asn Gln Ser Arg Ala Ala Val Gly Ala Glu Ser Gly Glu Ala  
 20 25 30  
 Ser Thr Trp Arg Gly Ser Trp Ala Val Ala Ala Pro Leu Glu Trp Leu  
 35 40 45  
 Ser Leu Trp Thr Ser Pro His Pro Thr Arg Ala Leu Ala Leu Ala Gly  
 50 55 60  
 Cys Pro Gln Met Ser Ala Trp Asp Trp Ser Gln Pro Leu Trp Gly Gly  
 65 70 75 80  
 Cys Ala Gly Arg Gly Asp Glu Gly Val Ser Arg Thr Val Tyr Val Pro  
 85 90 95  
 Leu Ser Ser Ser  
 100

<210> 309  
 <211> 432  
 <212> DNA  
 <213> Homo sapiens

<400> 309  
 caggctcgta ctattcgat ccctgtgcat atggctcgagg tcatcaataa gctggctcgc  
 60  
 gtccagcgtc agatgctcca ggacctaggt cgtgagccca ccccggaaga gcttgccaac  
 120  
 gaactcgata tgaccgcaga gaaggtcatt gaggtgcaga aatacggtcg cgagccgac  
 180  
 tcgctgcata cccactggg tgaggatggc gattctgagt tcggtgacct tattgaggat  
 240  
 tccgaggcca tcgtgccagc agacgccgtc aacttcaccc tgttcagga gcagctgcat  
 300  
 gatgtcctcg ataccttgtc cgagcgagag gccggtgtcg tgcgatgcg attcggttg  
 360  
 accgacggac agcccaagac cctggatgag atcggcaaag tctacggtgt tactcgggag  
 420  
 cgcacccgcc ag  
 432

<210> 310  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 310  
 Gln Ala Arg Thr Ile Arg Ile Pro Val His Met Val Glu Val Ile Asn  
 1 5 10 15  
 Lys Leu Ala Arg Val Gln Arg Gln Met Leu Gln Asp Leu Gly Arg Glu

```

      20      25      30
Pro Thr Pro Glu Glu Leu Ala Asn Glu Leu Asp Met Thr Ala Glu Lys
      35      40      45
Val Ile Glu Val Gln Lys Tyr Gly Arg Glu Pro Ile Ser Leu His Thr
      50      55      60
Pro Leu Gly Glu Asp Gly Asp Ser Glu Phe Gly Asp Leu Ile Glu Asp
65      70      75      80
Ser Glu Ala Ile Val Pro Ala Asp Ala Val Asn Phe Thr Leu Leu Gln
      85      90      95
Glu Gln Leu His Asp Val Leu Asp Thr Leu Ser Glu Arg Glu Ala Gly
      100      105      110
Val Val Ser Met Arg Phe Gly Leu Thr Asp Gly Gln Pro Lys Thr Leu
      115      120      125
Asp Glu Ile Gly Lys Val Tyr Gly Val Thr Arg Glu Arg Ile Arg Gln
      130      135      140

```

<210> 311  
 <211> 358  
 <212> DNA  
 <213> Homo sapiens

```

<400> 311
acgcgtatcg aaaatatccc tccattatt accgctcgcc ctgaactgat ggctcatgaa
60
ctgacgccag aatctcttga tgcgagcctg gagtgggccc atgtgggtgt cattggtcct
120
ggactgggac aacaagcgtg gggcaaaaaa gcgctacaaa aggtcgagaa ttgtcgtaaa
180
ccgatgctgt gggatgccga cgcgcttaac cttctggcaa tcaatcctga taaacgtcac
240
aatcgcatcc tgacgccaca ccccggcgag gccgcgcggc tgcttagctg cagcgtcgca
300
gaaattgaaa acgatcgctt acttntctgc gcacgtctgg taaaacggta acccgagt
358

```

<210> 312  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

```

<400> 312
Thr Arg Ile Glu Asn Ile Pro Pro Ile Ile Thr Ala Arg Pro Glu Leu
1      5      10      15
Met Ala His Glu Leu Thr Pro Glu Ser Leu Asp Ala Ser Leu Glu Trp
      20      25      30
Ala Asp Val Val Val Ile Gly Pro Gly Leu Gly Gln Gln Ala Trp Gly
      35      40      45
Lys Lys Ala Leu Gln Lys Val Glu Asn Cys Arg Lys Pro Met Leu Trp
      50      55      60
Asp Ala Asp Ala Leu Asn Leu Leu Ala Ile Asn Pro Asp Lys Arg His
65      70      75      80
Asn Arg Ile Leu Thr Pro His Pro Gly Glu Ala Ala Arg Leu Leu Ser
      85      90      95
Cys Ser Val Ala Glu Ile Glu Asn Asp Arg Leu Leu Xaa Cys Ala Arg

```

100 105 110  
 Leu Val Lys Arg  
 115  
 <210> 313  
 <211> 347  
 <212> DNA  
 <213> Homo sapiens  
 <400> 313  
 ncaactgaaa gcattgagat gagcgacgtg ctgtccccct tccacccac caaggccaac  
 60  
 acccctggtg gcgaaccgcg caccatccgc acctcgaacg cgcacatcat tgccgtcacc  
 120  
 agtggcгааг gcggcggtggg caagaccttt gtctccgcca acctggccgc cgcgctgacc  
 180  
 cgcctgggac tgcgcgtgct ggtactggac gccgacctgg gcctggccaa cttggacgtg  
 240  
 gtgctgaacc tctaccccaa ggtgacgctg cacgatgtgt tcaccggcaa ggcctcgctg  
 300  
 caagacgagg tggtcacggc ccccgggcggc ttccatgtgc tgetagc  
 347

<210> 314  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 314  
 Xaa Thr Glu Ser Ile Glu Met Ser Asp Val Leu Ser Pro Phe His Pro  
 1 5 10 15  
 Thr Lys Ala Asn Thr Pro Gly Gly Glu Pro Arg Thr Ile Arg Thr Ser  
 20 25 30  
 Asn Ala His Ile Ile Ala Val Thr Ser Gly Lys Gly Gly Val Gly Lys  
 35 40 45  
 Thr Phe Val Ser Ala Asn Leu Ala Ala Leu Thr Arg Leu Gly Leu  
 50 55 60  
 Arg Val Leu Val Leu Asp Ala Asp Leu Gly Leu Ala Asn Leu Asp Val  
 65 70 75 80  
 Val Leu Asn Leu Tyr Pro Lys Val Thr Leu His Asp Val Phe Thr Gly  
 85 90 95  
 Lys Ala Ser Leu Gln Asp Ala Val Val Thr Ala Pro Gly Gly Phe His  
 100 105 110  
 Val Leu Leu  
 115

<210> 315  
 <211> 544  
 <212> DNA  
 <213> Homo sapiens

<400> 315  
 nnacgcgttc gtcaacagga aaacaacaac ggcttctcgc tggaggggaac catgcttgcc  
 60

gaagatatct acgcgatcat gctgttttca tcgctcatcc tggctgtccc ggggccatcc  
 120  
 aacaccttgc tgctcagcgc ccgtttccat ttcggctcgc tgcgggcggc gcccttcac  
 180  
 ctgcttgagg cggtgggcta ctcgctatcc atttcggcat ggggctgggt attggcgcgc  
 240  
 ctgtccgaga gcaatccatg gatcatcagt ctgaccaagg cactctgcgc gctatatgtg  
 300  
 gcgcttctgg cggtgaagac ctggaatgcc ntcgatccgc agtgccgggc cggtaaattc  
 360  
 cgccatgggc ccttgcacct gttcgtggca accctgtcga acccgaaggc gctgatcttc  
 420  
 gccagcgtga tctttcccg caaggcgttc ctcgacttct ggaacaacta cacgatctcg  
 480  
 ctgctggcct tcttggttgt gctggcgccc atcgggatgc tttgggtcgg gctgggggcc  
 540  
 ggta  
 544

<210> 316  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 316  
 Ile Tyr Ala Ile Met Leu Phe Ser Ser Leu Ile Leu Val Val Pro Gly  
 1 5 10 15  
 Pro Ser Asn Thr Leu Leu Leu Ser Ala Arg Phe His Phe Gly Ser Leu  
 20 25 30  
 Arg Ala Ala Pro Phe Ile Leu Leu Glu Ala Leu Gly Tyr Ser Leu Ser  
 35 40 45  
 Ile Ser Ala Trp Gly Trp Val Leu Ala Arg Leu Ser Glu Ser Asn Pro  
 50 55 60  
 Trp Ile Ile Ser Leu Thr Lys Ala Leu Cys Ala Leu Tyr Val Ala Leu  
 65 70 75 80  
 Leu Ala Val Lys Thr Trp Asn Ala Xaa Asp Pro Gln Cys Gly Ala Gly  
 85 90 95  
 Asn Phe Arg His Gly Pro Leu Pro Leu Phe Val Ala Thr Leu Ser Asn  
 100 105 110  
 Pro Lys Ala Leu Ile Phe Ala Ser Val Ile Phe Pro Gly Lys Ala Phe  
 115 120 125  
 Leu Asp Phe Trp Asn Asn Tyr Thr Ile Ser Leu Leu Ala Phe Leu Val  
 130 135 140  
 Val Leu Ala Pro Ile Gly Met Leu Trp Val Gly Leu Gly Ala Gly  
 145 150 155

<210> 317  
 <211> 343  
 <212> DNA  
 <213> Homo sapiens

<400> 317  
 nggtcagcct ctgcgccagg caattctctt aagatacatg agctgctatg agtaccaaag  
 60

ccagagggtt gtccactgag agaagcacat tggaaaagggg ggcgtgggcc tgggactgtg  
 120  
 tggcacttta tgcacggggg gggcctaagg gggnggtcc accaaccatg cactgngggg  
 180  
 ggggtgtggg taacatgccg tgcattttgg ggggtgtgcca tgagtggcac accatggggg  
 240  
 tggcatgtgg ggcattgatg catgtggtgt tggcgagca aactcagctc ttacctggct  
 300  
 ggggccagcc tctaaaactt ctcacattgg gctcccttct gac  
 343

<210> 318

<211> 98

<212> PRT

<213> Homo sapiens

<400> 318

Met	Ser	Thr	Lys	Ala	Arg	Gly	Leu	Ser	Thr	Glu	Arg	Ser	Thr	Leu	Glu
1			5					10					15		
Arg	Gly	Ala	Trp	Ala	Trp	Asp	Cys	Val	Ala	Leu	Tyr	Ala	Arg	Gly	Gly
		20					25					30			
Pro	Lys	Gly	Gly	Gly	Pro	Pro	Thr	Met	His	Xaa	Gly	Trp	Gly	Val	Gly
		35					40					45			
Asn	Met	Pro	Cys	Ile	Leu	Gly	Val	Cys	His	Glu	Trp	His	Thr	Met	Gly
	50					55					60				
Val	Ala	Cys	Gly	Ala	Cys	Met	His	Val	Val	Leu	Ala	Gln	Gln	Thr	Gln
65					70					75				80	
Leu	Leu	Pro	Gly	Trp	Gly	Gln	Pro	Leu	Lys	Leu	Leu	Thr	Leu	Gly	Ser
			85					90						95	
Leu	Leu														

<210> 319

<211> 429

<212> DNA

<213> Homo sapiens

<400> 319

gaattctcga tgtaccccct cccggcagtc ctattctcga gctgagcggg cacagtggcc  
 60  
 ccgttaacag tgtggcttgg ggtccacca gccagagcac gttgcgaaat ggacctagta  
 120  
 agggcatgat atgtacagga ggcgacgatg ctcaagtgcct cgtatatgat ctgactagct  
 180  
 caactcttcg aacagcatct gctcaaggac ggcgctctcg aaacagtcca tataaaca  
 240  
 gccattcacc gggaatagac ggatggcgtg tcggcgagca agtgccggtg ctcgcttata  
 300  
 cggccccgctc tatggtcaac aatgctagct ggctcggcat gcctgcgcca taaaacgca  
 360  
 catcgctaca gagcaaacac cgcagccttt accgcagctt actcagttag tggactgagt  
 420  
 atacgtccn  
 429

<210> 320  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 320  
 Met Ile Cys Thr Gly Gly Asp Asp Ala Gln Cys Leu Val Tyr Asp Leu  
 1 5 10 15  
 Thr Ser Ser Thr Leu Arg Thr Ala Ser Ala Gln Gly Arg Arg Ser Arg  
 20 25 30  
 Asn Ser Pro Tyr Lys Gln Ser His Ser Pro Gly Ile Asp Gly Trp Arg  
 35 40 45  
 Val Gly Ala Glu Val Pro Val Leu Ala Tyr Thr Ala Pro Ser Met Val  
 50 55 60  
 Asn Asn Ala Ser Trp Leu Gly Met Pro Ala Pro Ser Lys Arg Thr Ser  
 65 70 75 80  
 Leu Gln Ser Lys His Arg Ser Leu Tyr Arg Ser Leu Leu Ser Glu Trp  
 85 90 95  
 Thr Glu Tyr Thr Ser  
 100

<210> 321  
 <211> 530  
 <212> DNA  
 <213> Homo sapiens

<400> 321  
 ngtgcacgac gtgctcgcca agtcctcgg gtcctctaata gcgatcaacg tgggtcacgc  
 60  
 caccgtcgat gcgttgacgc agctcgagga gcccgagag gtcgcccgtc gccgcggcaa  
 120  
 gtccgttgag gagatcgccc cagcagccat gctgcgtgcg cgcaaggagg ccgacgaggc  
 180  
 cgccgctgct gcccgcatgg aggaaaaggc ggggggtaac tgatgagcaa gctgaagatc  
 240  
 acccagatca agtctggcat cgctaccaag ccaaatacgc gtgagaccct gcgcagcctc  
 300  
 ggactgaagc gtattggtga cacggatcac aaggaggacc gcccgagatt ccgcggcatg  
 360  
 gtccggaccg ttcgtcacct cgtcaccatg gaagaggtgg actgacatgg ctattgagct  
 420  
 ccatgacctc aagcccgtc ctggtgcccc caaggccaag acccgcggtg gtcgtggtga  
 480  
 ggggtccaag ggtaagaccg ctggtcgagg taccaagggc accggtgcac  
 530

<210> 322  
 <211> 60  
 <212> PRT  
 <213> Homo sapiens

<400> 322  
 Met Ser Lys Leu Lys Ile Thr Gln Ile Lys Ser Gly Ile Ala Thr Lys

```

      1             5             10             15
Pro Asn His Arg Glu Thr Leu Arg Ser Leu Gly Leu Lys Arg Ile Gly
      20             25             30
Asp Thr Val Ile Lys Glu Asp Arg Pro Glu Phe Arg Gly Met Val Arg
      35             40             45
Thr Val Arg His Leu Val Thr Met Glu Glu Val Asp
      50             55             60

```

<210> 323  
 <211> 468  
 <212> DNA  
 <213> Homo sapiens

```

<400> 323
ntccggaccc gctgtggcca cgtattctgc cgttcctgta ttgctaccag tctaaagaac
60
aacaagtgga cctgtcctta ttgccgggca tatcttcctt cagaaggagt tccagcaact
120
gatgtagcca aaagaatgaa atcagagtat aagaactgcg ctgagtgtga caccctgggt
180
tgcctcagtg aaatgagggc acatattcgg acttgtcaga agtacataga taagtatgga
240
ccactacaag aacttgagga gacagcagca aggtgtgtat gtcccttttg tcagagggaa
300
ctgtatgaag acagcttgct ggatcattgt attactcatc acagatcgga acggaggcct
360
gtgttctgtc cactttgcca ttttaataccc gatgagaatc caagcagctt cagtggcagt
420
ttaataagac atctgcaagt tagtcacact ttggtttatg atgatttc
468

```

<210> 324  
 <211> 156  
 <212> PRT  
 <213> Homo sapiens

```

<400> 324
Xaa Arg Thr Arg Cys Gly His Val Phe Cys Arg Ser Cys Ile Ala Thr
1             5             10             15
Ser Leu Lys Asn Asn Lys Trp Thr Cys Pro Tyr Cys Arg Ala Tyr Leu
      20             25             30
Pro Ser Glu Gly Val Pro Ala Thr Asp Val Ala Lys Arg Met Lys Ser
      35             40             45
Glu Tyr Lys Asn Cys Ala Glu Cys Asp Thr Leu Val Cys Leu Ser Glu
      50             55             60
Met Arg Ala His Ile Arg Thr Cys Gln Lys Tyr Ile Asp Lys Tyr Gly
65             70             75             80
Pro Leu Gln Glu Leu Glu Glu Thr Ala Ala Arg Cys Val Cys Pro Phe
      85             90             95
Cys Gln Arg Glu Leu Tyr Glu Asp Ser Leu Leu Asp His Cys Ile Thr
      100            105            110
His His Arg Ser Glu Arg Arg Pro Val Phe Cys Pro Leu Cys His Leu
      115            120            125
Ile Pro Asp Glu Asn Pro Ser Ser Phe Ser Gly Ser Leu Ile Arg His

```

130 135 140  
 Leu Gln Val Ser His Thr Leu Val Tyr Asp Asp Phe  
 145 150 155

<210> 325

<211> 374

<212> DNA

<213> Homo sapiens

<400> 325

acgcgtgaag ggaggacgag gaagtaacgg gaagcacaag gccgctgctg gggagatggc  
 60  
 actggagccc cctaggaagc atctcacagg ctgtggccct tggcacgggg atctggggcc  
 120  
 aggtcagcgc caggtctggg tatcatgcga gtgcgggctc gctggggcgg gaaagagttt  
 180  
 ggagctctgc tcccaggga tcccactcc cgcagatgac ttgcccgaga gatttctgct  
 240  
 ggtggatttt gatggaaatt ctatttgatc gcaccactt ggttcactgt gtgcttcgg  
 300  
 gtccccaggt tttaggtgct tcatgccctg ctgggaacga gacacgctcc tgcctcagt  
 360  
 gaatcttcag tcta  
 374

<210> 326

<211> 108

<212> PRT

<213> Homo sapiens

<400> 326

Met Lys His Leu Lys Pro Gly Asp Pro Glu Ala His Ser Glu Pro Ser  
 1 5 10 15  
 Gly Cys Asp Gln Ile Glu Phe Pro Ser Lys Ser Thr Ser Arg Thr Leu  
 20 25 30  
 Ser Gly Lys Ser Ser Ala Gly Val Gly Ile Pro Trp Glu Gln Ser Ser  
 35 40 45  
 Lys Leu Phe Pro Ala Pro Ala Ser Pro His Ser His Asp Thr Gln Thr  
 50 55 60  
 Cys Ala Arg Pro Gly Pro Arg Ser Pro Cys Gln Gly Pro Gln Pro Val  
 65 70 75 80  
 Arg Cys Phe Leu Gly Gly Ser Ser Ala Ile Ser Pro Ala Ala Ala Leu  
 85 90 95  
 Cys Phe Pro Leu Leu Pro Arg Pro Pro Phe Thr Arg  
 100 105

<210> 327

<211> 538

<212> DNA

<213> Homo sapiens

<400> 327

cactataaaa tccagtttgg ggcccgtgtt ctttcctatt ggtctgtcag gtgaaaaact  
 60



ccggctgggg gaaaagcgtc cggtggtttg ttggtaaaga gggcgctga tgggctctgg  
 120  
 ggaatggagg atggcgcacc ggctgtgggt ggactgtgga aacggggggg ggcagtgccg  
 180  
 gggtagttgt cctgctggtc tggttttggg atcctgggct ggagaaatgc gatccaaaag  
 240  
 agctcgggat gggctcagag cgacccacga aaataccagg ggccaagtaa aatgaaccca  
 300  
 ccctttaaca gtgcacaaag cgctggcaca cggtcacgt ctggtgacgc aggctgcccg  
 360  
 aagcgctcca accattttgc aaacctggga gagcaagagg ggctctgcag gtctagccgc  
 420  
 cgccctgtc ccactctggc cagccggagt ttttcaccta cagaccaata ggaaagaaca  
 480  
 cgggccccaa actggatttt atagtctgag ctctcagcat ctaaggaatg atatgccc  
 538

<210> 328

<211> 125

<212> PRT

<213> Homo sapiens

<400> 328

Met	Val	Gly	Ala	Leu	Arg	Ala	Ala	Cys	Val	Thr	Arg	Arg	Gly	Pro	Cys
1				5				10					15		
Ala	Ser	Ala	Leu	Cys	Thr	Val	Lys	Gly	Trp	Val	His	Phe	Thr	Trp	Pro
			20				25						30		
Leu	Val	Phe	Ser	Trp	Val	Ala	Leu	Ser	Pro	Ser	Arg	Ala	Leu	Leu	Asp
		35				40						45			
Arg	Ile	Ser	Pro	Ala	Gln	Asp	Pro	Lys	Thr	Arg	Pro	Ala	Gly	Gln	Leu
	50				55						60				
Pro	Arg	His	Cys	His	Pro	Pro	Phe	Pro	Gln	Ser	Thr	His	Ser	Arg	Cys
65				70					75					80	
Ala	Ile	Leu	His	Ser	Pro	Glu	Pro	Ile	Thr	His	Pro	Leu	Tyr	Gln	Gln
			85					90						95	
Thr	Thr	Gly	Arg	Phe	Ser	Pro	Ser	Arg	Ser	Phe	Ser	Pro	Asp	Arg	Pro
			100					105					110		
Ile	Gly	Lys	Asn	Thr	Gly	Pro	Lys	Leu	Asp	Phe	Ile	Val			
		115					120					125			

<210> 329

<211> 407

<212> DNA

<213> Homo sapiens

<400> 329

tccggagagt tccctcccca ggaattcctt ctaagaatcc atgtggaaat agagcctgaa  
 60  
 gctcttcagt ctttctgctc cactgagcag tgttttcttg atacccttgg taccctgcca  
 120  
 gcagcctcgt tatgactcct aactccattg ccctccatgg cccctggggc ctctctctct  
 180  
 ctttctctcc aggtagtaga gcactgcttc tggcttcttg tgcacagaag ggtttccac  
 240

agctgagagc tgggctccta ctgacatagt tatttccttt atatactgcc ccaccttctt  
 300  
 ctggtagcac acagcaacct tgcatagtag ctggtatcat taccttccca atcaacaggc  
 360  
 cttgatttct tataggactt tttctctcag atttacattg cttcttt  
 407

<210> 330

<211> 113

<212> PRT

<213> Homo sapiens

<400> 330

Met Ile Pro Ala Thr Met Gln Gly Cys Cys Val Leu Pro Glu Glu Gly  
 1 5 10 15  
 Gly Ala Gly Tyr Lys Gly Asn Asn Tyr Val Ser Arg Ser Pro Ala Leu  
 20 25 30  
 Ser Cys Gly Lys Pro Phe Cys Ala Gln Glu Ala Arg Ser Ser Ala Leu  
 35 40 45  
 Leu Pro Gly Glu Lys Glu Arg Glu Ser Ala Gln Gly Pro Trp Arg Ala  
 50 55 60  
 Met Glu Leu Gly Val Ile Thr Arg Leu Leu Ala Gly Tyr Gln Gly Tyr  
 65 70 75 80  
 Gln Glu Asn Thr Ala Gln Trp Ser Arg Lys Thr Glu Glu Leu Gln Ala  
 85 90 95  
 Leu Phe Pro His Gly Phe Leu Glu Gly Ile Pro Gly Glu Gly Thr Leu  
 100 105 110  
 Arg

<210> 331

<211> 523

<212> DNA

<213> Homo sapiens

<400> 331

tgtaccgaac ctgctggtct cgagggcctt gctgggctcg tcgtacgcac agctgacgaa  
 60  
 tccaccggcc cccatcccgg cgccactttc gctgaggcca tggagtcgat cggagccagc  
 120  
 tacgacggat cggccgggtt ggccggaagt cacgtcggcg tcgatgtgcc cgtgacaagg  
 180  
 ttcgacgcag cggtgaact cttcgtcgaa ttgttgaaca ccacgagcct ggttgaagag  
 240  
 gacatcgccc gtcagatcga cgcggcgcca gcctccctgg cccagaccag ccagcgcgga  
 300  
 tcggccctag ccgagatggc agcagcacgt gcgctatggc cagtggggtc acggtcgtcc  
 360  
 ctgcccacga tcggtaccct ctcgtcggtg gaaaagctca acgccgcagc cgcacgagaa  
 420  
 ttctggggcg cgcactggac gatctccgat gccgtgctgg tggttgccgg agagggagtc  
 480  
 gaggacctcg acttgtcaat attcaaggag tggacgacca gct  
 523

<210> 332  
 <211> 174  
 <212> PRT  
 <213> Homo sapiens

<400> 332  
 Cys Thr Glu Pro Ala Gly Leu Glu Gly Leu Ala Gly Leu Val Val Arg  
 1 5 10 15  
 Thr Ala Asp Glu Ser Thr Gly Pro His Pro Gly Ala Thr Phe Ala Glu  
 20 25 30  
 Ala Met Glu Ser Ile Gly Ala Ser Tyr Asp Gly Ser Ala Gly Leu Ala  
 35 40 45  
 Gly Ser His Val Gly Val Asp Val Pro Val Thr Arg Phe Asp Ala Ala  
 50 55 60  
 Ala Glu Leu Phe Val Glu Leu Leu Asn Thr Thr Ser Leu Val Glu Glu  
 65 70 75 80  
 Asp Ile Ala Arg Gln Ile Asp Ala Ala Arg Ala Ser Leu Ala Gln Thr  
 85 90 95  
 Ser Gln Arg Gly Ser Ala Leu Ala Glu Met Ala Ala Arg Ala Leu  
 100 105 110  
 Trp Pro Val Gly Ser Arg Ser Ser Leu Pro Thr Ile Gly Thr Leu Ser  
 115 120 125  
 Ser Val Glu Lys Leu Asn Ala Ala Ala Arg Glu Phe Trp Ala Ala  
 130 135 140  
 His Trp Thr Ile Ser Asp Ala Val Leu Val Val Ala Gly Glu Gly Val  
 145 150 155 160  
 Glu Asp Leu Asp Leu Ser Ile Phe Lys Glu Trp Thr Thr Ser  
 165 170

<210> 333  
 <211> 372  
 <212> DNA  
 <213> Homo sapiens

<400> 333  
 nntgttcgtc gtgtcgaccc ggaactcaag gcccgagcga tgacggtgaa ggtgccaacc  
 60  
 gatccccatc accgcccggg agttccattg aagtctgcga aggaccgtat ggacatcatt  
 120  
 tctgcttacc gagaactcgg aagctatcgc gccgcagccg aggtgtgcgg caccaccac  
 180  
 aagaccgtca agcgggtggt cgatcggttt gaagccggcg atccaccac cggtggcaag  
 240  
 gaacgggccc gcaactacga tgcggtggcc cagctcgtcg cgcagcgagt cgcgcggtca  
 300  
 caccggccga tcaactgcaa acggctgcta ccggtagcgc gagcggcagg atatgagggg  
 360  
 tcggcgcgga at  
 372

<210> 334  
 <211> 88  
 <212> PRT

<213> Homo sapiens

<400> 334

```

Met Asp Ile Ile Ser Ala Tyr Arg Glu Leu Gly Ser Tyr Arg Ala Ala
 1           5           10           15
Ala Glu Val Cys Gly Thr Thr His Lys Thr Val Lys Arg Val Val Asp
      20           25           30
Arg Phe Glu Ala Gly Asp Pro Pro Thr Gly Gly Lys Glu Arg Ala Arg
      35           40           45
Asn Tyr Asp Ala Val Ala Gln Leu Val Ala Gln Arg Val Ala Arg Ser
      50           55           60
His Gly Arg Ile Thr Ala Lys Arg Leu Leu Pro Val Ala Arg Ala Ala
      65           70           75           80
Gly Tyr Glu Gly Ser Ala Arg Asn
      85

```

<210> 335

<211> 356

<212> DNA

<213> Homo sapiens

<400> 335

```

gtgcacgcct tgctgggcga gggcgatgcg cctgcgcgca ccttcgtgga cggtagccttt
60
ggcaggggag ggcattcgcg gctcatcctg cagcgggttg ggccgcaagg ccgcctgggtg
120
gcgttcgaca aggacaccga agccattcaa gcagcggcgc gcatcacgga tgcgcgcttt
180
tccatcnggc accagggggt cagccatctc ggggaactgc ccgccgccag cgtgtccggt
240
gtgctgctgg acctgggcgt gagctccccg cagatcgacg acccccagcg cgggttcagt
300
tttcgtttcg atggtccgct ggacatgcgc atggacacca ctccgatgca tggatg
356

```

<210> 336

<211> 118

<212> PRT

<213> Homo sapiens

<400> 336

```

Val His Ala Leu Leu Gly Glu Gly Asp Ala Pro Ala Arg Thr Phe Val
 1           5           10           15
Asp Gly Thr Phe Gly Arg Gly Gly His Ser Arg Leu Ile Leu Gln Arg
      20           25           30
Leu Gly Pro Gln Gly Arg Leu Val Ala Phe Asp Lys Asp Thr Glu Ala
      35           40           45
Ile Gln Ala Ala Ala Arg Ile Thr Asp Ala Arg Phe Ser Ile Xaa His
      50           55           60
Gln Gly Phe Ser His Leu Gly Glu Leu Pro Ala Ala Ser Val Ser Gly
      65           70           75           80
Val Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Ile Asp Asp Pro Gln
      85           90           95
Arg Gly Phe Ser Phe Arg Phe Asp Gly Pro Leu Asp Met Arg Met Asp

```

100 105 110  
 Thr Thr Pro Met His Gly  
 115  
 <210> 337  
 <211> 447  
 <212> DNA  
 <213> Homo sapiens  
 <400> 337  
 cagcctctct ccgaccgcgc cgggtgtgaag cacgggcatg ccggtgtgca agtggcacca  
 60  
 cagccaaaac agcgagctca cacttcaaac tccttcaaag accccaggcc tctgtaagaa  
 120  
 ccgctcatct ctgtgccac agtcccccg cttccatgtg acccagaaat ggaaccacgc  
 180  
 agcagaggcg gggatcacag gtgaagcagc tgtgaacatt tgcttcaggc ttctgtgcaa  
 240  
 acaggcgcca tcatgtcagc cggtgagcag gagcaacgtg cgtgggtcag ggggtggcca  
 300  
 caggtccaac ttataagaa atgacagatt ccctgatggc catagggatc tgcagggcca  
 360  
 gcagcaggca taggacttcc ggtggccctg cgtcttcac aacactgagt attgtcaggg  
 420  
 tttctgtact gtttttacag ccaattg  
 447  
 <210> 338  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens  
 <400> 338  
 Met Pro Val Cys Lys Trp His His Ser Gln Asn Ser Glu Leu Thr Leu  
 1 5 10 15  
 Gln Thr Pro Ser Lys Thr Pro Gly Leu Cys Lys Asn Arg Ser Ser Leu  
 20 25 30  
 Cys Pro Gln Leu Pro Arg Phe His Val Thr Gln Lys Trp Asn His Ala  
 35 40 45  
 Ala Glu Ala Gly Ile Thr Gly Glu Ala Ala Val Asn Ile Cys Phe Arg  
 50 55 60  
 Leu Leu Cys Lys Gln Ala Pro Ser Cys Gln Pro Val Ser Arg Ser Asn  
 65 70 75 80  
 Val Arg Gly Ser Gly Gly His Thr Ser Asn Phe Ile Arg Asn Asp  
 85 90 95  
 Arg Phe Pro Asp Gly His Arg Asp Leu Gln Gly Gln Gln Gln Ala  
 100 105 110  
 <210> 339  
 <211> 588  
 <212> DNA  
 <213> Homo sapiens  
 <400> 339

tctagaatga agcgctgtat cctagcaccg gcagacgtac caagactatc aagggcgtca  
 60  
 gatcgtttat cctgcagttg ccattcatca gacaaatcca gtggaacca atggaagaca  
 120  
 ccgacctgca agcgctgatg gccagactcg aattgctaata tgatcgggtc gagcaactta  
 180  
 agagtcaaaa cggactccta ttagctcagg aaaagacctg ggcgcganaa cgcgctcacc  
 240  
 tcattgaaaa aaacgaaatc gcccgcgta aggtcgaatc gatgatttcg cgcctgaagg  
 300  
 ccctggagca agactatgag ttaagcaata gcgttacgtg cagatcctcg acaaagaata  
 360  
 ttcgatcatc tgcccccagg aagaacgcag cacctggtga gtgctgccg ctacctggaa  
 420  
 ggccaaaagg cgtgaaatcc gcagcagcgg caaagtcacg ggtgccgacc gcatcgccgt  
 480  
 gatggccgcg ctgaacatca cccacgatct gctgcataag caggaacggc ctgacgttca  
 540  
 ggccagcggc tcaacgcgcg agcaagtgcg tgacctgctg gaacgcgt  
 588

<210> 340  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 340  
 Met Glu Asp Thr Asp Leu Gln Ala Leu Met Ala Arg Leu Glu Leu Leu  
 1 5 10 15  
 Ile Asp Arg Val Glu Gln Leu Lys Ser Gln Asn Gly Leu Leu Leu Ala  
 20 25 30  
 Gln Glu Lys Thr Trp Ala Arg Xaa Arg Ala His Leu Ile Glu Lys Asn  
 35 40 45  
 Glu Ile Ala Arg Arg Lys Val Glu Ser Met Ile Ser Arg Leu Lys Ala  
 50 55 60  
 Leu Glu Gln Asp Tyr Glu Leu Ser Asn Ser Val Thr Cys Arg Ser Ser  
 65 70 75 80  
 Thr Lys Asn Ile Arg Ser Ser Ala Pro Arg Lys Asn Ala Ala Pro Gly  
 85 90 95  
 Glu Cys Cys Pro Leu Pro Gly Arg Pro Lys Gly Val Lys Ser Ala Ala  
 100 105 110  
 Ala Ala Lys Ser Ser Val Pro Thr Ala Ser Pro  
 115 120

<210> 341  
 <211> 401  
 <212> DNA  
 <213> Homo sapiens

<400> 341  
 ngccgcgcgg cctacctgct gtacctggcc tatgccacct ggcgtgaccg ctcggccttt  
 60  
 gcaatgaacg acacgccgac agttgcgacc gcgcgcagcc tgatcctgcg tggcttcttg  
 120

ctgaacattc ttaaccccaa gctgacaatt ttcttctctgg ccttctctgcc tcaattcgta  
 180  
 acgccaggcg gcaccgcgcc ggccttgacag atgctgggtac tgagcggcgt gttcatggcg  
 240  
 atgacgcttg cagtgtttgt gctgtatggc ctgttggcga atgtgtttcg tcgtgcagtg  
 300  
 gtcgagtcgc cacgtgtgca gaactggctg cgacgcagtt ttgccacggc ctttgccggg  
 360  
 ctgggggttg acctggcggt tgccgacgcg tgaggacgcg t  
 401

<210> 342

<211> 130

<212> PRT

<213> Homo sapiens

<400> 342

Xaa	Arg	Ala	Ala	Tyr	Leu	Leu	Tyr	Leu	Ala	Tyr	Ala	Thr	Trp	Arg	Asp
1				5					10					15	
Arg	Ser	Ala	Phe	Ala	Met	Asn	Asp	Thr	Pro	Thr	Val	Ala	Thr	Ala	Arg
			20					25					30		
Ser	Leu	Ile	Leu	Arg	Gly	Phe	Leu	Leu	Asn	Ile	Leu	Asn	Pro	Lys	Leu
		35					40					45			
Thr	Ile	Phe	Phe	Leu	Ala	Phe	Leu	Pro	Gln	Phe	Val	Thr	Pro	Gly	Gly
	50					55					60				
Thr	Ala	Pro	Ala	Leu	Gln	Met	Leu	Val	Leu	Ser	Gly	Val	Phe	Met	Ala
65				70					75					80	
Met	Thr	Leu	Ala	Val	Phe	Val	Leu	Tyr	Gly	Leu	Leu	Ala	Asn	Val	Phe
			85						90				95		
Arg	Arg	Ala	Val	Val	Glu	Ser	Pro	Arg	Val	Gln	Asn	Trp	Leu	Arg	Arg
		100					105					110			
Ser	Phe	Ala	Thr	Ala	Phe	Ala	Gly	Leu	Gly	Leu	Asn	Leu	Ala	Phe	Ala
		115					120					125			
Gln	Arg														
	130														

<210> 343

<211> 389

<212> DNA

<213> Homo sapiens

<400> 343

gtgttgcgca actacatggc gtccctgccg ttcagcgtgg tcgagtcggc gcgcacgcac  
 60  
 ggggtgctcca acttccagat cttctggaag ctgatcgccc cgatggcgat gccggcgatg  
 120  
 gcggcggttcg cgacctgca gttcctgtgg gtgtggaacg acctgctcat cgccaagctc  
 180  
 ttctcacca acgacaaccc cacgggtgac gtcaagctcc aacagctttc cnngggcccc  
 240  
 aaggcccagg gtgcggagct gctgacggcg ggcgccttca tctccatcgt gctacccatg  
 300  
 atcgtcttct tcgtgctcca gaacttctg gtgcgcggta tgacgtcggg tgccgtcaag  
 360

gggtgaccgc tcaactgcag tggccccggg  
389

<210> 344

<211> 121

<212> PRT

<213> Homo sapiens

<400> 344

Val	Leu	Arg	Asn	Tyr	Met	Ala	Ser	Leu	Pro	Phe	Ser	Val	Val	Glu	Ser
1			5					10					15		
Ala	Arg	Ile	Asp	Gly	Cys	Ser	Asn	Phe	Gln	Ile	Phe	Trp	Lys	Leu	Ile
		20					25					30			
Ala	Pro	Met	Ala	Met	Pro	Ala	Met	Ala	Ala	Phe	Ala	Thr	Leu	Gln	Phe
		35					40				45				
Leu	Trp	Val	Trp	Asn	Asp	Leu	Leu	Ile	Ala	Lys	Leu	Phe	Leu	Thr	Asn
	50				55					60					
Asp	Asn	Pro	Thr	Val	Ile	Val	Lys	Leu	Gln	Gln	Leu	Ser	Xaa	Gly	Pro
65			70					75					80		
Lys	Ala	Gln	Gly	Ala	Glu	Leu	Leu	Thr	Ala	Gly	Ala	Phe	Ile	Ser	Ile
			85					90					95		
Val	Leu	Pro	Met	Ile	Val	Phe	Phe	Val	Leu	Gln	Asn	Phe	Leu	Val	Arg
			100					105					110		
Gly	Met	Thr	Ser	Gly	Ala	Val	Lys	Gly							
			115				120								

<210> 345

<211> 360

<212> DNA

<213> Homo sapiens

<400> 345

ctagtacttt atgctgatgg tgaacgtcgt tacatccttg cccctaaagg catggttgct  
60  
ggatgatgtga tccaatctgg tgaagatgca tcaattaaag taggtaactg cttaccgatg  
120  
cgtaatatc cagttggtag aacagtagac gctgtagaaa tgaacactgc taaaggtagca  
180  
caaattgcac gttctgctgg ttcttacagc caaattatag ctgctgatgg tgcttacggt  
240  
actctacggt tacgtagtgg tgaaatgcgt aaaatccctg ctgagtgctg tgcaacaatc  
300  
ggatgaagttg gtaatgcaga acatatgcta cgtcaactag gtaaagctgg tgctacgcgt  
360

<210> 346

<211> 120

<212> PRT

<213> Homo sapiens

<400> 346

Leu	Val	Leu	Tyr	Ala	Asp	Gly	Glu	Arg	Arg	Tyr	Ile	Leu	Ala	Pro	Lys
1			5					10					15		
Gly	Met	Val	Ala	Gly	Asp	Val	Ile	Gln	Ser	Gly	Glu	Asp	Ala	Ser	Ile



```

      20      25      30
Lys Val Gly Asn Cys Leu Pro Met Arg Asn Ile Pro Val Gly Thr Thr
      35      40      45
Val His Ala Val Glu Met Lys Pro Ala Lys Gly Ala Gln Ile Ala Arg
      50      55      60
Ser Ala Gly Ser Tyr Ser Gln Ile Ile Ala Arg Asp Gly Ala Tyr Val
      65      70      75      80
Thr Leu Arg Leu Arg Ser Gly Glu Met Arg Lys Ile Pro Ala Glu Cys
      85      90      95
Arg Ala Thr Ile Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Gln
      100      105      110
Leu Gly Lys Ala Gly Ala Thr Arg
      115      120

```

<210> 347  
 <211> 565  
 <212> DNA  
 <213> Homo sapiens

```

<400> 347
accggtgatg ccaaagggtgc tgtgacaagg ggattcatcg gttcgggcaa ggtcgtcacg
60
gcagctgccg tcatcatgat ttcggtgttc gtcttcttca tccccgaggg catgaacgcc
120
atcaaggaaa tcgccctggc cctggccgtc gggatcctca cggatgcctt cttggtgcgg
180
atgacctcg tccccgccgt gatggccctg ctaggtgaca aggcattggtg gttgccccgg
240
tggtctggatc gacgcctacc ccgcctcgac atcgaggag aagggatcac ccacaggaa
300
aagctggccg cctggcccac agcggatcac accgagggcc tgcacgccga ggggatcggg
360
gtggaggggc tcttcgaagg cctcgatctg cacgtcgaac cgcgtcaggt gcaagccgtc
420
gtcggatcgc agaacagtgt ctcgccgctc ctgctggcga tcgggggacg gctgcccttg
480
gatcacggcc ggatgaggtc gggaggattg ctgctaccgc agcgggcttc cagagtgcgt
540
cgggtgacgt ggttcctcga cgcgt
565

```

<210> 348  
 <211> 188  
 <212> PRT  
 <213> Homo sapiens

```

<400> 348
Thr Gly Asp Ala Lys Gly Ala Val Thr Arg Gly Phe Ile Gly Ser Gly
1      5      10      15
Lys Val Val Thr Ala Ala Ala Val Ile Met Ile Ser Val Phe Val Phe
20      25      30
Phe Ile Pro Glu Gly Met Asn Ala Ile Lys Glu Ile Ala Leu Ala Leu
35      40      45
Ala Val Gly Ile Leu Thr Asp Ala Phe Leu Val Arg Met Thr Leu Val

```

```

      50              55              60
Pro Ala Val Met Ala Leu Leu Gly Asp Lys Ala Trp Trp Leu Pro Gly
65              70              75              80
Trp Leu Asp Arg Arg Leu Pro Arg Leu Asp Ile Glu Gly Glu Gly Ile
      85              90              95
Thr His Glu Glu Lys Leu Ala Ala Trp Pro Thr Ala Asp His Thr Glu
      100              105              110
Ala Leu His Ala Glu Gly Ile Gly Val Glu Gly Leu Phe Glu Gly Leu
      115              120              125
Asp Leu His Val Glu Pro Arg Gln Val Gln Ala Val Val Gly Ser Gln
      130              135              140
Asn Ser Val Ser Ala Val Leu Leu Ala Ile Gly Arg Leu Pro Leu
      145              150              155              160
Asp His Gly Arg Met Arg Ser Gly Gly Leu Leu Leu Pro Glu Arg Ala
      165              170              175
Ser Arg Val Arg Arg Val Thr Trp Phe Leu Asp Ala
      180              185

```

<210> 349  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

```

<400> 349
ntgctggcca cggataatga ccgtactctg cgtgatgtcg ttgccgctga ccctacccat
60
gagctcgggtt cggctaccgc tcatacgttt gcggaacaatt tgccgttccct tcttaaactg
120
ctcgcggcag aagagccact atcgttgcag gctcatccca gtttggcgca agcacaggaa
180
gggtacgggc gggagaatcg caaaggggtg ccattagatg cccagaccg gaattaccac
240
gatcccaacc ataaaccgga gcttattgtt gggctgacgc gattccacgc actagccggc
300
ttccgtgaac cacaacgcac acttgagctt tttgacgcg
339

```

<210> 350  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

```

<400> 350
Xaa Leu Ala Thr Asp Asn Asp Arg Thr Leu Arg Asp Val Val Ala Ala
1      5      10      15
Asp Pro Thr His Glu Leu Gly Ser Ala Thr Ala His Thr Phe Ala Asp
      20      25      30
Asn Leu Pro Phe Leu Leu Lys Leu Leu Ala Ala Glu Glu Pro Leu Ser
      35      40      45
Leu Gln Ala His Pro Ser Leu Ala Gln Ala Gln Glu Gly Tyr Gly Arg
      50      55      60
Glu Asn Arg Lys Gly Val Pro Leu Asp Ala Pro Asp Arg Asn Tyr His
      65      70      75      80
Asp Pro Asn His Lys Pro Glu Leu Ile Val Gly Leu Thr Arg Phe His

```

	85		90		95										
Ala	Leu	Ala	Gly	Phe	Arg	Glu	Pro	Gln	Arg	Thr	Leu	Glu	Leu	Phe	Asp
	100						105						110		
Ala															

<210> 351  
 <211> 354  
 <212> DNA  
 <213> Homo sapiens

<400> 351  
 gcgcgccccca gtgccgagac ccgggggcttc aggagccggc cccgggagag aagagtgcgg  
 60  
 cgggcgacgg agaaaacaac tccaaagtgt gcgaaaggca ccgccctac tcccgggtg  
 120  
 ccgcgcctc cccgccccca gccctggcat ccagagtacg ggtcgagccc gnggccatgg  
 180  
 agccccctg gggaggcggc accaggagc ctgggccccg gggctccgcc gcgacccat  
 240  
 cgggtagacc acagaagctc cgggaccctt ccggcacctc tggacagccc aggatgctgt  
 300  
 tggccaccn ntctctctc tctctcttg aggcgctctg gcccatccag accg  
 354

<210> 352  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 352  
 Ala Arg Pro Ser Ala Glu Thr Arg Gly Phe Arg Ser Arg Pro Arg Glu  
 1 5 10 15  
 Arg Arg Val Arg Arg Arg Thr Glu Lys Thr Thr Pro Lys Leu Ala Lys  
 20 25 30  
 Gly Thr Ala Pro Thr Pro Gly Leu Pro Pro Pro Pro Arg Pro Gln Pro  
 35 40 45  
 Trp His Pro Glu Tyr Gly Ser Ser Pro Xaa Pro Trp Ser Pro Pro Gly  
 50 55 60  
 Glu Ala Ala Pro Gly Ser Leu Gly Pro Gly Ala Pro Pro Arg Pro His  
 65 70 75 80  
 Arg Val Asp His Arg Ser Ser Gly Thr Leu Pro Ala Pro Leu Asp Ser  
 85 90 95  
 Pro Gly Cys Cys Trp Pro Pro Xaa Pro Pro Pro Pro Trp Arg Arg  
 100 105 110  
 Ser Gly Pro Ser Arg Pro  
 115

<210> 353  
 <211> 1469  
 <212> DNA  
 <213> Homo sapiens

<400> 353

nntcatgaag gcttgaactt gcgtgatctt cagcctgcgg acctggcggg tgacggcggt  
60  
attgagccgg tggacctcgt ggtcggagat gtctctttta tctccttgac gatgacctt  
120  
gaacccattt cagctgttgt cagccacac ggccctcatgc tgttgctggt gaagcctcaa  
180  
tttgagggtg gttgcaaggc tttgggagcc catggcggtg tcacggaccc ggccctgccc  
240  
ttgcaggcca tcgcgggtgt catggcagca gcggtagatt tgggttgccg tatgcgtgac  
300  
gagtgcgata gcccgttgcc cgggcaggat ggaaacgttg agcacttcgt cttgctggaa  
360  
cgtacgggtc ggtgacagac gtccgggcat atcatgggccc gctactgtgg tcttgtgaac  
420  
gacacgagcc cttcgagata cgttgtcgtc gtcacccatg ccacgcggga cgacgtttt  
480  
gacgcggctg ccgaattcat ctctgaaatg gcggggcgag acattggttg cgcggttccg  
540  
gatgatcagg tgaagccgat gtcaagcaag ctgccaggga tcgatcttga aagcttgga  
600  
gagttcggcc acgagggcga ggtggtcgtc gtctttggcg gcgacggcac gatcttgcca  
660  
gctgctgaat ggtcattacc tcgccacgtt cccatgattg gcgtcaacct tggccatgct  
720  
ggttttctgg ctgagctgga gcgctccgat atggcggatc tagtgaacaa ggtgtgttcg  
780  
cgcgactaca ccgttgagga tcgcctcgtg cttaaaacca ccgtcaccga gcattccgga  
840  
caacaccgtt ggagttcttt tgccgtcaac gagttgtctc tggaaaaggc agcccgcgcg  
900  
cgcatgctcg acgttctggc gtctgtcgac gagttgccgg tgcaacgctg gagttgcgac  
960  
gggatcctgg tctcgacccc gaccggatcg acggcctacg cgttctcagc tggcgggccc  
1020  
gtcatgtggc ccgatctcga cggcatgctc atggtgccgt tgagcgetca cgctctcttt  
1080  
gctcgaccgc tggatcatgag ccagctgct cgagtggacc ttgacatcca gccagacggt  
1140  
tcagaatcgg cggttctgtg gtgcgacggg cggcgatcgt gcaccgtacg accgggggaa  
1200  
agaatcaccg tcgtccgcca tcccgaaccg ctgcgcattg ctcgtctggc cgcgcagccc  
1260  
ttcacatcgc gtctggtcaa gaagtttgag ctcccggta cggggtggcg tcagggtcgt  
1320  
gaccgtcatc acctagagga gacttcgtga tacgtagtgt gcgaattcgt ggactcggcg  
1380  
tcacgatga gacggtcctc gaacctcat ccgcgctgac ggcagtcacc ggcgagaccg  
1440  
gcgccggaaa gaccatggtg gtcaccggt  
1469

&lt;210&gt; 354

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 354

```

Met Gly Arg Tyr Cys Gly Leu Val Asn Asp Thr Ser Pro Ser Arg Tyr
 1           5           10           15
Val Val Val Val Thr His Ala Thr Arg Asp Asp Ala Phe Asp Ala Ala
 20           25           30
Ala Glu Phe Ile Ser Glu Met Ala Gly Arg Asp Ile Gly Cys Ala Val
 35           40           45
Pro Asp Asp Gln Val Lys Pro Met Ser Ser Lys Leu Pro Gly Ile Asp
 50           55           60
Leu Glu Ser Leu Gly Glu Phe Ala His Glu Ala Glu Val Val Val Val
 65           70           75           80
Phe Gly Gly Asp Gly Thr Ile Leu Arg Ala Ala Glu Trp Ser Leu Pro
 85           90           95
Arg His Val Pro Met Ile Gly Val Asn Leu Gly His Val Gly Phe Leu
100           105           110
Ala Glu Leu Glu Arg Ser Asp Met Ala Asp Leu Val Asn Lys Val Cys
115           120           125
Ser Arg Asp Tyr Thr Val Glu Asp Arg Leu Val Leu Lys Thr Thr Val
130           135           140
Thr Glu His Ser Gly Gln His Arg Trp Ser Ser Phe Ala Val Asn Glu
145           150           155           160
Leu Ser Leu Glu Lys Ala Ala Arg Arg Arg Met Leu Asp Val Leu Ala
165           170           175
Ser Val Asp Glu Leu Pro Val Gln Arg Trp Ser Cys Asp Gly Ile Leu
180           185           190
Val Ser Thr Pro Thr Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly
195           200           205
Pro Val Met Trp Pro Asp Leu Asp Ala Met Leu Met Val Pro Leu Ser
210           215           220
Ala His Ala Leu Phe Ala Arg Pro Leu Val Met Ser Pro Ala Ala Arg
225           230           235           240
Val Asp Leu Asp Ile Gln Pro Asp Gly Ser Glu Ser Ala Val Leu Trp
245           250           255
Cys Asp Gly Arg Arg Ser Cys Thr Val Arg Pro Gly Glu Arg Ile Thr
260           265           270
Val Val Arg His Pro Asp Arg Leu Arg Ile Ala Arg Leu Ala Ala Gln
275           280           285
Pro Phe Thr Ser Arg Leu Val Lys Lys Phe Glu Leu Pro Val Ser Gly
290           295           300
Trp Arg Gln Gly Arg Asp Arg His His Leu Glu Glu Thr Ser
305           310           315

```

&lt;210&gt; 355

&lt;211&gt; 558

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 355

```

nggatccac ctctggaat ggaaaccac ataccagttc tcttctcga tttgaatgcg
60
gatgacctca gtgccaatga gcagcttggt ggccccatg catccggcgt gaactccatc
120

```

ctgcccagg agcatggcag ccagtttttc tacctgcccc tcataaagca cagtgatgat  
 180  
 gaggtttcag ccacagcctc ttgggattcc tcggtgcatg attctgttca cttgaatggg  
 240  
 gtcacaccac agaataaaag gatttaccta attgtgaaaa ccacagttca actcagccac  
 300  
 cctgctgcta tggagttagt attacgaaaa cgaattgcag ccaatatatta caacaaacag  
 360  
 agtttcacgc agagtttgaa gaggagaata tccttgaaaa atatatttta ttctgtggt  
 420  
 gtaacctatg aaatagtatc caatatacca aaggcaactg aggagataga ggaccgggaa  
 480  
 acgctggctc tcctggcagc aaggagttaa aacgaaggca catcagatgg gaagacgtac  
 540  
 attgagaagt acactcga  
 558

<210> 356  
 <211> 186  
 <212> PRT  
 <213> Homo sapiens

<400> 356  
 Xaa Ile Pro Pro Pro Gly Met Glu Thr His Ile Pro Val Leu Phe Leu  
 1 5 10 15  
 Asp Leu Asn Ala Asp Asp Leu Ser Ala Asn Glu Gln Leu Val Gly Pro  
 20 25 30  
 His Ala Ser Gly Val Asn Ser Ile Leu Pro Lys Glu His Gly Ser Gln  
 35 40 45  
 Phe Phe Tyr Leu Pro Ile Ile Lys His Ser Asp Asp Glu Val Ser Ala  
 50 55 60  
 Thr Ala Ser Trp Asp Ser Ser Val His Asp Ser Val His Leu Asn Gly  
 65 70 75 80  
 Val Thr Pro Gln Asn Glu Arg Ile Tyr Leu Ile Val Lys Thr Thr Val  
 85 90 95  
 Gln Leu Ser His Pro Ala Ala Met Glu Leu Val Leu Arg Lys Arg Ile  
 100 105 110  
 Ala Ala Asn Ile Tyr Asn Lys Gln Ser Phe Thr Gln Ser Leu Lys Arg  
 115 120 125  
 Arg Ile Ser Leu Lys Asn Ile Phe Tyr Ser Cys Gly Val Thr Tyr Glu  
 130 135 140  
 Ile Val Ser Asn Ile Pro Lys Ala Thr Glu Glu Ile Glu Asp Arg Glu  
 145 150 155 160  
 Thr Leu Ala Leu Leu Ala Ala Arg Ser Glu Asn Glu Gly Thr Ser Asp  
 165 170 175  
 Gly Lys Thr Tyr Ile Glu Lys Tyr Thr Arg  
 180 185

<210> 357  
 <211> 323  
 <212> DNA  
 <213> Homo sapiens

<400> 357

acgcgtgcgt gtgttgtgtg agtcgggtgt gtgcatgcgt gtgggtgtgc agcaggtggg  
 60  
 gtacgatcag gctgaaggct gatcaggcac aaggctctgg gggagagccc tggttccagc  
 120  
 cctgggggtca gagcagcagg ggccagaaag acggcagggg tgagcactgc acccgctggg  
 180  
 cagggcaggg ccacagaagg cagggcatgg aggccacgtg aagggttga cagagtggat  
 240  
 ggatgtctcc ggaagcacct gcgtggccca gtcagcagga tcagactcgc atgtgtcagg  
 300  
 gtcaccatgg gtcagcgagg atn  
 323

<210> 358  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens

<400> 358  
 Met Val Thr Leu Thr His Ala Ser Leu Ile Leu Leu Thr Gly Pro Arg  
 1 5 10 15  
 Arg Cys Phe Arg Arg His Pro Ser Thr Leu Ser Ser Pro Ser Arg Gly  
 20 25 30  
 Leu His Ala Leu Pro Ser Val Ala Leu Pro Cys Pro Ala Gly Ala Val  
 35 40 45  
 Leu Thr Pro Ala Val Phe Leu Ala Pro Ala Ala Leu Thr Pro Gly Leu  
 50 55 60  
 Glu Pro Gly Leu Ser Pro Arg Ala Leu Cys Leu Ile Ser Leu Gln Pro  
 65 70 75 80  
 Asp Arg Thr Pro Pro Ala Ala His Pro His Ala Cys Thr His Pro Thr  
 85 90 95  
 His Thr Thr His Ala Arg  
 100

<210> 359  
 <211> 265  
 <212> DNA  
 <213> Homo sapiens

<400> 359  
 acgcgtaccg acaagcgccc ggtgatggcc gaccttcgcg aatcgggcgc aatcgagcag  
 60  
 gatcgggaca tgatcgtctt catctaccgc gacgattact acaacaagga aaattcgccg  
 120  
 gacaaggggc tggccgagat catcatcggc aagcatcggg ggggccccac cggctcgtgc  
 180  
 aagctgaagt tcttcggcga gtacacccgt ttcgacaacc tggcccacaa ctcggttggt  
 240  
 tcgttcgaat aacggatgat tccgg  
 265

<210> 360  
 <211> 83  
 <212> PRT

<213> Homo sapiens

<400> 360

```

Thr Arg Thr Asp Lys Arg Pro Val Met Ala Asp Leu Arg Glu Ser Gly
 1           5           10           15
Ala Ile Glu Gln Asp Ala Asp Met Ile Val Phe Ile Tyr Arg Asp Asp
      20           25           30
Tyr Tyr Asn Lys Glu Asn Ser Pro Asp Lys Gly Leu Ala Glu Ile Ile
      35           40           45
Ile Gly Lys His Arg Gly Gly Pro Thr Gly Ser Cys Lys Leu Lys Phe
      50           55           60
Phe Gly Glu Tyr Thr Arg Phe Asp Asn Leu Ala His Asn Ser Val Gly
65           70           75           80
Ser Phe Glu

```

<210> 361

<211> 453

<212> DNA

<213> Homo sapiens

<400> 361

```

gctttgcagg aggaaatctc tatctctggc tgcaagatga ggctgagcta cctgagcagc
60
cggacccttg gctacaaatc tgcctgagg atcagcctca cccaccgac catcccttc
120
aacctcatga aggtgcacct catggtagcg gtggagggcc gctcttcag gaagtggttc
180
gctgcagccc cagacctgtc ctattatttc atttgggaca agacagacgt ctacaaccag
240
aagggtgttg ggctttcaga agcctttggt tccgtggggt atgaatatga atcctgcccc
300
gatctaatacc tgtgggaaaa aagaacaaca gtgctgcagg gctatgaaat tgacgcgtcc
360
aagcttggag gatggagcct agacaaacat catgcctca acattcaaag tggcatcctg
420
cacaaaggga atgngagaa ccagtttgtg tct
453

```

<210> 362

<211> 151

<212> PRT

<213> Homo sapiens

<400> 362

```

Ala Leu Gln Glu Glu Ile Ser Ile Ser Gly Cys Lys Met Arg Leu Ser
 1           5           10           15
Tyr Leu Ser Ser Arg Thr Pro Gly Tyr Lys Ser Val Leu Arg Ile Ser
      20           25           30
Leu Thr His Pro Thr Ile Pro Phe Asn Leu Met Lys Val His Leu Met
      35           40           45
Val Ala Val Glu Gly Arg Leu Phe Arg Lys Trp Phe Ala Ala Ala Pro
      50           55           60
Asp Leu Ser Tyr Tyr Phe Ile Trp Asp Lys Thr Asp Val Tyr Asn Gln

```



```

65          70          75          80
Lys Val Phe Gly Leu Ser Glu Ala Phe Val Ser Val Gly Tyr Glu Tyr
      85          90          95
Glu Ser Cys Pro Asp Leu Ile Leu Trp Glu Lys Arg Thr Thr Val Leu
      100          105          110
Gln Gly Tyr Glu Ile Asp Ala Ser Lys Leu Gly Gly Trp Ser Leu Asp
      115          120          125
Lys His His Ala Leu Asn Ile Gln Ser Gly Ile Leu His Lys Gly Asn
      130          135          140
Gly Glu Asn Gln Phe Val Ser
145          150

```

<210> 363  
 <211> 502  
 <212> DNA  
 <213> Homo sapiens

```

<400> 363
ggtacacaaa aagtttgcca cagtattcac actccagggtc tccataaacc ttccagatcc
60
gctcacacaa gctggtgttc atttgcttct tctgtaaact gttcaggacc ttcataaaaag
120
cggtgatgcc tgaccggtgc tcaggggagc ctttgcaaga gtcaggctga tgtgtgatgg
180
tgtccccacc accagctact ggaggagga ggtctgaggg ctcagctggg tttgacctga
240
gacacctgct gggatctggg tcaccagctg aaagcacagc catgttctgc cttcccccta
300
ggggggtctg ggcgccatgg ctttctgat ctgaccagc actctggggc ttggacagca
360
gtagtgtgat cacttcacct tgcgtctgga ctgagcttct gtgctgcatg tctgggggct
420
tctcaggagc agcatgagcc tctgcggagg aggtatcatt tttcaacaaa aaatcatctg
480
aaaccacctc ttgagaatgc ag
502

```

<210> 364  
 <211> 136  
 <212> PRT  
 <213> Homo sapiens

```

<400> 364
Met Gln His Arg Ser Ser Val Gln Thr Gln Gly Glu Val Ile Thr Leu
1          5          10          15
Leu Leu Ser Lys Ala Gln Ser Ala Gly Ser Asp Gln Glu Ser His Gly
      20          25          30
Ala Gln Ser Pro Leu Gly Glu Gly Gln Asn Met Ala Val Leu Ser Ala
      35          40          45
Gly Asp Pro Asp Pro Ser Arg Cys Leu Arg Ser Asn Pro Ala Glu Ala
      50          55          60
Ser Asp Leu Leu Pro Pro Val Ala Gly Gly Gly Asp Thr Ile Thr His
65          70          75          80
Gln Pro Asp Ser Cys Lys Ala Ala Pro Glu His Arg Ser Gly Ile Thr

```

```

      85              90              95
Ala Phe Met Lys Val Leu Asn Ser Leu Gln Lys Lys Gln Met Asn Thr
      100              105              110
Ser Leu Cys Glu Arg Ile Trp Lys Val Tyr Gly Asp Leu Glu Cys Glu
      115              120              125
Tyr Cys Gly Lys Leu Phe Trp Tyr
130              135

```

<210> 365  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<400> 365  
 atctcaacgg atgcatccat caaggagatg atccccccag gtgctcttgt tatgctcaca  
 60  
 ccactgatcg ttgggattct atttgggggt gagaccctct ctggagtcct tgctggtgcc  
 120  
 cttgtctctg gtgttcagat tgccatttct gcatccaaca ctggtggtgc ctgggacaac  
 180  
 gccaaagaagt acattgaggc tggagtttca gagcatgccca ggacccttgg cccaaaaggt  
 240  
 tctgaccctc acaaggcggc tgtcattggt gacaccattg gagatcctct caaggacacg  
 300  
 tctggccctt ccctcaacat cctcatcaag ctt  
 333

<210> 366  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 366  
 Ile Ser Thr Asp Ala Ser Ile Lys Glu Met Ile Pro Pro Gly Ala Leu  
 1 5 10 15  
 Val Met Leu Thr Pro Leu Ile Val Gly Ile Leu Phe Gly Val Glu Thr  
 20 25 30  
 Leu Ser Gly Val Leu Ala Gly Ala Leu Val Ser Gly Val Gln Ile Ala  
 35 40 45  
 Ile Ser Ala Ser Asn Thr Gly Gly Ala Trp Asp Asn Ala Lys Lys Tyr  
 50 55 60  
 Ile Glu Ala Gly Val Ser Glu His Ala Arg Thr Leu Gly Pro Lys Gly  
 65 70 75 80  
 Ser Asp Pro His Lys Ala Ala Val Ile Gly Asp Thr Ile Gly Asp Pro  
 85 90 95  
 Leu Lys Asp Thr Ser Gly Pro Ser Leu Asn Ile Leu Ile Lys Leu  
 100 105 110

<210> 367  
 <211> 381  
 <212> DNA  
 <213> Homo sapiens

<400> 367

gcgttcgctc cactacccgg cggcggcgga acccttgacg agctactcga agcatggaca  
 60  
 tggcagcagc tcggtgtaca cagcaaaccg gtgngccttg tacgactcga cnncttctgg  
 120  
 gcaccgctga ccgcgctact caaccacatg accatcgaaa gcttcattcg ccctgaggac  
 180  
 cgcgcctcgc tcgtgatcgc cgataccata catcagctga tggccgatct tgagggatgg  
 240  
 accccaccac caccgaagtg gcgctcgtga catagaacaa atgattctga ctatggctca  
 300  
 ttgacatctg cgcagcggct actagctcca ttgacttcaa atcgggcctt ggccgaggct  
 360  
 cngttcaggt ggcccgaat g  
 381

<210> 368

<211> 89

<212> PRT

<213> Homo sapiens

<400> 368

Ala	Phe	Val	Ala	Leu	Pro	Gly	Gly	Gly	Gly	Thr	Leu	Asp	Glu	Leu	Leu
1				5					10					15	
Glu	Ala	Trp	Thr	Trp	Gln	Gln	Leu	Gly	Val	His	Ser	Lys	Pro	Val	Xaa
			20					25					30		
Leu	Val	Arg	Leu	Asp	Xaa	Phe	Trp	Ala	Pro	Leu	Thr	Ala	Leu	Leu	Asn
		35					40					45			
His	Met	Thr	Ile	Glu	Ser	Phe	Ile	Arg	Pro	Glu	Asp	Arg	Ala	Ser	Leu
	50					55				60					
Val	Ile	Ala	Asp	Thr	Ile	His	Gln	Leu	Met	Ala	Asp	Leu	Glu	Gly	Trp
65					70					75				80	
Thr	Pro	Pro	Pro	Pro	Lys	Trp	Arg	Ser							
					85										

<210> 369

<211> 313

<212> DNA

<213> Homo sapiens

<400> 369

gatacatgat cctctcatac cgcacacaca ccgctcccct ctgccgcaat tcgcagacaa  
 60  
 acttgccgag gcttcacagc aagccgtcaa ggctgcttcc tgtgggctac cgatagtctc  
 120  
 gtacgcgagt tctcggacat caacgccaac gtcgggcaag atactgtcaa cgccatctac  
 180  
 acattctacg agcagcaagc gaccagtttc cttegccagc tgaacgacct cccacccgaa  
 240  
 gagcttcccc acgtcatcga ggacttcttc cgcctgtcca ctgatgtcct tctttacat  
 300  
 ttccagcaag ctt  
 313

<210> 370

<211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 370

```

Ser Ser His Thr Ala His Thr Pro Leu Pro Ser Ala Ala Ile Arg Arg
1      5      10      15
Gln Thr Cys Ala Gly Phe Thr Ala Ser Arg Gln Gly Cys Phe Leu Trp
20      25      30
Ala Thr Asp Ser Leu Val Arg Glu Phe Ser Asp Ile Asn Ala Asn Val
35      40      45
Gly Gln Asp Thr Val Asn Ala Ile Tyr Thr Phe Tyr Glu Gln Gln Ala
50      55      60
Thr Ser Phe Leu Arg Gln Leu Asn Asp Leu Pro Pro Glu Glu Leu Pro
65      70      75      80
Asp Val Ile Glu Asp Phe Phe Arg Leu Ser Thr Asp Val Leu Leu Tyr
85      90      95
His Phe Gln Gln Ala
100

```

<210> 371  
 <211> 380  
 <212> DNA  
 <213> Homo sapiens

<400> 371

```

atgacgggtc acgtcatcct ggcgattcca caggtggtga cgtcatggat cggcctcatc
60
tgcatcgcca ttggcacggg ctttatcaag ccgaacctct ccacggtggt aggaggtctt
120
tacgatgacg gtgacccccg ccgcgatcag ggtttcctgt acttctacat gtcgatcagt
180
attggatctc tcttcgcgcc gatcgtcacc ggcctcctca aggaccatta cggctaccac
240
gtaggtttca ttgccgctgc tatcggtatg gctctgggtc tgatcgctt cttccacggt
300
cgttccaaac tgcgtgagct cgccttcgac atccccaatc cgctggcccc cggcgagggt
360
cgccggatgg tgctccgcgg
380

```

<210> 372  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<400> 372

```

Met Thr Gly His Val Ile Leu Ala Ile Pro Gln Val Val Thr Ser Trp
1      5      10      15
Ile Gly Leu Ile Cys Ile Ala Ile Gly Thr Gly Phe Ile Lys Pro Asn
20      25      30
Leu Ser Thr Val Val Gly Gly Leu Tyr Asp Asp Gly Asp Pro Arg Arg
35      40      45
Asp Gln Gly Phe Leu Tyr Phe Tyr Met Ser Ile Ser Ile Gly Ser Leu

```

```

      50              55              60
Phe Ala Pro Ile Val Thr Gly Leu Leu Lys Asp His Tyr Gly Tyr His
65              70              75              80
Val Gly Phe Ile Ala Ala Ala Ile Gly Met Ala Leu Gly Leu Ile Ala
      85              90              95
Phe Phe His Gly Arg Ser Lys Leu Arg Glu Leu Ala Phe Asp Ile Pro
      100              105              110
Asn Pro Leu Ala Pro Gly Glu Gly Arg Arg Met Val Leu Arg
      115              120              125

```

<210> 373  
 <211> 475  
 <212> DNA  
 <213> Homo sapiens

```

<400> 373
acatgttgga aaaattgcct cccactctgg tgctacaggt atgaatctca gccacagtga
60
tgactgtggc agctacaggc ctgatgaaca cccaccaag aaaaggagca tcatgtgcct
120
gcttctctct ggttctctaaa tcctttggcc aaacattttc cccacaaccc tccactccag
180
ttggctgggc actgcctctc agaaagaagt cccagggtccc tgtcagcccc agagcgctg
240
catggactct gccactgtc cctttccaac acggaggccc ccaattctgg ggaccctac
300
accctaccct gtaccaccac atccccatgc ctgctccaga cagcactaac ctcccatgac
360
agtgggacca aagcagttct taaagggtcca atccactcag ttcttaaagt aaaaacagtt
420
gcccatgagt ccccccaaa gacgtccgca catatgccaa acattcggtg tgcac
475

```

<210> 374  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

```

<400> 374
Met Gly Met Trp Trp Tyr Arg Val Gly Cys Arg Gly Pro Gln Asn Trp
1              5              10              15
Gly Pro Pro Cys Trp Lys Gly Thr Val Gly Arg Val His Ala Gly Ala
      20              25              30
Leu Gly Leu Thr Gly Thr Trp Asp Phe Phe Leu Arg Gly Ser Asp Gln
      35              40              45
Pro Thr Gly Val Glu Gly Cys Gly Glu Asn Val Trp Pro Lys Asp Leu
      50              55              60
Gly Thr Arg Glu Lys Gln Ala His Asp Ala Pro Phe Leu Gly Gly Val
65              70              75              80
Phe Ile Arg Pro Val Ala Ala Thr Val Ile Thr Val Ala Glu Ile His
      85              90              95
Thr Cys Ser Thr Arg Val Gly Gly Asn Phe Ser Asn Met
      100              105

```

<210> 375  
 <211> 332  
 <212> DNA  
 <213> Homo sapiens

<400> 375  
 nnacgcgtcg cctccacctc gaaaccgcgc gccggtcgtt ttttcaccat ggccgaccgc  
 60  
 aaggcccaag ttgcgacggt cacggacacg ctgtatttca cgccgtcgca atgggatgga  
 120  
 tgcattggcac ggatgcgtgg ggataagata tcagcactga agtggaatca gatgcagatg  
 180  
 gcggcatgct ccttcatagc ggcatgtggg gcgaagctgg gctgcccgc gcgcactatg  
 240  
 ggcaaggcgc agctgctgta ccagcgtttc catctatttc atgcgccgac tgagttttcg  
 300  
 ttacatgagg tggctttgac gtgtctcttc ac  
 332

<210> 376  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 376  
 Xaa Arg Val Ala Ser Thr Ser Lys Pro Ala Gly Gly Arg Phe Phe Thr  
 1 5 10 15  
 Met Ala Asp Arg Lys Ala Gln Val Ala Thr Val Thr Asp Thr Leu Tyr  
 20 25 30  
 Phe Thr Pro Ser Gln Trp Asp Gly Cys Met Ala Arg Met Arg Gly Asp  
 35 40 45  
 Lys Ile Ser Ala Leu Lys Trp Asn Gln Met Gln Met Ala Ala Cys Ser  
 50 55 60  
 Phe Ile Ala Ala Val Gly Ala Lys Leu Gly Cys Pro Gln Arg Thr Met  
 65 70 75 80  
 Gly Thr Ala Gln Leu Leu Tyr Gln Arg Phe His Leu Phe His Ala Pro  
 85 90 95  
 Thr Glu Phe Ser Leu His Glu Val Ala Leu Thr Cys Leu Phe  
 100 105 110

<210> 377  
 <211> 369  
 <212> DNA  
 <213> Homo sapiens

<400> 377  
 cgcgtgccag gtatgtcaac tgatctgtcg gatatttccg aggttgagta ccgtcaactg  
 60  
 aggctggaac gagggtgct gtgttcgggt tggactcagg gaactgccgc agacgccgag  
 120  
 aacgctatgg cggagctgaa agcccttgct gaaacggcgg gatctcaggt actcgaagct  
 180  
 gtcattgaac gtcggactac cccggatccg gcgacgtaca ttggttcggg caaggtggct  
 240

gagcttgccg aggtgggtgcg ggcgactggt gccgatactg tcatttgtga cggatgaactt  
 300  
 gacgccgctc agttgcgcaa cctcgaggat cgggtcaagn gcaaagttgt ggaccgggtcg  
 360  
 gtctgattc  
 369

<210> 378  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 378  
 Arg Val Pro Gly Met Ser Thr Asp Leu Ser Asp Ile Ser Glu Val Glu  
 1 5 10 15  
 Tyr Arg Gln Leu Arg Leu Glu Arg Val Val Leu Cys Ser Val Trp Thr  
 20 25 30  
 Gln Gly Thr Ala Ala Asp Ala Glu Asn Ala Met Ala Glu Leu Lys Ala  
 35 40 45  
 Leu Ala Glu Thr Ala Gly Ser Gln Val Leu Glu Ala Val Met Gln Arg  
 50 55 60  
 Arg Thr Thr Pro Asp Pro Ala Thr Tyr Ile Gly Ser Gly Lys Val Ala  
 65 70 75 80  
 Glu Leu Ala Glu Val Val Arg Ala Thr Gly Ala Asp Thr Val Ile Cys  
 85 90 95  
 Asp Gly Glu Leu Asp Ala Ala Gln Leu Arg Asn Leu Glu Asp Arg Val  
 100 105 110  
 Lys Xaa Lys Val Val Asp Arg Ser Val  
 115 120

<210> 379  
 <211> 408  
 <212> DNA  
 <213> Homo sapiens

<400> 379  
 acgcgttact taaacttatc tgtaaataat aaattcatta tttctagttg gttaggtact  
 60  
 atgggctgtg gtttaccagg tgctatggca gctaaaattg cttatccaaa ccgtcaagca  
 120  
 gtagctatca caggcgacgg tgcgttccaa atggtaatgc aagactttgc tacagctggt  
 180  
 caatataact taccaatgac aatctttgta ttaaataaca aacaattgtc attcatataa  
 240  
 tatgaacaac aagctgctgg tgaattagag tatgccattg atttctctga tatggatcat  
 300  
 gctaaatttg ctgaagctgc tgggtgtaaa ggctatgttg tgagagatgt aagtcgtctt  
 360  
 gacgacatcg ttgaagaggc aatggctcaa gatgttccaa caatcggt  
 408

<210> 380  
 <211> 136  
 <212> PRT

<213> Homo sapiens

<400> 380

```

Thr Arg Tyr Leu Asn Leu Ser Val Asn Asn Lys Phe Ile Ile Ser Ser
 1           5           10          15
Trp Leu Gly Thr Met Gly Cys Gly Leu Pro Gly Ala Met Ala Ala Lys
      20           25           30
Ile Ala Tyr Pro Asn Arg Gln Ala Val Ala Ile Thr Gly Asp Gly Ala
      35           40           45
Phe Gln Met Val Met Gln Asp Phe Ala Thr Ala Val Gln Tyr Asn Leu
      50           55           60
Pro Met Thr Ile Phe Val Leu Asn Asn Lys Gln Leu Ser Phe Ile Lys
      65           70           75           80
Tyr Glu Gln Gln Ala Ala Gly Glu Leu Glu Tyr Ala Ile Asp Phe Ser
      85           90           95
Asp Met Asp His Ala Lys Phe Ala Glu Ala Ala Gly Gly Lys Gly Tyr
      100          105          110
Val Val Arg Asp Val Ser Arg Leu Asp Asp Ile Val Glu Glu Ala Met
      115          120          125
Ala Gln Asp Val Pro Thr Ile Val
      130          135

```

<210> 381

<211> 613

<212> DNA

<213> Homo sapiens

<400> 381

```

nacgcgtcat aggcggggccc agtgggaagac cacgccaaca cagttggttg agatccgcgt
60
tgaggggcaag gtccctgcgcg tcccgcgaaa tctgggtcaag gcctaccact ctgggctgat
120
cgacgtcgag gactgaaccc tgggagcctg ggcggtccag catgactgct caggctcatt
180
acaaaaacgc gtcgatcccg taggggtgtc gtcatgagca agcccgaagt gaccctgccc
240
gattccgccc ccgacgacct cgtcgttgag gacatcacca tcggcgacgg ccctgaagcg
300
tccgctggca acctcgtcga agtgcactac gtcggcggtg ccttaagcaa tggctgtgag
360
ttcgattctt cctggaaccc cggggagccg ctgaccttcc aactaggggc tggccagggtg
420
atccccgagt gggatgaagg tgtccaaggt atgaaggctg gtggacgacg caaactcgtc
480
atccccacc accttgetta cggctcgcaa ggaatctccg gtgtgatcgc tggcggtgag
540
acgctggtct tcgtctgcga ccttgtcaac atcatctgac gtgacccccg ctcaagcagt
600
cttcgcgccc ggg
613

```

<210> 382

<211> 137

<212> PRT



<213> Homo sapiens

<400> 382

```

Leu Leu Arg Leu Ile Thr Lys Thr Arg Arg Ser Arg Arg Val Val Val
 1           5           10           15
Met Ser Lys Pro Glu Val Thr Leu Pro Asp Ser Ala Pro Asp Asp Leu
      20           25           30
Val Val Glu Asp Ile Thr Ile Gly Asp Gly Pro Glu Ala Ser Ala Gly
      35           40           45
Asn Leu Val Glu Val His Tyr Val Gly Val Ala Leu Ser Asn Gly Arg
 50           55           60
Glu Phe Asp Ser Ser Trp Asn Arg Gly Glu Pro Leu Thr Phe Gln Leu
65           70           75           80
Gly Ala Gly Gln Val Ile Pro Glu Trp Asp Glu Gly Val Gln Gly Met
      85           90           95
Lys Val Gly Gly Arg Arg Lys Leu Val Ile Pro His His Leu Ala Tyr
      100          105          110
Gly Pro Gln Gly Ile Ser Gly Val Ile Ala Gly Gly Glu Thr Leu Val
      115          120          125
Phe Val Cys Asp Leu Val Asn Ile Ile
      130          135

```

<210> 383

<211> 352

<212> DNA

<213> Homo sapiens

<400> 383

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nggagcaaca cctggctcctt gggaatgaag tgtaggagtt gcatttgctg aggttggtgt
60
ttgccaaaga gatgccagct tcttcgaact actgctgtgc aactcttcat gttcaaaacc
120
cagttttctg tttttcacac ctgaacatac accccctgc agttgggtgg ctccccggtt
180
accagctggg ctctatctac agagagagca atggcttccc ttcccttgaa ggaagtctca
240
ccctcacaag gacacttgat ccgctgcaaa gcagaaagtg tgcggaccct ttgggaaggg
300
cgttcttttc ttgttttagaa cctaggattc tgtttttccc aaacaggatc an
352

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<210> 384

<211> 93

<212> PRT

<213> Homo sapiens

<400> 384

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Met Pro Ala Ser Ser Asn Tyr Cys Cys Ala Thr Leu His Val Gln Asn
 1           5           10           15
Pro Val Phe Cys Phe Ser His Leu Asn Ile His Pro Pro Ala Val Gly
      20           25           30
Trp Leu Pro Arg Tyr Gln Leu Gly Ser Ile Tyr Arg Glu Ser Asn Gly
      35           40           45
Phe Pro Ser Leu Glu Gly Ser Leu Thr Leu Thr Arg Thr Leu Asp Pro

```

50                      55                      60  
 Leu Gln Ser Arg Lys Cys Ala Asp Pro Leu Gly Arg Ala Phe Phe Ser  
 65                      70                      75                      80  
 Cys Leu Glu Pro Arg Ile Leu Phe Phe Pro Asn Arg Ile  
                     85                      90

<210> 385  
 <211> 342  
 <212> DNA  
 <213> Homo sapiens

<400> 385  
 gcggcgccca cgaaatgcaa aatgcgccct tcaccggacg ccagggtgat cgagccgccca  
 60  
 gcacctcggg caatgtcctg ggcctgactg gcacacgcaa tcaaagcgag caacaacaca  
 120  
 caaaaacgca tcatgaggca gacgccaggg aagtacaga agccgcagca ggcgcgcggc  
 180  
 gattggaaat atcggtgagg ctaatggtca ccagcgcttg cagggtgtat tcggtggcca  
 240  
 attcgcgga cgacagcacc gccagttcca gtcgcccgc cagcaccagg cgacgcaagc  
 300  
 tgcggcgcaa ctccgggtgc accaacaaca ccgactgtt ca  
 342

<210> 386  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 386  
 Met Gln Asn Ala Pro Phe Thr Gly Arg Gln Val Asp Arg Ala Ala Ser  
 1                      5                      10                      15  
 Thr Ser Gly Asn Val Leu Gly Leu Thr Gly Thr Arg Asn Gln Ser Glu  
                     20                      25                      30  
 Gln Gln His Thr Lys Thr His His Glu Ala Asp Ala Arg Glu Val Thr  
                     35                      40                      45  
 Glu Ala Ala Ala Gly Ala Arg Arg Leu Glu Ile Ser Val Arg Leu Met  
                     50                      55                      60  
 Val Thr Ser Ala Cys Arg Leu Tyr Ser Val Ala Asn Ser Arg Asn Asp  
 65                      70                      75                      80  
 Ser Thr Ala Ser Ser Ser Ser Pro Arg Ser Thr Arg Arg Arg Lys Leu  
                     85                      90                      95  
 Arg Arg Asn Ser Gly Cys Thr Asn Asn Thr Ala Leu Phe  
                     100                      105

<210> 387  
 <211> 379  
 <212> DNA  
 <213> Homo sapiens

<400> 387  
 acgcgtgacg cgccggcatc ggaagcggtg actgcagaga agaccgcgca cgtggctgtg  
 60

ggacgtgctg gcacgtctga catggtgcgt ggacccgcct tctcttcgcc tgcgcatgcc  
 120  
 atgcaagagg agcttgacaa tgtgcgtgat ctgcccattg cgcggcagca agcgctcgat  
 180  
 gctgttcggt ccgagctgct cgaagcgcag caagcatgtg cctcgtgcca gctgcagctg  
 240  
 cagcatgtgc cagatgatcg tgtgcgagcg catcccatat accaggcgct ccatgcggac  
 300  
 gttgcttaca tgcagcaaga acttgatcac gtacgagacg cattggcttc ggcagaatct  
 360  
 gagaatgcga gcctgcgcg  
 379

<210> 388

<211> 114

<212> PRT

<213> Homo sapiens

<400> 388

Met	Arg	Leu	Val	Arg	Asp	Gln	Val	Leu	Ala	Ala	Cys	Lys	Gln	Arg	Pro
1				5					10					15	
His	Gly	Ala	Pro	Gly	Ile	Trp	Asp	Ala	Leu	Ala	His	Asp	His	Leu	Ala
			20					25					30		
His	Ala	Ala	Ala	Ala	Ala	Gly	Thr	Arg	His	Met	Leu	Ala	Ala	Leu	Arg
		35					40					45			
Ala	Ala	Arg	Asn	Glu	Gln	His	Arg	Ala	Leu	Ala	Ala	Ala	His	Gly	Arg
	50					55					60				
Asp	His	Ala	His	Cys	Gln	Ala	Pro	Leu	Ala	Trp	His	Ala	Gln	Ala	Lys
65					70				75					80	
Arg	Arg	Arg	Val	His	Ala	Pro	Cys	Gln	Thr	Cys	Gln	His	Val	Pro	Gln
			85					90						95	
Pro	Arg	Ala	Arg	Ser	Leu	Gln	Ser	Thr	Leu	Pro	Met	Pro	Ala	Arg	
			100				105							110	
His	Ala														

<210> 389

<211> 382

<212> DNA

<213> Homo sapiens

<400> 389

ngatggccga ctgtccact gtcagtacgc gaagctcgcc gtcgagtcgg tccacgtccg  
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 ggctccac gtgtccgca accctccgaa gcgatgacct ggcccgggg cggaacgag  
 120  
 gtattgcgtt tggagacgct tggggtaaat tacggccagg tgcgcgccgt cgatgccctg  
 180  
 acgaccaccg tagagcgcgg caccatcacc tgctcatgg gtcgaaatgg atcaggcaag  
 240  
 tcgtctctga tgtgggcgat ccaaggggca acaaagtcct cagggagggt actggtcaac  
 300  
 cagcaggggt cttgggctga ccccgcaaa gccgacgccg cgaccgctcg acgaatggtg  
 360

agcttagtcc cgcagtcagc cn  
382

<210> 390  
<211> 127  
<212> PRT  
<213> Homo sapiens

<400> 390  
Xaa Trp Pro Thr Val Pro Leu Ser Val Arg Glu Ala Arg Arg Arg Val  
1 5 10 15  
Gly Pro Arg Pro Gly Leu Pro Arg Ala Pro Gln Pro Ser Glu Ala Met  
20 25 30  
Thr Trp Pro Gly Gly Gly Asn Glu Val Leu Arg Leu Glu Thr Leu Gly  
35 40 45  
Val Asn Tyr Gly Gln Val Arg Ala Val Asp Ala Leu Thr Thr Thr Val  
50 55 60  
Glu Arg Gly Thr Ile Thr Cys Leu Met Gly Arg Asn Gly Ser Gly Lys  
65 70 75 80  
Ser Ser Leu Met Trp Ala Ile Gln Gly Ala Thr Lys Ser Ser Gly Arg  
85 90 95  
Val Leu Val Asn His Glu Gly Ser Trp Ala Asp Pro Arg Lys Ala Asp  
100 105 110  
Ala Ala Thr Ala Arg Arg Met Val Ser Leu Val Pro Gln Ser Ala  
115 120 125

<210> 391  
<211> 456  
<212> DNA  
<213> Homo sapiens

<400> 391  
nnacgcgttg ccgctctgtg aggcgcctat cacggtgaca ctctcgggtgc tatgagcgtg  
60  
tgcgacccta tcggtggcat gcacgccttg ttcagecgact ctattcccca gcagatcttc  
120  
ctgcccgcgc cctccttctt tcgccgccga cgaggccgac gtggagacgt ggtgcagcga  
180  
ggccgatgaa tcctggacac ccaccgcgac gacctggccg ggatcattgt cgagcccatc  
240  
ttgcaaggag ccggaggcat gtggccgtgg tctccgtcct gtctgaagca cctgcgccgt  
300  
cgtgctgatg aacttgacct agttcttata gccgacgagg tcgctactgg atttgggcgg  
360  
actggcaaac ttttcgcatg cgagtgggcc gatatcgctc ctgacatcat ggtggttggg  
420  
aaatccatga ctggcggata cctgaccag tcggcc  
456

<210> 392  
<211> 55  
<212> PRT  
<213> Homo sapiens

&lt;400&gt; 392

Gly Ala Tyr His Gly Asp Thr Leu Gly Ala Met Ser Val Cys Asp Pro  
 1 5 10 15  
 Ile Gly Gly Met His Ala Xaa Phe Ser Asp Ser Ile Pro Gln Ile  
 20 25 30  
 Phe Leu Pro Ala Pro Ser Phe Phe Arg Arg Arg Arg Gly Arg Arg Gly  
 35 40 45  
 Asp Val Val Gln Arg Gly Arg  
 50 55

&lt;210&gt; 393

&lt;211&gt; 371

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 393

nacgcgttgc tcgtcattgg tggctactcg gcctacgaag gtatctacac catgatgact  
 60  
 gagcgggacc ggtaccgggc ttccgtatt ccgacgggtg gcacccgggc ttctatcgac  
 120  
 aacaacctcc ccggttcgga actgtccatc ggcaccgaca ccgctctcaa cgtcatcgtc  
 180  
 gaggcgatgg acaagattaa ggagtcgggt atcgcgtcca gacgctgctt cgtcgtcgag  
 240  
 acgatgggtc gtgactgcgg atacctcgcg ttgatgtcgg gtatcgagc tggcgtgag  
 300  
 cggatctata ccaacgagga cggatatctc ctggacgac tagccaacga cgtccattgg  
 360  
 ttgcgggagt c  
 371

&lt;210&gt; 394

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 394

Xaa Ala Leu Leu Val Ile Gly Gly Tyr Ser Ala Tyr Glu Gly Ile Tyr  
 1 5 10 15  
 Thr Met Met Thr Glu Arg Asp Arg Tyr Pro Ala Phe Arg Ile Pro Thr  
 20 25 30  
 Val Cys Ile Pro Ala Ser Ile Asp Asn Asn Leu Pro Gly Ser Glu Leu  
 35 40 45  
 Ser Ile Gly Thr Asp Thr Ala Leu Asn Val Ile Val Glu Ala Met Asp  
 50 55 60  
 Lys Ile Lys Glu Ser Gly Ile Ala Ser Arg Arg Cys Phe Val Val Glu  
 65 70 75 80  
 Thr Met Gly Arg Asp Cys Gly Tyr Leu Ala Leu Met Ser Gly Ile Ala  
 85 90 95  
 Ala Gly Ala Glu Arg Ile Tyr Thr Asn Glu Asp Gly Ile Ser Leu Asp  
 100 105 110  
 Asp Leu Ala Asn Asp Val His Trp Leu Arg Glu  
 115 120

<210> 395  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 395  
 gaattctagt tgggagattc attgaccaga cttttggaat aaacactagt catcatgcta  
 60  
 gcgacagggt gtcttgtgca tggtagaaag gcagtccaag cctatgtctc tgaaacctgc  
 120  
 tctcatttct gttttctact ttacgattta tgttatctca tactcccat gttgcctgtt  
 180  
 ctccagtttt ttacttgtg ttatttccat tcttctattc ctgctcaatt tctgcctcag  
 240  
 ggcagaattg tgtccaacag ctcttaaatg cagcgagaa actgtgatgt taaaaacatc  
 300  
 ttgttatccg gccccaaaac atgttgtcct tggtaactct tactggtttg t  
 351

<210> 396  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 396  
 Met Val Glu Arg Gln Ser Lys Pro Met Ser Leu Lys Pro Ala Leu Ile  
 1 5 10 15  
 Ser Val Phe Tyr Phe Thr Ile Tyr Val Ile Ser Tyr Ser Pro Cys Cys  
 20 25 30  
 Leu Phe Ser Ser Phe Phe Thr Cys Val Ile Ser Ile Leu Leu Phe Leu  
 35 40 45  
 Leu Asn Phe Cys Leu Arg Ala Glu Leu Cys Pro Thr Ala Leu Lys Cys  
 50 55 60  
 Ser Ala Glu Thr Val Met Leu Lys Thr Ser Cys Tyr Pro Ala Pro Lys  
 65 70 75 80  
 His Val Val Leu Gly Asn Ser Tyr Trp Phe  
 85 90

<210> 397  
 <211> 483  
 <212> DNA  
 <213> Homo sapiens

<400> 397  
 gccgtcatta aagagatcac cctctcctc caacctgggtg atgtcctcgt cgacgggtgt  
 60  
 aatgcttatt ttggtgatac ccgccgccgt gaggaggaaa tacgtccac cggcattcac  
 120  
 tatgttggtg ctggcatctc cgggtgggga gtcggggccc tgagggtccc atcaattatg  
 180  
 cctggcgggg ttaaggaatc ttacgaaatc atcggaccgg tcttagaaaa aatctccgcc  
 240  
 cagctcgacg gtgaaccctg ctgcgcatgg atgggtactg acggcgccgg acacttcgtc  
 300

aagatggtcc ataatggcat cgagtacgcc gatatgcagt tcattggcga ggcgcccttc  
 360  
 ctttttgcgn tgcccgcggg tttagaccaat gctgaggccg ccgatgcctt cgagtcgtgg  
 420  
 aaccatggcg acctcaattc ctacctgctc gaaatcactt ctcggtact gcggtccaag  
 480  
 gat  
 483

<210> 398

<211> 161

<212> PRT

<213> Homo sapiens

<400> 398

Ala	Val	Ile	Lys	Glu	Ile	Thr	Pro	Leu	Leu	Gln	Pro	Gly	Asp	Val	Leu
1			5					10					15		
Val	Asp	Gly	Gly	Asn	Ala	Tyr	Phe	Gly	Asp	Thr	Arg	Arg	Arg	Glu	Glu
	20							25				30			
Glu	Ile	Arg	Pro	Thr	Gly	Ile	His	Tyr	Val	Gly	Thr	Gly	Ile	Ser	Gly
	35					40				45					
Gly	Gly	Val	Gly	Ala	Leu	Arg	Val	Pro	Ser	Ile	Met	Pro	Gly	Gly	Val
	50				55					60					
Lys	Glu	Ser	Tyr	Glu	Ile	Gly	Pro	Val	Leu	Glu	Lys	Ile	Ser	Ala	
65				70				75					80		
His	Val	Asp	Gly	Glu	Pro	Cys	Cys	Ala	Trp	Met	Gly	Thr	Asp	Gly	Ala
		85						90					95		
Gly	His	Phe	Val	Lys	Met	Val	His	Asn	Gly	Ile	Glu	Tyr	Ala	Asp	Met
		100						105					110		
Gln	Phe	Ile	Gly	Glu	Ala	Pro	Phe	Leu	Phe	Ala	Xaa	Pro	Ala	Gly	Leu
		115					120					125			
Thr	Asn	Ala	Glu	Ala	Ala	Asp	Ala	Phe	Glu	Ser	Trp	Asn	His	Gly	Asp
	130					135					140				
Leu	Asn	Ser	Tyr	Leu	Val	Glu	Ile	Thr	Ser	Arg	Val	Leu	Arg	Ala	Lys
145				150						155				160	
Asp															

<210> 399

<211> 314

<212> DNA

<213> Homo sapiens

<400> 399

nngggaatga agaccacca gcccttcctt tctcaaatc ttctccaggc ttctgtgcat  
 60  
 ggctcatcca cccatccact cattcaccca tctatccatc cactcatcca cccatccagt  
 120  
 cactcactca ttgtccatc cactcatgta cccatccact cattcgccca tttatccatc  
 180  
 cactcaacca tccactcatc caccatcca nctcatcatc cgtccagtca cccatctatc  
 240  
 caccatgta tccatccact catccacca tccactcatc tgtccatcca cttatccacc  
 300

catctactca ccca  
314

<210> 400

<211> 104

<212> PRT

<213> Homo sapiens

<400> 400

Xaa	Gly	Met	Lys	Thr	Thr	Gln	Pro	Phe	Leu	Ser	Ser	Asn	Leu	Leu	Gln
1				5					10				15		
Ala	Ser	Val	His	Gly	Ser	Ser	Thr	His	Pro	Leu	Ile	His	Pro	Ser	Ile
			20				25					30			
His	Pro	Leu	Ile	His	Pro	Ser	Ser	His	Ser	Leu	Ile	Cys	Pro	Ser	Thr
		35				40					45				
His	Val	Pro	Ile	His	Ser	Phe	Ala	His	Leu	Ser	Ile	His	Ser	Thr	Ile
	50				55				60						
His	Ser	Ser	Thr	His	Pro	Xaa	His	His	Pro	Ser	Ser	His	Pro	Ser	Ile
65				70					75				80		
His	Pro	Cys	Ile	His	Pro	Leu	Ile	His	Pro	Ser	Thr	His	Leu	Ser	Ile
			85					90					95		
His	Leu	Ser	Thr	His	Leu	Leu	Thr								
			100												

<210> 401

<211> 2165

<212> DNA

<213> Homo sapiens

<400> 401

gagaaaaatgg aactacctgt atataaatta ggtgagcaaa cagtataca ggtagtttta  
60  
agaagcaaat atatacagtc aatttaacag tgtttacttc tctggattgt ttaatgggtg  
120  
caaaatgaaa gatctattga agtttacta tacattgcat tgattgaacc ttggagagtt  
180  
ttatgaaaaa gaggggcatc ccttgccatc tgtttgccag tcttccttgc cccttccttt  
240  
gaaatgcctg cctctttttt gccagattg tttcctgacc atccgaactc agatgggggc  
300  
ctctaagttc ttcttgata ttcacaaatc cttcacaag gccacgtgc gaagtgaatg  
360  
atctggaggt gcctgggcat ctgtgttga agggagtcaa gactcaccag ccagtcagtt  
420  
tgtgggctac agttgtccca caaaaatcag gcatgttcac ctccctctg ggccctaca  
480  
gctgggactg atcatagcct cagattagaa gaaatactga cttctaactc tataagccag  
540  
cactcctggg taaggagtga agctctgttg gccatgccgc tttggactgc tgggcagagc  
600  
tgagcctaca gttttgtact ggggtgcacg gatgacagct gggaagatgg aaaggcagct  
660  
tgaggattta tagcagctaa agggtaaatg ctgttatgca aaaggccccc atatgaactt  
720



cctacaggtg tagccgcagc caagtgtctg tacagctgct gagaatttgt cggatgatga  
780  
aaaattcctc tttgcatcac aagcgagtgg aaagccaggg gctgcatgag tggagaaagc  
840  
acagtctggt ttttcaagta ctgcagagaa tgagaatacc cagccgggag cctggagtgt  
900  
aggccccagt tacacaggct cccggaatac agacctggga agatagggga ggagagggga  
960  
agcttggtggc cttttgatcc gcccccgaa tgcccaccgt gcgctgcttt gctgccttca  
1020  
tctcctgctc agaggccttc tcttcccag agacctcctt ggatgggtct aaggagaca  
1080  
ctgccccggc ctttttccct gcaatcacaa ggtccaaatc ctccaggctg cgcttgatcg  
1140  
gccgcgccgc cccaatgttc tacgggctca ttttccgggt caggattggg tggaccatgc  
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1260  
attcagggtg ttttttaggg cctgacatgg tcatgggtga taccgcacag gctttgggtg  
1320  
gacagtctcg actctggctg cctaagacct ggaactggga gatgcctttg ctctcctggg  
1380  
gccctgtggt ggaatgagcc agggccagga ccttgccggt aggtttgtgc gggttcttgg  
1440  
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1500  
cttgacaggtg cagggacgtg agataattta catggagctt ttcttgggtg ctgtgggaag  
1560  
gaaaagaact gttttccgat tccctgtaca tgtccctgga agggatattg gatgtctgtt  
1620  
cattatgaag atgggtgctc gtgtgtctgt agaggctatg gagatgaggg gacgagtaga  
1680  
agtcagccag gaagctaggc atgtgggaat gggggagggc ccttttctct aagagtattt  
1740  
ccttgccctc ctgaatttct tgcttcagga cgtaggagtc agcaaggggg ttaaggtgat  
1800  
gcttgagaga gctgcagcgg tggggatctg atcgactcag tttctcatgc ttaaagatgt  
1860  
cattgatggt ctttctctct tccgagggtc tgcttctgaa actctggacg tgctgaatca  
1920  
ctgatggcgg gctgaccgcc atatggtcag tgctttggcc atggtgggtc tgggacaaac  
1980  
tggaacacaa gtcaccccta gcaatcagtt tctttttgct gatcaaaggg ggtggggagc  
2040  
cataagggtg gctgctggag aggttgcccc cactcacttg ggacaaaagc ttttcttgg  
2100  
ccagtgggga catcatgcct gggttgcccc tagagtagag caggggcgtg taattaagtc  
2160  
catgg  
2165

&lt;210&gt; 402

&lt;211&gt; 87

&lt;212&gt; PRT

<213> Homo sapiens

<400> 402

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Glu Tyr Pro Ala Gly Ser Leu Glu Leu Arg Pro Glu Leu His Arg Leu
 1           5           10           15
Pro Glu Tyr Arg Pro Gly Lys Ile Gly Glu Glu Arg Gly Ser Leu Trp
          20           25           30
Pro Phe Asp Pro Pro Pro Glu Cys Pro Pro Cys Ala Ala Leu Leu Pro
          35           40           45
Ser Ser Pro Ala Gln Arg Pro Ser Pro Ser Gln Arg Pro Pro Trp Met
          50           55           60
Gly Leu Arg Glu Thr Leu Pro Gly Pro Phe Ser Leu Gln Ser Gln Gly
65           70           75           80
Pro Asn Pro Pro Gly Cys Ala
          85

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<210> 403

<211> 369

<212> DNA

<213> Homo sapiens

<400> 403

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cccatgggtg tgtcccagga cggcgtcatg aagcgtcagg taaatgacaa ggaaacggtc
60
gcgcacttgt tcgaatacac gacgcaagtg tctgtcgact cgacgccgca actcgtccag
120
ccttcgcccc cgtcgcacga caacctcgtg cctgtccaga tgatcttttg cttcaagcag
180
cgcaacgcga aaaagatcaa tagccaccgc tgggtatttc atgcactggg ccgcatgcta
240
cagcccgaca tggtcgtctt ggtggacgtc ggcacgaagc ccggccacct cgccctatac
300
catctatggc aggcattcta tcaccgacct accttggggc gtgcttgccg cgaaattcat
360
gctatgatac
369

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<210> 404

<211> 123

<212> PRT

<213> Homo sapiens

<400> 404

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Pro Met Gly Val Ser Gln Asp Gly Val Met Lys Arg Gln Val Asn Asp
 1           5           10           15
Lys Glu Thr Val Ala His Leu Phe Glu Tyr Thr Thr Gln Val Ser Val
          20           25           30
Asp Ser Thr Pro Gln Leu Val Gln Pro Ser Pro Thr Ser His Asp Asn
          35           40           45
Leu Val Pro Val Gln Met Ile Phe Cys Phe Lys Gln Arg Asn Ala Lys
          50           55           60
Lys Ile Asn Ser His Arg Trp Val Phe His Ala Leu Gly Arg Met Leu
65           70           75           80
Gln Pro Asp Met Val Val Leu Val Asp Val Gly Thr Lys Pro Gly His

```

```

      85              90              95
Leu Ala Leu Tyr His Leu Trp Gln Ala Phe Tyr His Arg Pro Thr Leu
      100              105              110
Gly Gly Ala Cys Gly Glu Ile His Ala Met Ile
      115              120

```

<210> 405  
 <211> 840  
 <212> DNA  
 <213> Homo sapiens

```

<400> 405
gaattcccg cgcaccagctc gaagctggag cactttgtgt ctatcctgct gaagtgttc
60
gactcgccct ggaccacgag ggccctgtcg gagacagtgg tggaggagag cgacccaag
120
ccggccttca gcaagatgaa tgggtccatg gacaaaaagt catcgaccgt cagtggaggac
180
gtggaggcca ccgtgcccat gctgcagcgg accaagtcac ggatcgagca gggatcgtg
240
gaccgctcag agacgggctg gctggacaag aaggaggggg agcaagccaa ggcgctgttt
300
gagaaggtga agaagttccg gacccatgtg gaggaggggg acattgtgta ccgcctctac
360
atgcggcaga ccatcatcaa ggtgatcaag ttcacctca tcatctgcta caccgtctac
420
tacgtgcaca acatcaagtt cgacgtggac tgcaccgtgg acattgagag cctgacgggc
480
taccgcacct accgctgtgc ccacccctg gccacactct tcaagatcct ggcgctcttc
540
tacatcagcc tagtcatctt ctacggcctc atctgcatgt atacactgtg gtggatgcta
600
cggcgctccc tcaagaagta ctcgtttgag tcatccgtg aggagagcag ctacagcgac
660
atccccgacg tcaagaacga cttcgccctc atgctgcacc tcattgacca atacgacccg
720
ctctactcca agcgcttcgc cgtcttcctg tcggaggtga gtgagaacaa gctgcggcag
780
ctgaacctca acaacgagtg gacgctggac aagctccggt acggagagaa gacaacgcgt
840

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<210> 406  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

```

<400> 406
Leu Ile Cys Met Tyr Thr Leu Trp Trp Met Leu Arg Arg Ser Leu Lys
1           5           10           15
Lys Tyr Ser Phe Glu Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile
20          25          30
Pro Asp Val Lys Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln
35          40          45
Tyr Asp Pro Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val

```

50                      55                      60  
 Ser Glu Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu  
 65                      70                      75                      80  
 Asp Lys Leu Arg Tyr Gly Glu Lys Thr Thr Arg  
                     85                      90

<210> 407  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens

<400> 407  
 gcctattgta ccagctctcc agggctgggg acttgctaga gcagggttcc cagtgtcccc  
 60  
 aggctctact ttgctctgcc tggctctcagg gtgtagggga tggagagctg gacttccagc  
 120  
 ctgcttcttg gctgtctagg ggccaggggc tcgggacaca gagctcctgg aggccgagca  
 180  
 caagccttgg gcagaggtga ggcagagctc tgactgtttc attcgactac gttgccaagg  
 240  
 agatgctcgc tcggagtggg tgctctggct ctgggattcc aaaccaagct gccttctctg  
 300  
 atgtggcctt agtgctctgg gcggatgtac cttggctctg cctggaccct ctctctcttc  
 360  
 caggcctctg tcccaccagg atgatgcta tccagagctc attgtcctct cccacttctc  
 420  
 ccccgagctt cccattccgt gtctctctgg agggcccatc atcatcctgg tggaggtgtt  
 480  
 gcactgagga ccacagcagc cctcgcatte ccacgggcaa aggggtatgt gtagg  
 535

<210> 408  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 408  
 Met Leu Ala Arg Ser Gly Cys Ser Gly Ser Gly Ile Pro Asn Gln Ala  
 1                      5                      10                      15  
 Ala Phe Ser Asp Val Ala Leu Val Leu Trp Ala Asp Val Pro Trp Leu  
                     20                      25                      30  
 Cys Leu Asp Pro Leu Ser Leu Pro Gly Leu Cys Pro Thr Arg Met Met  
                     35                      40                      45  
 Pro Ile Gln Ser Ser Leu Ser Ser Pro Thr Ser Ser Pro Ser Phe Pro  
                     50                      55                      60  
 Phe Arg Val Ser Leu Glu Gly Pro Ser Ser Ser Trp Trp Arg Cys Cys  
 65                      70                      75                      80  
 Thr Glu Asp His Ser Ser Pro Arg Ile Pro Thr Gly Lys Gly Val Cys  
                     85                      90                      95  
 Val

<210> 409  
 <211> 375

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 409

ngtgtcatgg gtgtctatac cagcgatgag gccaaagactg ccaagacttt tggatttggg  
 60  
 ggacttccga ttacgactaa tatttctctt gccacaact tcaatatgga tgaaatttct  
 120  
 gatattgtct tccgtgtcaa tgataccagt ttgacaccaa ctgtgggacc agaattagct  
 180  
 agaaaattga ccgaaattgc tggctcttcag caaggggagt atcaggtgtc agatgcgact  
 240  
 gcagccttcc aagaagtgca acaattgttc ggctttataa ctacgattat tagtgccatt  
 300  
 gcaggaattt ccctttttgt tggagggact ggtgttatga acatcatgct ggtttcggtg  
 360  
 acggagcgta cgcgt  
 375

&lt;210&gt; 410

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 410

Xaa	Val	Met	Gly	Val	Tyr	Thr	Ser	Asp	Glu	Ala	Lys	Thr	Ala	Lys	Thr
1				5					10					15	
Phe	Gly	Ile	Gly	Gly	Leu	Pro	Ile	Thr	Thr	Asn	Ile	Ser	Leu	Ala	Asn
			20					25					30		
Asn	Phe	Asn	Met	Asp	Glu	Ile	Ser	Asp	Ile	Val	Phe	Arg	Val	Asn	Asp
		35					40					45			
Thr	Ser	Leu	Thr	Pro	Thr	Val	Gly	Pro	Glu	Leu	Ala	Arg	Lys	Leu	Thr
	50					55					60				
Glu	Ile	Ala	Gly	Leu	Gln	Gln	Gly	Glu	Tyr	Gln	Val	Ser	Asp	Ala	Thr
65					70					75				80	
Ala	Ala	Phe	Gln	Glu	Val	Gln	Gln	Leu	Phe	Gly	Phe	Ile	Thr	Thr	Ile
			85					90					95		
Ile	Ser	Ala	Ile	Ala	Gly	Ile	Ser	Leu	Phe	Val	Gly	Gly	Thr	Gly	Val
		100						105					110		
Met	Asn	Ile	Met	Leu	Val	Ser	Val	Thr	Glu	Arg	Thr	Arg			
		115					120					125			

&lt;210&gt; 411

&lt;211&gt; 409

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 411

ccacatactt caccctcttc accccctcca cctactccac cacctggcag tcgccatcga  
 60  
 ggatgggacg caactccacg tccacatgct ccggaccacg cggcgtgtgg tggatgtgca  
 120  
 gcacgcggtc ggggcccctt gagctcgaag gcgcggcgca tcgggcagtg ctcgccggcc  
 180

tggtcgcagg gcacgtcgta ctgggtcgag acgcggaagc acttgtggcc gatgtaggcg  
 240  
 cgatcggtcg tcccgaactg gcgctgatag gccgtgtaca caacacaaac tgttgacttc  
 300  
 ccggtccacc acgatcatgg gctgggactc gtgttcagg tggggggcca gggcttgggc  
 360  
 ctgcggtgag cgctgggggt ggatggggca tagcgtcggg gaggaggtg  
 409

<210> 412  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 412  
 Met Pro His Pro Pro His Ala Leu Thr Ala Gly Pro Ser Pro Gly Pro  
 1 5 10 15  
 Pro Pro Gly Thr Arg Val Pro Ala His Asp Arg Gly Gly Pro Gly Val  
 20 25 30  
 Gln Gln Phe Val Leu Cys Thr Arg Pro Ile Ser Ala Ser Ser Gly Gln  
 35 40 45  
 Pro Ile Ala Pro Thr Ser Ala Thr Ser Ala Ser Ala Ser Arg Thr Ser  
 50 55 60  
 Thr Thr Cys Pro Ala Thr Arg Pro Ala Ser Thr Ala Arg Cys Ala Ala  
 65 70 75 80  
 Pro Ser Ser Ser Arg Gly Pro Asp Arg Val Leu His Ile His His Thr  
 85 90 95  
 Pro Arg Gly Pro Glu His Val Asp Val Glu Leu Arg Pro Ile Leu Asp  
 100 105 110  
 Gly Asp Cys Gln Val Val Glu  
 115

<210> 413  
 <211> 357  
 <212> DNA  
 <213> Homo sapiens

<400> 413  
 ccgggcatcc caccaccggg tgtcatgaac caagtagtgg cccctatggg agggactcca  
 60  
 gcaccgggtg gaagtccata tggacaacag gtgggagttt tggggcctcc agggcagcag  
 120  
 gcaccacctc catatcccg cccacatcca gctggacccc ctgtcatata gcagccaaca  
 180  
 acacccatgt ttgtagctcc cccccaaag acccagcggc ttcttctc agaggcctac  
 240  
 ctgaaataca ttgaaggact cagtgcggag tccaacagca ttagcaagtg ggatcagaca  
 300  
 ctggcagctc ggagacgca cgtccatttg tcgaaagaac aggagagccg cctaccc  
 357

<210> 414  
 <211> 119  
 <212> PRT

<213> Homo sapiens

<400> 414

```

Pro Gly Ile Pro Pro Pro Gly Val Met Asn Gln Val Val Ala Pro Met
 1           5           10           15
Val Gly Thr Pro Ala Pro Gly Gly Ser Pro Tyr Gly Gln Gln Val Gly
      20           25           30
Val Leu Gly Pro Pro Gly Gln Gln Ala Pro Pro Pro Tyr Pro Gly Pro
      35           40           45
His Pro Ala Gly Pro Pro Val Ile Gln Gln Pro Thr Thr Pro Met Phe
      50           55           60
Val Ala Pro Pro Pro Lys Thr Gln Arg Leu Leu His Ser Glu Ala Tyr
      65           70           75           80
Leu Lys Tyr Ile Glu Gly Leu Ser Ala Glu Ser Asn Ser Ile Ser Lys
      85           90           95
Trp Asp Gln Thr Leu Ala Ala Arg Arg Arg Asp Val His Leu Ser Lys
      100          105          110
Glu Gln Glu Ser Arg Leu Pro
      115

```

<210> 415

<211> 332

<212> DNA

<213> Homo sapiens

<400> 415

```

tctagagcca acttggttat cgtaatgaat agagagacta catctatatc aattattacg
60
ctctatagta atcatgaagc ttgggttata tgtatgacaa aaattgcaga aaaatcgaaa
120
caagaatatg gcgacttact aaaagaaaaa gaccatttac aagatatgga acagcttgag
180
atgactatcg tctcgatcca tacgccgtat ccgtccattg tcagaattca aggaaaaatc
240
aacacattac agccagagct ttggcaagct cccaatttag caattcggtt aattgtgagc
300
aatccgccag agggacaacc catctcacgc gt
332

```

<210> 416

<211> 102

<212> PRT

<213> Homo sapiens

<400> 416

```

Met Asn Arg Glu Thr Thr Ser Ile Ser Ile Ile Thr Leu Tyr Ser Asn
 1           5           10           15
His Glu Ala Trp Val Ile Cys Met Thr Lys Ile Ala Glu Lys Ser Lys
      20           25           30
Gln Glu Tyr Gly Asp Leu Leu Lys Glu Lys Asp His Leu Gln Asp Met
      35           40           45
Glu Gln Leu Glu Met Thr Ile Val Ser Ile His Thr Pro Tyr Pro Ser
      50           55           60
Ile Val Arg Ile Gln Gly Lys Ile Asn Thr Leu Gln Pro Glu Leu Trp

```

```

<210> 417
<211> 483
<212> DNA
<213> Homo sapiens

```

```
<210> 418
<211> 161
<212> PRT
<213> Homo sapiens
```

639



130                      135                      140  
 Gly Pro Arg Ala Leu Asn Ala Asn Gly Ile Lys Val Leu Ala Asp Pro  
 145                      150                      155                      160  
 Arg

<210> 419  
 <211> 797  
 <212> DNA  
 <213> Homo sapiens

<400> 419  
 atttcacccc aggaaaacca gtaaggacca atgattaagc ccaaggttgg gtaccgagtt  
 60  
 cggatccata agtaccggcc gcccaggggtg ctggaatttg ggctcccccc ggtgaaaata  
 120  
 tccatgcagc cgcgttgtct taggtagaaa agggagactg ggggtgggtg ggctgagctc  
 180  
 aagcccctgc ctacatactt tagtagtaac gactcccgat ctgcatccaa cacatttacc  
 240  
 gaacttctag taagcgcccc ccgctgcaag cgaaagcact cccctgccaa gaaacagatc  
 300  
 ttttccactt aaaattccca aactcagacc ttccactttt tactgaacaa aaagcgtgta  
 360  
 catgatctga agggttgaca tgacattttc taaattgggc gaatcaggaa gaggttgatg  
 420  
 aaaatccttg acgttttctg gggataggac atttgtgtgt gataacgttc ttaagtcgaa  
 480  
 tttcagtgtg gcagtgcacg cagattcttc attggtgtta gtgtatttcc atacggtatg  
 540  
 tattagtaca agaaatagtg ttccctttga cactcgaacc caaggagtgg tccgaggctt  
 600  
 tttgaggcaa cgtaggatca atgtctctga agcagatttg gtgaaggatg caggtctcat  
 660  
 aatttacaga gcaatcacag ccttctttga aacggagaaa ttagattcta tgaaattttg  
 720  
 tcagtgcaga tagatatgat gtggagaaac ggggaaaatt gagtacaaaa agatgaggct  
 780  
 tgaatgatgg ctggcca  
 797

<210> 420  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 420  
 Met Arg Pro Ala Ser Phe Thr Lys Ser Ala Ser Glu Thr Leu Ile Leu  
 1                      5                      10                      15  
 Arg Cys Leu Lys Lys Pro Arg Thr Thr Pro Trp Val Arg Val Ser Lys  
 20                      25                      30  
 Gly Thr Leu Phe Leu Val Leu Ile His Thr Val Trp Lys Tyr Thr Asn  
 35                      40                      45  
 Thr Asn Glu Glu Ser Ala Cys Thr Ala Thr Leu Lys Phe Asp Leu Arg

```

      50              55              60
Thr Leu Ser His Thr Asn Val Leu Ser Pro Glu Asn Val Lys Asp Phe
65              70              75              80
His Gln Pro Leu Pro Asp Ser Pro Asn Leu Glu Asn Val Met Ser Thr
      85              90              95
Leu Gln Ile Met Tyr Thr Leu Phe Val Gln
      100              105

```

<210> 421  
 <211> 406  
 <212> DNA  
 <213> Homo sapiens

```

<400> 421
ggatccacca tgatggagcc caccacacca tcctcagtec acctgctgca gcttctccat
60
aaccacaacac aggtcaatct tgtctcccta aacacacccat gtgctctcat gctgccatgg
120
tttgctctggg gccctctcta cctcctctgc tttctggaga acccttgca cctctccaag
180
ccttcaagtt ggaaagtga cagtcagcat atgtctctag ctcagccctt actgcgtgga
240
ttcatgaaga ttggttcact gtcagccctt gaccagaacg tgtgttttag gaaagcagga
300
accaagtctt accaatgtct gtagtcccag cctccaccct ggcatacagt aggtgctcat
360
tgaatgtggg agggaaagag gagacacatg gaagggaatg tcattc
406

```

<210> 422  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

```

<400> 422
Met Met Glu Pro Thr His Pro Ser Ser Val His Leu Leu Gln Leu Leu
1      5      10      15
His Asn Pro Thr Gln Val Asn Leu Val Ser Leu Asn Thr Pro Cys Ala
20      25      30
Leu Met Leu Pro Trp Phe Ala Trp Gly Pro Leu Tyr Leu Leu Cys Phe
35      40      45
Leu Glu Asn Pro Cys Thr Pro Pro Lys Pro Ser Ser Trp Lys Val Asn
50      55      60
Ser Gln His Met Ser Leu Ala Gln Pro Leu Leu Arg Gly Phe Met Lys
65      70      75      80
Ile Gly Ser Leu Ser Ala Pro Asp Gln Asn Val Cys Phe Arg Lys Ala
85      90      95
Gly Thr Lys Ser Tyr Gln Cys Leu
100

```

<210> 423  
 <211> 628  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 423

ngccacccta cgcctcgcct gcaatggcaa cttcagatcc ccggtggcac cgtagtctta  
 60  
 gagccaccgg ttctgagcgg ggaggacgac ggggttgggg cggaggaagg agaggagaa  
 120  
 ggagatgggg atttgctgac gcagacccaa gcccaaacgc cgactccagc acccgcttgg  
 180  
 ccggcgcccc cagccacacc gcgcttcctg gccctcgcaa atggtccct gttggtgccc  
 240  
 ctctgagtg ccaaggaggc gggcgtctac acttgccgtg cacacaatga gctgggcgcc  
 300  
 aactctacgt caatacgcgt ggcggtggca gcaaccgggc ccccaaaaca cgcgcctggc  
 360  
 gccgggggag aaccgcagcg acaggccccg acctctgagc gcaagtccac agccaagggc  
 420  
 cggggcaaca gcgtcctgcc ttccaaaccc gagggcaaaa tcaaaggcca aggcctggcc  
 480  
 aaggtcagca ttctcgggga gaccgagacg gagccggagg aggacacaag tgaggagag  
 540  
 gaggccgaag accagatcct cgcggaccgg gcggaggagc agcgctgtgg caacggggac  
 600  
 ccctctcggt acgtttctaa ccacgcgt  
 628

&lt;210&gt; 424

&lt;211&gt; 209

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 424

Xaa	His	Pro	Thr	Pro	Arg	Leu	Gln	Trp	Gln	Leu	Gln	Ile	Pro	Gly	Gly
1				5				10					15		
Thr	Val	Val	Leu	Glu	Pro	Pro	Val	Leu	Ser	Gly	Glu	Asp	Asp	Gly	Val
			20				25					30			
Gly	Ala	Glu	Gly	Glu	Gly	Gly	Gly	Asp	Gly	Asp	Leu	Leu	Thr	Gln	
		35				40					45				
Thr	Gln	Ala	Gln	Thr	Pro	Thr	Pro	Ala	Pro	Ala	Trp	Pro	Ala	Pro	Pro
		50				55				60					
Ala	Thr	Pro	Arg	Phe	Leu	Ala	Leu	Ala	Asn	Gly	Ser	Leu	Leu	Val	Pro
65				70				75						80	
Leu	Leu	Ser	Ala	Lys	Glu	Ala	Gly	Val	Tyr	Thr	Cys	Arg	Ala	His	Asn
			85					90					95		
Glu	Leu	Gly	Ala	Asn	Ser	Thr	Ser	Ile	Arg	Val	Ala	Val	Ala	Ala	Thr
			100				105					110			
Gly	Pro	Pro	Lys	His	Ala	Pro	Gly	Ala	Gly	Gly	Glu	Pro	Asp	Gly	Gln
		115				120					125				
Ala	Pro	Thr	Ser	Glu	Arg	Lys	Ser	Thr	Ala	Lys	Gly	Arg	Gly	Asn	Ser
		130				135				140					
Val	Leu	Pro	Ser	Lys	Pro	Glu	Gly	Lys	Ile	Lys	Gly	Gln	Gly	Leu	Ala
145				150						155				160	
Lys	Val	Ser	Ile	Leu	Gly	Glu	Thr	Glu	Thr	Glu	Pro	Glu	Glu	Asp	Thr
			165				170					175			
Ser	Glu	Gly	Glu	Glu	Ala	Glu	Asp	Gln	Ile	Leu	Ala	Asp	Pro	Ala	Glu

180 185 190  
 Glu Gln Arg Cys Gly Asn Gly Asp Pro Ser Arg Tyr Val Ser Asn His  
 195 200 205  
 Ala

<210> 425  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

<400> 425  
 ccggccgctcg aagactttga ggacgatgta gctcgcagcg cagcggttacg agccctggag  
 60  
 tacgtggatt tgaccccagg cactnaagtg cgcgtcatcg ccattgacac cgtgttccta  
 120  
 ggatcgtgca cgaatggccg tgaggactta cggctggctg ctgagggttcc caaaggacga  
 180  
 catatcgacg cgggcacccg gatgctcgtc gccctggat ctgctcgtgt ccgtctgcag  
 240  
 gctatggagg aaggcctcga cgagatcggg tcccggtttg ctgacatctt tcgcaataac  
 300  
 tctgcgaaca atggcttggt actggctcag gttgaccccg aggtcgtcga agagttgtgg  
 360  
 gactttgccg agcagcatcc tggtagacg ctcaccgtct ccctcgagaa tcggacgac  
 420  
 aaccttccgg gtcgcacgac ctaccggttc catattgatg acgtcacgcg t  
 471

<210> 426  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 426  
 Pro Ala Val Glu Asp Phe Glu Asp Asp Val Ala Arg Ser Ala Ala Leu  
 1 5 10 15  
 Arg Ala Leu Glu Tyr Val Asp Leu Thr Pro Gly Thr Xaa Val Arg Val  
 20 25 30  
 Ile Ala Ile Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Gly Arg Glu  
 35 40 45  
 Asp Leu Arg Leu Ala Ala Glu Val Pro Lys Gly Arg His Ile Ala Ala  
 50 55 60  
 Gly Thr Arg Met Leu Val Ala Pro Gly Ser Ala Arg Val Arg Leu Gln  
 65 70 75 80  
 Ala Met Glu Glu Gly Leu Asp Glu Ile Gly Ser Arg Phe Ala Asp Ile  
 85 90 95  
 Phe Arg Asn Asn Ser Ala Asn Asn Gly Leu Leu Leu Ala Gln Val Asp  
 100 105 110  
 Pro Glu Val Val Glu Glu Leu Trp Asp Phe Ala Glu Gln His Pro Gly  
 115 120 125  
 Glu Gln Leu Thr Val Ser Leu Glu Asn Arg Thr Ile Asn Leu Pro Gly  
 130 135 140  
 Arg Thr Thr Tyr Pro Phe His Ile Asp Asp Val Thr Arg

145

150

155

&lt;210&gt; 427

&lt;211&gt; 546

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 427

ctagcggtag tagaaggat gcagtttgat cgcggtact tgttccgta tttcatcaac  
60  
aatcaagaaa caatgaatgc agagctagaa aacccattta ttcttcttgt tgataagaaa  
120  
atttctaata tccgtgactt gctaccaatt ttggaagggtg ttgctaaagc atcgcgccca  
180  
ttgttgatca ttgcggaaga cgttgaaggc gaagcgttgg caaccttggt tgtaaacact  
240  
atgcgcggca tcgtaaaagt agcggcagcg aaagcgccag gttttggtga tcgccgtaaa  
300  
gcaatgcttc aagacattgc tgtgctaacg ggttcaactg ttatttcaga agaaattggc  
360  
attaagcttg aagaagcgac aattgaacag ttgggtacag cgaagcgcgt tacattgaca  
420  
aaagaaagta caacgattgt tgatggtgcg ggtgttgacg ctaatattac tggtcgtgtt  
480  
gagcaaattc gtgcagaaat tgctaactct tcttctggct acgataaaga gaaattgcaa  
540  
gaacgc  
546

&lt;210&gt; 428

&lt;211&gt; 182

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 428

Leu	Ala	Val	Val	Glu	Gly	Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro
1				5					10				15		
Tyr	Phe	Ile	Asn	Asn	Gln	Glu	Thr	Met	Asn	Ala	Glu	Leu	Glu	Asn	Pro
			20					25					30		
Phe	Ile	Leu	Leu	Val	Asp	Lys	Lys	Ile	Ser	Asn	Ile	Arg	Asp	Leu	Leu
		35				40					45				
Pro	Ile	Leu	Glu	Gly	Val	Ala	Lys	Ala	Ser	Arg	Pro	Leu	Leu	Ile	Ile
	50				55					60					
Ala	Glu	Asp	Val	Glu	Gly	Glu	Ala	Leu	Ala	Thr	Leu	Val	Val	Asn	Thr
65					70				75					80	
Met	Arg	Gly	Ile	Val	Lys	Val	Ala	Ala	Ala	Lys	Ala	Pro	Gly	Phe	Gly
			85					90					95		
Asp	Arg	Arg	Lys	Ala	Met	Leu	Gln	Asp	Ile	Ala	Val	Leu	Thr	Gly	Ser
		100					105					110			
Thr	Val	Ile	Ser	Glu	Glu	Ile	Gly	Ile	Lys	Leu	Glu	Glu	Ala	Thr	Ile
		115				120					125				
Glu	Gln	Leu	Gly	Thr	Ala	Lys	Arg	Val	Thr	Leu	Thr	Lys	Glu	Ser	Thr
	130					135				140					
Thr	Ile	Val	Asp	Gly	Ala	Gly	Val	Ala	Ala	Asn	Ile	Thr	Gly	Arg	Val

145                      150                      155                      160  
 Glu Gln Ile Arg Ala Glu Ile Ala Asn Ser Ser Ser Gly Tyr Asp Lys  
                                  165                      170                      175  
 Glu Lys Leu Gln Glu Arg  
                                  180

<210> 429  
 <211> 425  
 <212> DNA  
 <213> Homo sapiens

<400> 429  
 gctagcagcc cttacaggag acgggctaata aataatgcag cagtggctcc gacaacttgc  
 60  
 ccgttgacgc cggtcacgga tccatttgct tttagtagac aggcgctcca aagtacacca  
 120  
 ctgggcagtt cgtccaaaag cagtccacct gtcttgcaag gccagcccc cgcagggttt  
 180  
 tctcaacacc ccggtttgct tgtgccttac acacaatgca aaaaatagct ctcagggacc  
 240  
 ctgtgagccc ctgcctggac ctctgacaca gccagagca catgccagtc cgttttctgg  
 300  
 tgcattgaca ccttcagcac ctctggggcc tgagatgaac aggagtgcag aggtcgggtcc  
 360  
 cagttcagag cctgaagttc agactctgcc atatcttct cactacattc caggagtga  
 420  
 tcctg  
 425

<210> 430  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 430  
 Met Gln Gln Trp Leu Arg Gln Leu Ala Arg Cys Ser Arg Ser Arg Ile  
 1                      5                      10                      15  
 His Leu Leu Leu Val Asp Arg Arg Ser Lys Val His His Trp Ala Val  
                                  20                      25                      30  
 Arg Pro Lys Ala Val His Leu Ser Cys Lys Ala Gln Pro Pro Gln Gly  
                                  35                      40                      45  
 Phe Leu Asn Thr Pro Val Cys Leu Cys Leu Thr His Asn Ala Lys Asn  
                                  50                      55                      60  
 Ser Ser Gln Gly Pro Cys Glu Pro Leu Pro Gly Pro Leu Thr Gln Pro  
 65                      70                      75                      80  
 Arg Ala His Ala Ser Pro Phe Ser Gly Ala Leu Thr Pro Ser Ala Pro  
                                  85                      90                      95  
 Pro Gly Pro Glu Met Asn Arg Ser Ala Glu Val Gly Pro Ser Ser Glu  
                                  100                      105                      110  
 Pro Glu Val Gln Thr Leu Pro Tyr Leu Pro His Tyr Ile Pro Gly Val  
                                  115                      120                      125  
 Asp Pro  
 130

<210> 431  
 <211> 192  
 <212> DNA  
 <213> Homo sapiens

<400> 431  
 ctagccatcc accagcgtac acacacggga gagaggccct acactggcct cgggtgcaac  
 60  
 cgccgcttcc gccagcgcac ggccctcgtc atccaccagc gcatccacac gggcgagaag  
 120  
 cctnaccgt gcccggaactg cgagcggcgc ttctcctcct cctctcgcct ggtcagtcac  
 180  
 cggcgtgtgc ac  
 192

<210> 432  
 <211> 64  
 <212> PRT  
 <213> Homo sapiens

<400> 432  
 Leu Ala Ile His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Thr Gly  
 1 5 10 15  
 Leu Gly Cys Asn Arg Arg Phe Arg Gln Arg Thr Ala Leu Val Ile His  
 20 25 30  
 Gln Arg Ile His Thr Gly Glu Lys Pro Xaa Pro Cys Pro Asp Cys Glu  
 35 40 45  
 Arg Arg Phe Ser Ser Ser Ser Arg Leu Val Ser His Arg Arg Val His  
 50 55 60

<210> 433  
 <211> 635  
 <212> DNA  
 <213> Homo sapiens

<400> 433  
 nngccggcgg ctgcgttggg atacgacgtc gctgcgattg ggcgtgagta tctttggtac  
 60  
 ctcattggagg agcgtggcgc gtatgcggag gccgccgcgc tcatgccgct gctgctccgg  
 120  
 accgaccgag gcgcgtggga cacgtttgtg tgctgctacc tcgagcggca ccaaagggat  
 180  
 gcgatactcc cgcacattcc gacgcaggac cccagctga gtgagatggt gtacgatctc  
 240  
 gtgctggtgc atctgctgca gcacgatccc acgcagctgt tggcgacgct ccgcgcatgg  
 300  
 ccgagtcaca tctactcgaa gcaggcgggtg gctgcggcga tcggcgatca cgcacgaacc  
 360  
 agccgcacgc tgctcgagtg cctcgcacag ctgtacatgg ccgcacatca gcccggcaag  
 420  
 gctctgacat actacatgcg cctgcgtgat ccatgcgtgt ttgatctcat tcgcgagtac  
 480  
 gatctgctga tcgatgtgca gcaccacatc ggcacgctcg tcgagctcga tcaggaatgc  
 540

gccggctcca ctgagccgcg ctccagcgcg cttatgccgc tgctcgtgcc atataccac  
 600  
 tcgattccca tccagcgcg catggcgag ctcga  
 635

<210> 434  
 <211> 211  
 <212> PRT  
 <213> Homo sapiens

<400> 434  
 Xaa Pro Ala Ala Leu Gly Tyr Asp Val Ala Ala Ile Gly Arg Glu  
 1 5 10 15  
 Tyr Leu Trp Tyr Leu Met Glu Glu Arg Gly Ala Tyr Ala Glu Ala Ala  
 20 25 30  
 Ala Leu Met Pro Leu Leu Leu Arg Thr Asp Arg Gly Ala Trp Asp Thr  
 35 40 45  
 Phe Val Cys Cys Tyr Leu Glu Arg His Gln Arg Asp Ala Ile Leu Pro  
 50 55 60  
 His Ile Pro Thr Gln Asp Pro Gln Leu Ser Glu Met Val Tyr Asp Leu  
 65 70 75 80  
 Val Leu Val His Leu Leu Gln His Asp Pro Thr Gln Leu Leu Ala Thr  
 85 90 95  
 Leu Arg Ala Trp Pro Ser His Ile Tyr Ser Lys Gln Ala Val Ala Ala  
 100 105 110  
 Ala Ile Gly Asp His Ala Arg Thr Ser Arg Thr Leu Leu Glu Cys Leu  
 115 120 125  
 Ala Gln Leu Tyr Met Ala Ala His Gln Pro Gly Lys Ala Leu Thr Tyr  
 130 135 140  
 Tyr Met Arg Leu Arg Asp Pro Cys Val Phe Asp Leu Ile Arg Glu Tyr  
 145 150 155 160  
 Asp Leu Leu Ile Asp Val Gln His His Ile Gly Thr Leu Val Glu Leu  
 165 170 175  
 Asp Gln Glu Cys Ala Gly Ser Thr Glu Pro Arg Ser Ser Ala Leu Met  
 180 185 190  
 Pro Leu Leu Val Pro Tyr Thr His Ser Ile Pro Ile Gln Arg Ala Met  
 195 200 205  
 Ala Gln Leu  
 210

<210> 435  
 <211> 493  
 <212> DNA  
 <213> Homo sapiens

<400> 435  
 nncgtacgtt cgcgtatattt ccgcgccccg gaagctatcg ataataaagt tcaaccgctg  
 60  
 atccagcgtt agcaatggcg ggcacaggaa gggacttag gcatgcagaa agaaaagctt  
 120  
 tccgctctga tggatgggta atcggtcgac agcgagctgt tgagttctct gtcgcaagat  
 180  
 cgaacgcttc aacaaagctg gcagggctat cacctgatac gtgacacact gcgaggtgat  
 240



gtcgggcaag tgatgcatct cgacatcgcc gatcgcgtag ccgctgcact tgagaaagaa  
 300  
 cccgcccggc tgggtgccttc cgccgttcag gaatctcagc cgcagcctca cacctggcag  
 360  
 aaaatgccgt tctgggacaa agtgcgtccc tgggcgagcc agattacgca aatcggtatg  
 420  
 gcggcctgcg tgtcgctggc ggtgatcgtc ggcgtgcagc agtacaacca gccttctgcg  
 480  
 ccatcgaacg cgt  
 493

<210> 436

<211> 130

<212> PRT

<213> Homo sapiens

<400> 436

Met	Gln	Lys	Glu	Lys	Leu	Ser	Ala	Leu	Met	Asp	Gly	Glu	Ser	Phe	Asp
1				5					10					15	
Ser	Glu	Leu	Leu	Ser	Ser	Leu	Ser	Gln	Asp	Arg	Thr	Leu	Gln	Gln	Ser
			20					25					30		
Trp	Gln	Gly	Tyr	His	Leu	Ile	Arg	Asp	Thr	Leu	Arg	Gly	Asp	Val	Gly
		35					40					45			
Gln	Val	Met	His	Leu	Asp	Ile	Ala	Asp	Arg	Val	Ala	Ala	Ala	Leu	Glu
	50					55				60					
Lys	Glu	Pro	Ala	Arg	Leu	Val	Pro	Ser	Ala	Val	Gln	Glu	Ser	Gln	Pro
65					70					75				80	
Gln	Pro	His	Thr	Trp	Gln	Lys	Met	Pro	Phe	Trp	Asp	Lys	Val	Arg	Pro
			85						90					95	
Trp	Ala	Ser	Gln	Ile	Thr	Gln	Ile	Gly	Met	Ala	Ala	Cys	Val	Ser	Leu
			100					105					110		
Ala	Val	Ile	Val	Gly	Val	Gln	Gln	Tyr	Asn	Gln	Pro	Ser	Ala	Pro	Ser
		115					120						125		
Asn	Ala														
	130														

<210> 437

<211> 447

<212> DNA

<213> Homo sapiens

<400> 437

ntggtaaccg gtgtccctga tatggaccct gctgtgtag agcgtaaatt atttatttta  
 60  
 cgtaattatg taacacgcat ctgtttggag tctgttaatg gaattaagga caacttttac  
 120  
 attaatacat tctcatataa aacaatcggt tataaaggtc agttaaccac tgaacaagtg  
 180  
 ccacaatatt tcttagattt acaaaatcca agtatggtaa cggcattagc gcttggtcat  
 240  
 tcacgtttct caacaaatac atttcctcgt tggcgtttag cacaaccatt ccgttacatc  
 300  
 gtcataatg gcgaaatcaa tacggttcgc ggtaatatca attggatgaa agcacgtgaa  
 360

gcgttacttg aagctgaatt ttctactcgc tcagaattag atatgttaat gccaatctgt  
 420  
 acggatggta tgtctgactc ggcaagg  
 447

<210> 438  
 <211> 149  
 <212> PRT  
 <213> Homo sapiens

<400> 438  
 Xaa Val Thr Gly Val Pro Asp Met Asp Pro Ala Val Leu Glu Arg Lys  
 1 5 10 15  
 Leu Phe Ile Leu Arg Asn Tyr Val Thr Arg Ile Cys Leu Glu Ser Val  
 20 25 30  
 Asn Gly Ile Lys Asp Asn Phe Tyr Ile Asn Thr Phe Ser Tyr Lys Thr  
 35 40 45  
 Ile Val Tyr Lys Gly Gln Leu Thr Thr Glu Gln Val Pro Gln Tyr Phe  
 50 55 60  
 Leu Asp Leu Gln Asn Pro Ser Met Val Thr Ala Leu Ala Leu Val His  
 65 70 75 80  
 Ser Arg Phe Ser Thr Asn Thr Phe Pro Arg Trp Arg Leu Ala Gln Pro  
 85 90 95  
 Phe Arg Tyr Ile Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn  
 100 105 110  
 Ile Asn Trp Met Lys Ala Arg Glu Ala Leu Leu Glu Ala Glu Phe Phe  
 115 120 125  
 Thr Arg Ser Glu Leu Asp Met Leu Met Pro Ile Cys Thr Asp Gly Met  
 130 135 140  
 Ser Asp Ser Ala Arg  
 145

<210> 439  
 <211> 395  
 <212> DNA  
 <213> Homo sapiens

<400> 439  
 nacgcgtgaa gggagagtgg ggccgagccc caggaggctg tcctgcagca gctgcaccag  
 60  
 cttcccagg ggcggctgga cctggccacg caaagcctga cggtggagac ctgcagggcc  
 120  
 ctgggcaagc tgctgccgag ggagacgctg tgcacggagc tggtcctgag tgactgcatg  
 180  
 ctcagcgagg aagggggccac actgctgctc cgaggcctgt gtgccaacac cgtgctgcgc  
 240  
 tttctggact taaagggcaa caaccttcgg gctgcagggg ccgaggctct gggaaaactc  
 300  
 ctccaacaga acaagtccat tcagagcctc acgctggagt ggaacagcct gggcacgtgg  
 360  
 gacgatgcct tcgccacctt ctgcgggggc ctggc  
 395

<210> 440

<211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 440  
 Arg Glu Ser Gly Ala Glu Pro Gln Glu Ala Val Leu Gln Gln Leu His  
 1 5 10 15  
 Gln Leu Pro Arg Gly Arg Leu Asp Leu Ala Thr Gln Ser Leu Thr Val  
 20 25 30  
 Glu Thr Cys Arg Ala Leu Gly Lys Leu Leu Pro Arg Glu Thr Leu Cys  
 35 40 45  
 Thr Glu Leu Val Leu Ser Asp Cys Met Leu Ser Glu Glu Gly Ala Thr  
 50 55 60  
 Leu Leu Leu Arg Gly Leu Cys Ala Asn Thr Val Leu Arg Phe Leu Asp  
 65 70 75 80  
 Leu Lys Gly Asn Asn Leu Arg Ala Ala Gly Ala Glu Ala Leu Gly Lys  
 85 90 95  
 Leu Leu Gln Gln Asn Lys Ser Ile Gln Ser Leu Thr Leu Glu Trp Asn  
 100 105 110  
 Ser Leu Gly Thr Trp Asp Asp Ala Phe Ala Thr Phe Cys Gly Gly Leu  
 115 120 125

<210> 441  
 <211> 364  
 <212> DNA  
 <213> Homo sapiens

<400> 441  
 gccagctact acgtgaacat gttcgatgcc gagcagggct tcttcgacag gcgcagcccg  
 60  
 ggcgccgaggt tccaagccgg cttggatccg gaatcctggg gcggtctgtt cactgagacc  
 120  
 gacgggtgga acttcgcctt ccacgctcca caggacggcc gggggctggc cgcgctctac  
 180  
 ggcggtccga aaggcttgga gaacaagctc gatgcctttt tcgcgacgcc ggaaaacgcg  
 240  
 gacaagccgg cgtacggcgg aatccacgaa atggtcgagg ccagagcggg ccggatgggc  
 300  
 caattgggca tgtccaacga gccctcgac catattcctt acatctacaa ctatgccggc  
 360  
 gcgc  
 364

<210> 442  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 442  
 Ala Gln Tyr Tyr Val Asn Met Phe Asp Ala Glu Gln Gly Phe Phe Asp  
 1 5 10 15  
 Arg Arg Ser Pro Gly Gly Glu Phe Gln Ala Gly Leu Asp Pro Glu Ser  
 20 25 30  
 Trp Gly Gly Leu Phe Thr Glu Thr Asp Gly Trp Asn Phe Ala Phe His

```

      35              40              45
Ala Pro Gln Asp Gly Arg Gly Leu Ala Ala Leu Tyr Gly Gly Pro Lys
      50              55              60
Gly Leu Glu Asn Lys Leu Asp Ala Phe Phe Ala Thr Pro Glu Asn Ala
65              70              75              80
Asp Lys Pro Ala Tyr Gly Gly Ile His Glu Met Val Glu Ala Arg Ala
      85              90              95
Val Arg Met Gly Gln Leu Gly Met Ser Asn Glu Pro Ser His His Ile
      100             105             110
Pro Tyr Ile Tyr Asn Tyr Ala Gly Ala
      115             120

```

<210> 443  
 <211> 430  
 <212> DNA  
 <213> Homo sapiens

```

<400> 443
accgggttacg gctcagtgca acaagagatg ttcgccaaca acctcgtgcg gatgccgctg
60
ctcatggtgct tggcaatccc ctctgccaag atcctctcga cgacctgtc catcggatcg
120
ggcgggtccgg cggcgctcttc cggccctggc atgggtcatcg gcggagccac tggcgcgga
180
ctgtggcgcc tcctcgaggg gctgccaggt atcccatcct caccgatgag ttctgtcatt
240
gtcggcatga tcgcctgctt cgggtcgggt gcccatgccc cactcggcgt gctgctcatg
300
gttggcgaga tgaccggaaa cctgtcgtg ctgctcctg gcatgatcgc cgtcgccgtc
360
gctggccgag ttgtcgggga cacttcgatc tacacctctc agctcaagga tcgcctggag
420
ggcgacgcgt
430

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<210> 444  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

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<400> 444
Thr Gly Tyr Gly Ser Val Gln Gln Glu Met Phe Ala Asn Asn Leu Val
1              5              10              15
Arg Met Pro Leu Leu Met Val Leu Ala Ile Pro Phe Ala Lys Ile Leu
20              25              30
Ser Thr Thr Leu Ser Ile Gly Ser Gly Gly Pro Ala Ala Ser Ser Gly
35              40              45
Pro Gly Met Val Ile Gly Gly Ala Thr Gly Ala Ala Leu Trp Arg Leu
50              55              60
Leu Glu Gly Leu Pro Gly Ile Pro Ser Ser Pro Met Ser Phe Val Ile
65              70              75              80
Val Gly Met Ile Ala Cys Phe Gly Ala Val Ala His Ala Pro Leu Gly
85              90              95
Val Leu Leu Met Val Gly Glu Met Thr Gly Asn Leu Ser Leu Leu Ala

```

	100		105		110										
Pro	Gly	Met	Ile	Ala	Val	Ala	Val	Ala	Gly	Arg	Val	Val	Gly	Asp	Thr
	115				120				125						
Ser	Ile	Tyr	Thr	Ser	Gln	Leu	Lys	Asp	Arg	Leu	Glu	Gly	Asp	Ala	
	130				135					140					

<210> 445  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 445  
 ccatggggct gcctagcctc tggggaggcc cctcagctgg tgacaccagc agggcagatt  
 60  
 tcttgcttta ttgctcacc tgtccagggt tccctctggt tgtgaggag ctgctgccac  
 120  
 cttgggtcca ggaagcatga agctccgcag gtcagcctcc tgggtggagg acttttcctt  
 180  
 agttttcttt gctcttctgc tctgagtcca gccctggctg gaccttgat cccttctctc  
 240  
 tttatcagga aattttctga ctttcttctt ttgccttttc aagatctgtg atgccatctc  
 300  
 caagtgggaa caagccatga aggagctgca ccccgaaag tctgagggtg ggacacgcgt  
 360

<210> 446  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

Met	Ala	Cys	Ser	His	Leu	Glu	Met	Ala	Ser	Gln	Ile	Leu	Lys	Arg	Gln
1				5				10					15		
Lys	Lys	Lys	Val	Arg	Lys	Phe	Pro	Asp	Lys	Glu	Arg	Arg	Asp	Gln	Arg
			20				25					30			
Ser	Ser	Gln	Gly	Trp	Thr	Gln	Ser	Arg	Arg	Ala	Lys	Lys	Thr	Lys	Glu
		35				40					45				
Lys	Ser	Ser	His	Gln	Glu	Ala	Asp	Leu	Arg	Ser	Phe	Met	Leu	Pro	Gly
	50				55					60					
Pro	Lys	Val	Ala	Ala	Ala	Pro	Ser	Gln	Thr	Glu	Gly	Thr	Leu	Asp	Arg
65				70				75					80		
Val	Ser	Asn	Lys	Ala	Arg	Asn	Leu	Pro	Cys	Trp	Cys	His	Gln	Leu	Arg
			85				90						95		
Gly	Leu	Pro	Arg	Gly											
			100												

<210> 447  
 <211> 487  
 <212> DNA  
 <213> Homo sapiens

<400> 447  
 acgcgtgaag ggggaaattg ctgctgccac ctgaggatta atcattaccc tggaaccctt  
 60

cccaaggcca tcaaggaaca cgcacccctt accagacctt ccagctgctg ggggctctcc  
 120  
 gagtgaggct gaggtcatgg agaaggaat ggggggcccc catggccagc tggacctgat  
 180  
 cactgcctcc cactcagcc acagccctca gggccctgtg ccagtcaga agccattca  
 240  
 gggacacctt tggccaatgt tctgtttcat ctgcgaggca accttcccca gtgcccac  
 300  
 catagcgttt tccccaaac accctcagga aggagggacc actacctgtg cagggggggg  
 360  
 caggagcctc ctgagagcct catatgggga ggaagtggta ccatctcacc cccattgcct  
 420  
 ttctctccta ctccacctg gccagcttcc ctcaagtccc ctctgcctc agtgcccctt  
 480  
 cacgcgt  
 487

&lt;210&gt; 448

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 448

Met	Glu	Lys	Gly	Met	Gly	Gly	Pro	His	Gly	Gln	Leu	Asp	Leu	Ile	Thr
1				5					10					15	
Ala	Ser	Pro	Leu	Ser	His	Ser	Pro	Gln	Gly	Pro	Val	Pro	Val	Gln	Lys
			20					25					30		
Pro	Ile	Gln	Gly	His	Leu	Trp	Pro	Met	Phe	Cys	Phe	Ile	Cys	Glu	Ala
		35				40					45				
Thr	Phe	Pro	Ser	Ala	Pro	Thr	Ile	Ala	Phe	Ser	Pro	Lys	His	Pro	Gln
	50					55					60				
Glu	Gly	Gly	Thr	Thr	Thr	Cys	Ala	Gly	Gly	Ala	Arg	Ser	Leu	Leu	Arg
65				70					75				80		
Ala	Ser	Tyr	Gly	Glu	Glu	Val	Val	Pro	Ser	His	Pro	His	Cys	Leu	Ser
			85					90					95		
Leu	Leu	Leu	Pro	Pro	Gly	Gln	Leu	Pro	Ser	Val	Pro	Leu	Leu	Pro	Gln
			100				105						110		
Cys	Pro	Phe	Thr	Arg											
			115												

&lt;210&gt; 449

&lt;211&gt; 353

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 449

gagctcagcc agttggagtt tgagaagcgg cagctgcaca gggacttgga gcaggccaag  
 60  
 gagaagggggg agcgggcaga gaagctggag agggagctac agcgactcca ggaggagaac  
 120  
 gggaggctgg ccaggaaggt gacctccctg gagacagcca ccgagaaagt cgaggccctg  
 180  
 gagcatgaga gccagggcct gcagctggag aaccggactc tgaggaagtc tctggacacc  
 240

ttgcagaacg tgtccctgca gcttgagggc ctggagcgtg acaacaagca gctggacgca  
 300  
 gagaacctgg agctgcgcag gctggtggag accatgcgga gacgacaacg cgt  
 353

<210> 450  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 450  
 Glu Leu Ser Gln Leu Glu Phe Glu Lys Arg Gln Leu His Arg Asp Leu  
 1 5 10 15  
 Glu Gln Ala Lys Glu Lys Gly Glu Arg Ala Glu Lys Leu Glu Arg Glu  
 20 25 30  
 Leu Gln Arg Leu Gln Glu Glu Asn Gly Arg Leu Ala Arg Lys Val Thr  
 35 40 45  
 Ser Leu Arg Thr Ala Thr Glu Lys Val Glu Ala Leu Glu His Glu Ser  
 50 55 60  
 Gln Gly Leu Gln Leu Glu Asn Arg Thr Leu Arg Lys Ser Leu Asp Thr  
 65 70 75 80  
 Leu Gln Asn Val Ser Leu Gln Leu Glu Gly Leu Glu Arg Asp Asn Lys  
 85 90 95  
 Gln Leu Asp Ala Glu Asn Leu Glu Leu Arg Arg Leu Val Glu Thr Met  
 100 105 110  
 Arg Arg Arg Gln Arg  
 115

<210> 451  
 <211> 444  
 <212> DNA  
 <213> Homo sapiens

<400> 451  
 gtgatgcggc tgactaagcc tactttattc accaatatcc cagtaacatg tgaagagaaa  
 60  
 gacttacctg gagatctctt taaccagctg atgagagatg atccttcaac cgttaatggt  
 120  
 gcagaagttt taatgttggg agaaatgctg actttaccac agaattttgg gaatatattt  
 180  
 ttgggagaga ccttttccag ttatatcagc gttcataatg atagcaatca agttgtaaaa  
 240  
 gacatattag taaaagctga tcttcagaca agttctcagc gtttaaactt ttcagcctcc  
 300  
 aatgctgcag tggctgaact taaaccggat tgttgattg atgatgtcat acatcatgaa  
 360  
 gtcaaagaaa ttggaacaca catcttggtg tgtgctgtga gttatacaac tcaggctgga  
 420  
 gaaaaaatgt atttcagaaa attt  
 444

<210> 452  
 <211> 148  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 452

```

Val Met Arg Leu Thr Lys Pro Thr Leu Phe Thr Asn Ile Pro Val Thr
 1           5           10           15
Cys Glu Glu Lys Asp Leu Pro Gly Asp Leu Phe Asn Gln Leu Met Arg
 20           25           30
Asp Asp Pro Ser Thr Val Asn Gly Ala Glu Val Leu Met Leu Gly Glu
 35           40           45
Met Leu Thr Leu Pro Gln Asn Phe Gly Asn Ile Phe Leu Gly Glu Thr
 50           55           60
Phe Ser Ser Tyr Ile Ser Val His Asn Asp Ser Asn Gln Val Val Lys
 65           70           75           80
Asp Ile Leu Val Lys Ala Asp Leu Gln Thr Ser Ser Gln Arg Leu Asn
 85           90           95
Leu Ser Ala Ser Asn Ala Ala Val Ala Glu Leu Lys Pro Asp Cys Cys
100           105           110
Ile Asp Asp Val Ile His His Glu Val Lys Glu Ile Gly Thr His Ile
115           120           125
Leu Val Cys Ala Val Ser Tyr Thr Thr Gln Ala Gly Glu Lys Met Tyr
130           135           140
Phe Arg Lys Phe
145

```

&lt;210&gt; 453

&lt;211&gt; 373

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 453

```

gctagctctg accccacctt tgccaagtgg cactaggggtg gccaatgggg actaggggtg
60
tataattgga aaatacagtc tcccctgttg tccaagaaag gccccagatg acctggggct
120
tgaaaaggcac tcccgtctggg tgcttctctgg gagcaggtgg ggggcagcgg ggcggcgggg
180
cctgtctgtg ctgagcatcc ccagctccag ggcaggtgct gggctctgag cccactgggt
240
gcgttttggg atgggctggc ctgcgcggct gtcgtttcag agcacacaga agagaccctg
300
ccacaggagg agtgggagga gaagctgttg atgttctctgc gagacaccct ggccatcatt
360
tctgacaacg cgt
373

```

&lt;210&gt; 454

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 454

```

Met Met Ala Arg Val Ser Arg Arg Asn Ile Asn Ser Phe Ser Ser His
 1           5           10           15
Ser Ser Cys Gly Arg Val Ser Ser Val Cys Ser Glu Thr Thr Ala Ala

```



```

          20          25          30
Gln Ala Ser Pro Ser Gln Asn Ala Pro Val Gly Leu Arg Ala Gln His
          35          40          45
Leu Pro Trp Ser Trp Gly Cys Ser Ala Gln Thr Gly Pro Ala Ala Pro
          50          55          60
Leu Pro Pro Thr Cys Ser Gln Glu Ala Pro Ser Gly Ser Ala Phe Gln
          65          70          75          80
Ala Pro Gly His Leu Gly Pro Phe Leu Asp Asn Arg Gly Asp Cys Ile
          85          90          95
Phe Gln Leu Tyr Asn Pro Ser Pro His Trp Pro Pro
          100          105

```

<210> 455  
 <211> 602  
 <212> DNA  
 <213> Homo sapiens

```

<400> 455
cctaggcaaa gcatgcccac cctacctccc cttaccctta cccttcattt tcccctaagc
60
accatcacc accgatgtta ctgtatgtgt ttgcttacgc tgacagccca ccaccacac
120
tggaatgtcc gcacgacaaa ggcaggactc ttggctgcct tagccacagc tggatcccca
180
gagcttttga ggggtgttggg cacagagtgg agtgggtact taataagtat ctgtggaatg
240
aacatgtaca gagtgaagcc ctgtgcccag aacaggctca aaataagctc aattcctttc
300
cttgccactt actaagtcct ttttctctcg cccctctca ctgacctggt tttgatgcc
360
gacagcacag atgggctagg gaggcagggt gggaagcaga gatctgcgtc tcttgagct
420
ggagctggtg ggtggggctc cttcctggtg ctgcggaggc tcattgggga ggtggcagcg
480
acccttcag gagcctctgt cgctgcact cagatctgtg cctttccaca gcgccggag
540
gaagacttgc tcaggagata aattcaaaga caacaggaag ctggacgtgg tggctcacgc
600
gt
602

```

<210> 456  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

```

<400> 456
Met Pro Thr Leu Pro Pro Leu Thr Leu Thr Leu His Phe Pro Leu Ser
1          5          10          15
Thr His His His Arg Cys Tyr Cys Met Cys Leu Leu Thr Leu Thr Ala
          20          25          30
His His Pro His Trp Asn Val Arg Thr Thr Lys Ala Gly Leu Leu Ala
          35          40          45
Ala Leu Ala Thr Ala Gly Ser Pro Glu Leu Cys Arg Val Leu Gly Thr

```

```

      50              55              60
Glu Trp Ser Gly Tyr Leu Ile Ser Ile Cys Gly Met Asn Met Tyr Arg
65              70              75              80
Val Lys Pro Cys Ala Gln Asn Arg Leu Lys Ile Ser Ser Ile Pro Phe
      85              90              95
Leu Ala Thr Tyr
      100

```

<210> 457  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

```

<400> 457
acgcgtcatg tggatattcc tgggaggttc ccaggaacgt ttctggacgg gcccccgacc
60
agaggtcagg gaacttttct tattattctg cacgtgccca gggatagtca aaccaggtct
120
tcccccttctg ctggccgcaa cacgccagcc gccgccacga ccgcacgctg aattcatgac
180
ccgacacgcg acgtggcagc gagcacaccc accgctagga gaaagagcgc tcatcgaaga
240
tcgttttctg tccactggcc agcgccacta tgatcaggtg gggatatccgc ccggcggcgg
300
gagcacccggg acgccggggc gccg
324

```

<210> 458  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

```

<400> 458
Met Trp Ile Phe Leu Gly Gly Ser Gln Glu Arg Phe Trp Thr Gly Pro
1              5              10              15
Arg Pro Glu Val Arg Glu Leu Phe Leu Leu Phe Cys Thr Cys Pro Gly
      20              25              30
Ile Val Lys Pro Gly Leu Pro Leu Leu Leu Ala Ala Thr Arg Gln Pro
      35              40              45
Pro Pro Arg Pro His Ala Glu Phe Met Thr Arg His Ala Thr Trp Gln
      50              55              60
Arg Ala His Pro Pro Leu Gly Glu Arg Ala Leu Ile Glu Asp Arg Phe
65              70              75              80
Leu Ser Thr Gly Gln Arg His Tyr Asp Gln Val Gly Tyr Pro Pro Gly
      85              90              95
Gly Gly Ser Thr Gly Thr Pro Gly Arg
      100              105

```

<210> 459  
 <211> 415  
 <212> DNA  
 <213> Homo sapiens

<400> 459

acgcgttcat tcggcatctg cttccatgga tttcctgcgg ggaggcgcgg ccgagagtgc  
60  
gggtgtcgaa caccgacctt cagtgatcgt ttcaaccacc ggccgagatg ggtcctgacg  
120  
ctgggcttca agccgcttgc gctcgcgctc ctgatctcgg gcagcgcgat tccggtgggt  
180  
tatgctgccg gcagacgact gcgcacgccc ctcacgaggt atctgcacat gcttaaaggg  
240  
agaggcctca cccgacagct gggcatcgga tttacgaagc ccacgacgaa tcttcctcgc  
300  
ctcctcaaag ccgatcatcg gcatgccagg tttgtgggtg aatgcttcga tcaacacact  
360  
aggatcggtg gggtccacca catacaccga gcggcaatcg agcggatacg acctc  
415

<210> 460

<211> 105

<212> PRT

<213> Homo sapiens

<400> 460

Met	Pro	Met	Ile	Gly	Phe	Glu	Glu	Ala	Arg	Lys	Ile	Arg	Arg	Gly	Leu
1			5					10				15			
Arg	Lys	Ser	Asp	Ala	Gln	Leu	Ser	Gly	Glu	Ala	Ser	Pro	Phe	Lys	His
		20					25				30				
Val	Gln	Ile	Pro	Arg	Glu	Gly	Arg	Ala	Gln	Ser	Ser	Ala	Gly	Ser	Ile
		35				40					45				
Asn	His	Arg	Asn	Arg	Ala	Ala	Arg	Asp	Gln	Glu	Arg	Glu	Arg	Lys	Arg
	50				55					60					
Leu	Glu	Ala	Gln	Arg	Gln	Asp	Pro	Ser	Arg	Pro	Val	Val	Glu	Thr	Ile
65				70				75						80	
Thr	Glu	Val	Ser	Cys	Ser	Thr	Pro	Ala	Leu	Ser	Ala	Ala	Pro	Pro	Arg
			85				90						95		
Arg	Lys	Ser	Met	Glu	Ala	Asp	Ala	Glu							
		100					105								

<210> 461

<211> 357

<212> DNA

<213> Homo sapiens

<400> 461

acgcgttcga ggtcgggctaa atttatcatg cgcacgacaa agagagtagt ggctcacaac  
60  
cgggtcacat gcatgatgac aaaaactggc agaataagagt tgatgtcatc ccgtctacca  
120  
gtccttagaa ccagctcaga gagtcccggg gtcgggtaccg tcgagactca gtacacaact  
180  
gtcgcgatac cggacgaccc tcttcacatg gttgcagatg ggcgtctcaa tcacgtcact  
240  
gtcgtttacg aaacctacgg gaagctcaat acgtccagcg acaatgcggg ctatacctgt  
300  
catgcgctta ctggtgatgc ccatgcagcc ggatttcacc ccggtgtagt ccgtccg  
357

<210> 462  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 462  
 Thr Arg Ser Arg Ser Ala Lys Phe Ile Met Arg Thr Thr Lys Arg Val  
 1 5 10 15  
 Val Ala His Asn Arg Val Thr Cys Met Met Thr Lys Thr Gly Arg Ile  
 20 25 30  
 Glu Leu Met Ser Ser Arg Leu Pro Ala Pro Arg Thr Ser Ser Glu Ser  
 35 40 45  
 Pro Gly Val Gly Thr Val Glu Thr Gln Tyr Thr Thr Val Ala Ile Pro  
 50 55 60  
 Asp Asp Pro Leu His Leu Val Ala Asp Gly Arg Leu Asn His Val Thr  
 65 70 75 80  
 Val Ala Tyr Glu Thr Tyr Gly Lys Leu Asn Thr Ser Ser Asp Asn Ala  
 85 90 95  
 Val Tyr Thr Cys His Ala Leu Thr Gly Asp Ala His Ala Ala Gly Phe  
 100 105 110  
 His Pro Gly Val Val Arg Pro  
 115

<210> 463  
 <211> 434  
 <212> DNA  
 <213> Homo sapiens

<400> 463  
 gtgcacgggg tatgcgaggg atgcggcatt gccaccaatg ccgctgacct gcgcagatac  
 60  
 gaggcagctg gtgacgatga agtggtgcga tgcgaggaat gcgatcgat cctggtgcgt  
 120  
 accggagagt ccatctgagc ccttcttggtg gcggtgatgc cgggatatcc gtagaattag  
 180  
 cggtcggacg agccatccgg gtgatcgagg cagcgggtgag ttgtcgagga aagtcggggc  
 240  
 tccatagagc aggggtggtgg gtaacgcccc cccgggggtga cccgcgggaa agtgccacag  
 300  
 agaacagact gccggtttcg agccggtgag ggtgaaacgg tggagtaagt gcccaccgag  
 360  
 tcatcgggtga cggtgacggc atggcaaacc ccacctggag caaggccaag aagaccgtga  
 420  
 ggtcgcggac gcgt  
 434

<210> 464  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

<400> 464  
 Met Pro Ser Pro Ser Pro Met Thr Arg Trp Ala Leu Thr Pro Pro Phe

```

      1           5           10           15
His Pro His Arg Leu Glu Thr Gly Ser Leu Phe Ser Val Ala Leu Ser
      20           25           30
Arg Gly Ser Pro Arg Val Gly Val Thr His His Pro Ala Leu Trp Ser
      35           40           45
Pro Asp Phe Pro Arg Gln Leu Thr Ala Ala Ala Ile Thr Arg Met Ala
      50           55           60
Arg Pro Thr Ala Asn Ser Thr Asp Ile Pro Ala Ser Pro Pro Gln Glu
      65           70           75           80
Gly Leu Arg Trp Thr Leu Arg Tyr Ala Pro Gly Tyr Asp Arg Ile Pro
      85           90           95
Arg Ile Ala Pro Leu His Arg His Gln Leu Pro Arg Ile Cys Ala Gly
      100          105          110
Gln Arg His Trp Trp Gln Cys Arg Ile Pro Arg Ile Pro Arg Ala
      115          120          125

```

&lt;210&gt; 465

&lt;211&gt; 438

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 465

```

gatcatttag aatttatgga agaagctgat gtgaaagcta tgggtcaaatac tggcactgtg
60
gctgtattgc taccaggagc attttacacc ttgaaagaaa ctcaacttcc accgatgaat
120
ttgttacgtc agtacggagt agacattgct atttcgacgg atgctaatacc agggacgtcg
180
ccagcggttat cattacggtt aatgatgaat atggcatgta ccttgtttgg tatgacacct
240
gaaaccgccc ttgcaggggt aacaattcat gcggcaaaag cggtggggat tagcgattct
300
catggcactt tagaagttgg caaggtagct gattttgtct gctgggatgt ggaaagcccc
360
ggtgaacttt gttattggtt aggagagcag ttagtaaagc aacgtattca gcacggagta
420
tcccatgaat aatctaga
438

```

&lt;210&gt; 466

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 466

```

Asp His Leu Glu Phe Met Glu Glu Ala Asp Val Lys Ala Met Val Lys
      1           5           10           15
Ser Gly Thr Val Ala Val Leu Leu Pro Gly Ala Phe Tyr Thr Leu Lys
      20           25           30
Glu Thr Gln Leu Pro Pro Met Asn Leu Leu Arg Gln Tyr Gly Val Asp
      35           40           45
Ile Ala Ile Ser Thr Asp Ala Asn Pro Gly Thr Ser Pro Ala Leu Ser
      50           55           60
Leu Arg Leu Met Met Asn Met Ala Cys Thr Leu Phe Gly Met Thr Pro

```

```

65          70          75          80
Glu Thr Ala Leu Ala Gly Val Thr Ile His Ala Ala Lys Ala Leu Gly
          85          90          95
Ile Ser Asp Ser His Gly Thr Leu Glu Val Gly Lys Val Ala Asp Phe
          100          105          110
Val Cys Trp Asp Val Glu Ser Pro Gly Glu Leu Cys Tyr Trp Leu Gly
          115          120          125
Glu Gln Leu Val Lys Gln Arg Ile Gln His Gly Val Ser His Glu
          130          135          140

```

<210> 467  
 <211> 460  
 <212> DNA  
 <213> Homo sapiens

```

<400> 467
ntttccctgg ctattggcca tgtgggacac aacgttccgc ctaccccaaga gcggttaagc
60
tgcacccctg caccttcttc tcccaccgct tcaaagccac agtgaggaaac ttcggagctt
120
ctcgcaagtga agatggcggt ggaggaatgg atgccctggc tagaagaggc ggaatatctg
180
ttgatttgtt ggaccgacca caaaaacctg gagtatctcc acacaaccaa gtgcctcaac
240
tccaggcaag caagaagggc ccagctgttt acctggttcc acttttccct ctectaccgg
300
ccgggggtcca agaacatcag gctggatgcc ctttcttgcc actttatggg catgggcccc
360
ttcctccagg cttgcctgtc acccgggctc ccgtcaaacc ctggccttcg tgcgacaaca
420
ctcttggtgc cttctatggt tctgtatggt gccgcaattg
460

```

<210> 468  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

```

<400> 468
Gly Thr Ser Glu Leu Leu Ala Val Lys Met Ala Leu Glu Glu Trp Met
1          5          10          15
Pro Trp Leu Glu Glu Ala Glu Tyr Leu Leu Ile Val Trp Thr Asp His
20          25          30
Lys Asn Leu Glu Tyr Leu His Thr Thr Lys Cys Leu Asn Ser Arg Gln
35          40          45
Ala Arg Arg Ala Gln Leu Phe Thr Trp Phe His Phe Ser Leu Ser Tyr
50          55          60
Arg Pro Gly Ser Lys Asn Ile Arg Leu Asp Ala Leu Ser Cys His Phe
65          70          75          80
Met Gly Met Gly Pro Phe Leu Gln Ala Cys Leu Ser Pro Gly Leu Pro
85          90          95
Ser Asn Pro Gly Leu Arg Ala Thr Thr Leu Leu Val Pro Ser Met Val
100          105          110
Leu Tyr Val Ala Ala Ile

```

115

&lt;210&gt; 469

&lt;211&gt; 381

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 469

cttgtgcaca cgttattttt ccaatacaaa tagtttaaaa agtaaaactcc aaatacctat  
 60  
 aagccccctc aaagcacctt ccaaatatga accttgtaa tgcccaaggt ccagaggggt  
 120  
 cccccagaaa ggcccaggag cctggggcat gggaaagctg tcgggggtccc catgctgact  
 180  
 ccctggactc caagcgatat tccataaagc cagggcctcc tggctgcggg agggaggcct  
 240  
 tgacccaaaa tccattcggc cctggatact ggagaggcag aggcctctgc tgatgagaag  
 300  
 ccctgagttc ctggctagct gtgggtaacc acaaaaaatg cgggggggtga tgattttcga  
 360  
 agtccatcgg caaagaaaga c  
 381

&lt;210&gt; 470

&lt;211&gt; 110

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 470

Met	Asp	Phe	Glu	Asn	His	His	Pro	Pro	His	Phe	Leu	Trp	Leu	Thr	Thr
1				5					10					15	
Ala	Ser	Gln	Glu	Leu	Arg	Ala	Ser	His	Gln	Gln	Arg	Pro	Leu	Pro	Leu
		20						25					30		
Gln	Tyr	Pro	Gly	Pro	Asn	Gly	Phe	Trp	Val	Lys	Ala	Ser	Leu	Pro	Gln
		35					40					45			
Pro	Gly	Gly	Pro	Gly	Phe	Met	Glu	Tyr	Arg	Leu	Glu	Ser	Arg	Glu	Ser
	50					55					60				
Ala	Trp	Gly	Pro	Arg	Gln	Leu	Ser	His	Ala	Pro	Gly	Ser	Trp	Ala	Phe
65					70					75				80	
Leu	Gly	Asp	Pro	Ser	Gly	Pro	Trp	Ala	Leu	Thr	Arg	Phe	Ile	Phe	Gly
				85					90					95	
Arg	Cys	Phe	Glu	Gly	Ala	Tyr	Arg	Tyr	Leu	Glu	Phe	Thr	Phe		
			100					105					110		

&lt;210&gt; 471

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 471

accggtgact acctgcagca ctggattgac atgggtaaaa agggcggcga ccgcatgcca  
 60  
 gaggtcttcc tgggtaactg gttccgccgc ggcgacgatg gccgcttcct gtggccngg  
 120

cttggcgaaa acttcccggt cctanagtgg atcatcgacc gcattgaagg caacgtagag  
 180  
 gccgaggaca cgggtggtcgg acgcaccgcc cgcgccgagg acatcgactt gcaaggcctt  
 240  
 gacttcgatg tcgacgacgt tcgcgccgca ctgcgccgttg acccgaagga atgggaaggc  
 300  
 gatatgcaag acaacgccga gtacctgaac ttcttgggct cccgcgtgcc cgaggaagtg  
 360  
 tggaaccagt tccgcgcc  
 378

<210> 472  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<400> 472  
 Thr Gly Asp Tyr Leu Gln His Trp Ile Asp Met Gly Lys Lys Gly Gly  
 1 5 10 15  
 Asp Arg Met Pro Glu Val Phe Leu Val Asn Trp Phe Arg Arg Gly Asp  
 20 25 30  
 Asp Gly Arg Phe Leu Trp Pro Xaa Leu Gly Glu Asn Phe Pro Val Leu  
 35 40 45  
 Xaa Trp Ile Ile Asp Arg Ile Glu Gly Asn Val Glu Ala Glu Asp Thr  
 50 55 60  
 Val Val Gly Arg Thr Ala Arg Ala Glu Asp Ile Asp Leu Gln Gly Leu  
 65 70 75 80  
 Asp Phe Asp Val Asp Asp Val Arg Ala Ala Leu Ala Val Asp Pro Lys  
 85 90 95  
 Glu Trp Glu Gly Asp Met Gln Asp Asn Ala Glu Tyr Leu Asn Phe Leu  
 100 105 110  
 Gly Ser Arg Val Pro Glu Glu Val Trp Asn Gln Phe Arg Ala  
 115 120 125

<210> 473  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

<400> 473  
 accggttggt gggggaagg acccatccca tgccacctgt cctagaaaat gtttccctt  
 60  
 gttgagcagc tgctggatct agggctgctg ggtctaagtc caaaaaggga aaaaggaaaa  
 120  
 aggaccaag taaaagaagg gggaagctgc caaaaccccc cctgccaaaa ctctcccacc  
 180  
 ctgcttccat ttccctctcc agggaaacagg tgtacctccc ctctccctg tctctctcag  
 240  
 atgccccagg ggctctctac ttcattctct cgcacctgc caggagtggc ctcaggggta  
 300  
 gaggctccta gttggagaat ttgcttgag gaagggtgaa  
 339

<210> 474



<211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 474  
 Met Phe Pro Leu Val Glu Gln Leu Leu Asp Leu Gly Leu Leu Gly Leu  
 1 5 10 15  
 Ser Pro Lys Arg Glu Lys Gly Lys Arg His Gln Val Lys Glu Gly Gly  
 20 25 30  
 Ser Cys Gln Asn Pro Pro Cys Gln Asn Ser Pro Thr Leu Leu Pro Phe  
 35 40 45  
 Pro Ser Pro Gly Asn Arg Cys Thr Ser Pro Pro Pro Cys Pro Pro Gln  
 50 55 60  
 Met Pro Gln Gly Leu Ser Thr Ser Phe Leu Pro Thr Leu Pro Gly Val  
 65 70 75 80  
 Ala Ser Gly Val Glu Ala Pro Ser Trp Arg Ile Cys Leu Gln Glu Gly  
 85 90 95  
 Glu

<210> 475  
 <211> 345  
 <212> DNA  
 <213> Homo sapiens

<400> 475  
 acgcgtgaag ggtccctcc aaactctgag cctccttcca agccttgetg ggagctcccc  
 60  
 agcgctgcc ggagaggcct ctctccagg cgggcttccc gcgccgatgt gaaggagagg  
 120  
 ctgccccaga ggggtctgga tcgtaatcca gaaagggaca gtccacagc cataatcccg  
 180  
 aatgctggga ctcttcagta aaggaagaga tggctttttc gttcatctgc ctttctgaaa  
 240  
 ggtaaaatat ctccagatcc gggctctctg ggcgactgcg tatgtggggg tccctgaagc  
 300  
 ctttgatgga tcttgtaga agtgggtgt tcatcttggg gtttt  
 345

<210> 476  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 476  
 Met Asn Asn Pro Leu Leu Thr Arg Ser Ile Lys Gly Phe Arg Asp Pro  
 1 5 10 15  
 His Ile Arg Ser Arg Pro Glu Ser Pro Asp Leu Glu Ile Phe Tyr Leu  
 20 25 30  
 Ser Glu Arg Gln Met Asn Glu Lys Ala Ile Ser Ser Phe Thr Glu Glu  
 35 40 45  
 Ser Gln His Ser Gly Leu Trp Leu Trp Asp Cys Pro Phe Leu Asp Tyr  
 50 55 60  
 Asp Pro Asp Pro Ser Gly Ala Ala Ser Pro Ser His Arg Arg Gly Lys

```

65          70          75          80
Pro Ala Trp Arg Arg Gly Leu Ser Gly Arg Arg Trp Gly Ala Pro Ser
          85          90          95
Lys Ala Trp Lys Glu Ala Gln Ser Leu Glu Gly Thr Leu His Ala
          100          105          110

```

```

<210> 477
<211> 422
<212> DNA
<213> Homo sapiens

```

```

<400> 477
acgcgtggcc gagccagcgt gctcaaggaa atgggtcaacg gcactcttat taacggctgg
60
gactctcccc aggtggaacg ggcactggac ctgtgcatgg cgtgcaaagg gtgcgcccga
120
gattgcccca ccggaatcga catggccagc taccgcagca cggttcttga cgaaaaatac
180
cgtcaccgtc tccgccctcg ctcccacctg acgatggggc tgctgcccac gtgggaacgt
240
ttgctcaatc ggaccccagg agcgccgtcg ctggctaacg cagtgccttc gatgccggtc
300
ttcgcacgtc ttgctagatg gacagccggg gtggatcagc gtcgtccctt cccccgattc
360
cagccctcgg ccagattggc cagtcgcgag gccgccccgg ttaaggagat tgtggcggat
420
cc
422

```

```

<210> 478
<211> 140
<212> PRT
<213> Homo sapiens

```

```

<400> 478
Thr Arg Gly Arg Ala Ser Val Leu Lys Glu Met Val Asn Gly Thr Leu
1          5          10          15
Ile Asn Gly Trp Asp Ser Pro Glu Val Glu Arg Ala Leu Asp Leu Cys
          20          25          30
Met Ala Cys Lys Gly Cys Ala Arg Asp Cys Pro Thr Gly Ile Asp Met
          35          40          45
Ala Ser Tyr Arg Ser Thr Val Leu Asp Glu Lys Tyr Arg His Arg Leu
          50          55          60
Arg Pro Arg Ser His Leu Thr Met Gly Leu Leu Pro Met Trp Glu Arg
65          70          75          80
Leu Leu Asn Arg Thr Pro Gly Ala Pro Ser Leu Ala Asn Ala Val Leu
          85          90          95
Ser Met Pro Val Phe Ala Arg Leu Ala Arg Trp Thr Ala Gly Val Asp
          100          105          110
Gln Arg Arg Pro Leu Pro Arg Phe Gln Pro Ser Ala Arg Leu Ala Ser
          115          120          125
Pro Gln Ala Ala Pro Val Lys Glu Ile Val Ala Asp
          130          135          140

```

<210> 479  
 <211> 348  
 <212> DNA  
 <213> Homo sapiens

<400> 479  
 cgcgtggcca ttggccgggc gctgggtcgg caccgcgac tggtgattgc cgatgagccg  
 60  
 atctcggcgt tggacatgac catccagaag cagattcttg agctgttcga gcgcctgcag  
 120  
 gcgcagtacg gctttgcctg cctgttcac tcccacgacc tggcagcggg ggaacgcac  
 180  
 gccaccggg tggcgggtgat gagcgaggc aggggtggg aaatgggtgc ccgcgacgag  
 240  
 atcttcgacc gcccgacga cccctacacc cgcaagctgc tggccgccgc cagccccttg  
 300  
 gagaaacttg aaaacggtgg ctaccgcac cgccagggcc ccgtaccg  
 348

<210> 480  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 480  
 Arg Val Ala Ile Gly Arg Ala Leu Val Arg His Pro Arg Leu Val Ile  
 1 5 10 15  
 Ala Asp Glu Pro Ile Ser Ala Leu Asp Met Thr Ile Gln Lys Gln Ile  
 20 25 30  
 Leu Glu Leu Phe Glu Arg Leu Gln Ala Gln Tyr Gly Phe Ala Cys Leu  
 35 40 45  
 Phe Ile Ser His Asp Leu Ala Ala Val Glu Arg Ile Ala His Arg Val  
 50 55 60  
 Ala Val Met Ser Glu Gly Arg Val Val Glu Met Gly Ala Arg Asp Glu  
 65 70 75 80  
 Ile Phe Asp Arg Pro Gln His Pro Tyr Thr Arg Lys Leu Leu Ala Ala  
 85 90 95  
 Ala Ser Pro Leu Glu Lys Leu Glu Asn Gly Gly Tyr Arg Ile Arg Gln  
 100 105 110  
 Gly Pro Val Pro  
 115

<210> 481  
 <211> 441  
 <212> DNA  
 <213> Homo sapiens

<400> 481  
 aagcttctga ctgtggcatt ctccctgctt aatatgtcct caatatcccc tacttactgg  
 60  
 gcaaaatcct gcttatgctt tgggactagc tcaaagacca ctcccttgga tgggtgcctc  
 120  
 cctgcctgc cggttgccg tggcttcctc agtgtagga ttaccatcac attgcatcat  
 180

gagagcagaa gaccatctcc atgtgactgc tgccctgtct cccagcaggg cccacaanca  
 240  
 cccagtccag gacctggctc acgctgggtg gcggatgccc aggaatgggg ctctggatct  
 300  
 gcctcttctc ctgcaggacc aggaaaccgc tgccctgtcc ctgccccagg aaaccctcag  
 360  
 taaatcccca gtcatttgag ttccctctca gcgccagaga ccaataacac atctccacca  
 420  
 acctgaaaaa ccttcacgcg t  
 441

<210> 482  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 482  
 Lys Leu Leu Thr Val Ala Phe Ser Leu Leu Asn Met Ser Ser Ile Ser  
 1 5 10 15  
 Pro Thr Tyr Trp Ala Lys Ser Cys Leu Cys Phe Gly Thr Ser Ser Lys  
 20 25 30  
 Thr Thr Pro Leu Asp Gly Ala Phe Pro Ala Leu Pro Ala Cys Ala Gly  
 35 40 45  
 Phe Leu Ser Val Arg Ile Thr Ile Thr Leu His His Glu Ser Arg Arg  
 50 55 60  
 Pro Ser Pro Cys Asp Cys Cys Pro Cys Ser Gln Gln Gly Pro Gln Xaa  
 65 70 75 80  
 Pro Ser Pro Gly Pro Gly Ser Arg Trp Val Ala Asp Ala Gln Glu Trp  
 85 90 95  
 Gly Ser Gly Ser Ala Ser Ser Pro Ala Gly Pro Gly Asn Arg Cys Pro  
 100 105 110  
 Val Pro Ala Pro Gly Asn Pro Gln  
 115 120

<210> 483  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

<400> 483  
 acgcgttcat tccctgatgg ccacgcacga gctaacggag ggatggggcg aagggaaggc  
 60  
 caagggttgc tcgaagacca aggagtgtgc agggcaggac ctcgttttaa aggaatatcc  
 120  
 tctcaccaga gacacgcggc ggccaggcag ggccggagcg gggcctgtgc ccaggctccg  
 180  
 agcgtctgcc cagcccagca tccctgtccc cagccaggaa tatgtcttcg tggcatagag  
 240  
 ggagctcttg gagccacacc tgcgtgtgca catgtgtcac cccactgctg ggaggggctc  
 300  
 tcccgggacc ctgcagcgtg ggctgggccc  
 330

<210> 484

<211> 96  
 <212> PRT  
 <213> Homo sapiens

<400> 484  
 Met Gly Arg Arg Glu Gly Gln Gly Cys Leu Glu Asp Gln Gly Val Cys  
 1 5 10 15  
 Arg Ala Gly Pro Arg Phe Lys Gly Ile Ser Ser His Gln Arg His Ala  
 20 25 30  
 Ala Ala Arg Gln Gly Arg Ser Gly Ala Cys Ala Gln Ala Pro Ser Val  
 35 40 45  
 Cys Pro Ala Gln His Pro Cys Pro Gln Pro Gly Ile Cys Leu Arg Gly  
 50 55 60  
 Ile Glu Gly Ala Leu Gly Ala Thr Pro Ala Cys Ala His Val Ser Pro  
 65 70 75 80  
 His Cys Trp Glu Gly Leu Ser Arg Asp Pro Ala Ala Trp Ala Gly Pro  
 85 90 95

<210> 485  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<400> 485  
 acgcgtgctc gcgcggacga agtcggcgct gatcgcccag tcatgcgccc tgcccgtgcc  
 60  
 gcccgattcg gcgatcgccg cattcgggccg gccggaatcg agaaggaatg cgtggacgta  
 120  
 cgggggatac caaaggaatc ttgtcgaggg cttcgcgggc ctcgacgtgg atcacctgta  
 180  
 cccgacggac gtggggaagc cgtcccga gctcacggga ctccgcgaca tcgatgtgcg  
 240  
 atacgatttg caccgtcgtc ggctgcgtgc gcgacacatg ctccgcgatc gcctcagcgg  
 300  
 tgggtttccga cgtcagcagg aacgtggcga cgggtggcat ggcggtcgcc gttatgtcgg  
 360  
 cattcccatt cctcggg  
 377

<210> 486  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 486  
 Met Arg Pro Ala Arg Ala Ala Gln Phe Gly Asp Arg Arg Ile Arg Pro  
 1 5 10 15  
 Ala Gly Ile Glu Lys Glu Cys Val Asp Val Arg Gly Ile Pro Lys Glu  
 20 25 30  
 Ser Cys Arg Gly Leu Arg Gly Pro Arg Arg Gly Ser Pro Val Pro Asp  
 35 40 45  
 Gly Arg Gly Glu Ala Val Pro Gln Ala His Gly Thr Pro Arg His Arg  
 50 55 60  
 Cys Ala Ile Arg Phe Ala Pro Ser Ser Ala Ala Cys Ala Thr His Ala

```

65              70              75              80
Pro Arg Ser Pro Gln Arg Trp Phe Pro Thr Ser Ala Gly Thr Trp Arg
              85              90              95
Arg Val Ala Trp Arg Ser Pro Leu Cys Arg His Ser His Ser Ser
              100              105              110

```

<210> 487  
 <211> 459  
 <212> DNA  
 <213> Homo sapiens

```

<400> 487
nnacgcgtaa gatcgattgt ggatcagcac cgatgctggt ccccccgcagc ttgttgttgg
60
cgggtgttgt tgtaaggagt gtgtgtgatg cgtgttggtg ttcctactga ggtaagaat
120
agtgaagtttc gtgtggctgt gacgccggcg ggtgttcattg cggttggttg tcgtgggtcat
180
gagggtgttg ttcaggctgg tgctggtgtg ggttcgggta ttccggattc ggattttgtg
240
ggtgctggtg cgcgggttgt gggatgatgt gagtcggtgt ggggtgatgc tgatttggtg
300
ttgaaggatga aggagcctgt tgcggaggag tatgggcggt tgcattgaggg tttggttctt
360
tttacgtatc ttcatttggc tgctgatgag gcgttgactc gtgagctttt ggggcgtggg
420
gtgacgtcga ttgcgtatga gacggtggag ttggccgat
459

```

<210> 488  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

```

<400> 488
Met Arg Val Gly Val Pro Thr Glu Val Lys Asn Ser Glu Phe Arg Val
1              5              10              15
Ala Val Thr Pro Ala Gly Val His Ala Leu Val Gly Arg Gly His Glu
              20              25              30
Val Leu Val Gln Ala Gly Ala Gly Val Gly Ser Gly Ile Pro Asp Ser
              35              40              45
Asp Phe Val Gly Ala Gly Ala Arg Val Val Gly Asp Val Glu Ser Val
              50              55              60
Trp Gly Asp Ala Asp Leu Val Leu Lys Val Lys Glu Pro Val Ala Glu
65              70              75              80
Glu Tyr Gly Arg Leu His Glu Gly Leu Val Leu Phe Thr Tyr Leu His
              85              90              95
Leu Ala Ala Asp Glu Ala Leu Thr Arg Glu Leu Leu Gly Arg Gly Val
              100              105              110
Thr Ser Ile Ala Tyr Glu Thr Val Glu Leu Ala Asp
              115              120

```

<210> 489  
 <211> 542

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 489

nacgcgtttg gcgtactgag tgcggtggtg gatggcgacg acagtggcaa gccgctgctc  
 60  
 aaccagcacg gttgctacaa agtgcgcttt ccatttaccc gcgatcaaaa gccccagcact  
 120  
 cgggggttcgg catggctgcg caggggtgctg ttgtctgccg gttccagcca tggcatgcac  
 180  
 ttccgctgc tcaaaggcag tgaagtgttg gtgtcatttc tggggggcga ccccgaccgg  
 240  
 ccgattatcg ttggtgcgt accaaactcg gaaaccccg gcatggctcg tgagcgtaac  
 300  
 gccaccaga gcggcttctc cacggccgga gggcacttcc tggcgatgga agaccacccc  
 360  
 ggggctgccc atctgaagct ggggtgcctt ggccgcaaca gcgtcttcac actgggcaat  
 420  
 ggcaaagtcg ccggcgcgca actgcgcacc aacgccccac atgcaattga catcgtcttc  
 480  
 gctcaaacac gaagtgcccg gcgtgtactc attgtcgatg ggcaccgggg acccggcggc  
 540  
 cg  
 542

&lt;210&gt; 490

&lt;211&gt; 180

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 490

Xaa Ala Phe Gly Val Leu Ser Ala Val Val Asp Gly Asp Asp Ser Gly  
 1 5 10 15  
 Lys Pro Leu Leu Asn Gln His Gly Cys Tyr Lys Val Arg Phe Pro Phe  
 20 25 30  
 Thr Arg Asp Gln Lys Pro Ser Thr Arg Gly Ser Ala Trp Leu Arg Arg  
 35 40 45  
 Val Ser Leu Ser Ala Gly Ser Ser His Gly Met His Phe Pro Leu Leu  
 50 55 60  
 Lys Gly Ser Glu Val Leu Val Ser Phe Leu Gly Gly Asp Pro Asp Arg  
 65 70 75 80  
 Pro Ile Ile Val Gly Cys Val Pro Asn Ser Glu Thr Pro Ser Met Val  
 85 90 95  
 Val Glu Arg Asn Ala Thr Gln Ser Gly Phe Ser Thr Ala Gly Gly His  
 100 105 110  
 Phe Leu Ala Met Glu Asp His Pro Gly Ala Ala His Leu Lys Leu Gly  
 115 120 125  
 Ala Pro Gly Gly Asn Ser Val Phe Thr Leu Gly Asn Gly Lys Val Ala  
 130 135 140  
 Gly Ala Gln Leu Arg Thr Asn Ala Pro His Ala Ile Asp Ile Val Phe  
 145 150 155 160  
 Ala Gln Thr Arg Ser Ala Arg Arg Val Leu Ile Val Asp Gly His Arg  
 165 170 175  
 Gly Pro Gly Gly

180

<210> 491  
 <211> 825  
 <212> DNA  
 <213> Homo sapiens

<400> 491  
 nacgcgtcga ggcgacggtc ggcgccgtca tggcgactgt tctcgagggc acatgggaac  
 60  
 gcatcggtgc cggattccgg actgccttaa ccacagcctt ggaacgcacc gatgaatggg  
 120  
 tgggcggccc tgacagcaag cccctcaacg aagtcgagac actgcgccgg tgcgccgatg  
 180  
 aactcatcgg cgggcccgtc ggcgcggttg ccgcgatgca cggaggggtca atcgaattgg  
 240  
 tcgacgtgtc ggtcgggtgac gaagagcgca gagtcgacgt caccatgaag ggagcatgcc  
 300  
 gaggttgccc ggcagccatc agaccctaca tcagcgcctg gaacatcaac tgagtctgcg  
 360  
 nattgcgcga gccggtcacc gtgcgggaaa tctgacacct actccgacag ctccacctcg  
 420  
 acgagcacct ccacgacgag gccaaagccac tcgtagacgc attcctcctc ggcattccat  
 480  
 tcttccccgg ccgcccagac gacttcgtcg gcagtaacct ggtcgatgat ccctagcctg  
 540  
 gcggccatca tgccacgcag cgcattgaca gtacgaagcc aacgttgctg catcacaggg  
 600  
 ttcatggaga tacagccggt tcggtgcaac gtctccacat cagcacttaa ggactgagcg  
 660  
 tcttcccagc gcgcccgac atcctcggcg tcatggtcga catggaattg cgcgtcagct  
 720  
 gagtcgtcgt cagcataggc gctgggcagg atcaatcgac gcacctcgtc gtctcctctg  
 780  
 agtccagaaa actggctctc ccaaaaagcg aacgggtccc cctcc  
 825

<210> 492  
 <211> 58  
 <212> PRT  
 <213> Homo sapiens

<400> 492  
 Met Asn Gly Trp Ala Ala Leu Thr Ala Ser Pro Ser Thr Lys Ser Arg  
 1 5 10 15  
 His Cys Ala Gly Ala Pro Met Asn Ser Ser Ala Gly Pro Ser Ala Arg  
 20 25 30  
 Leu Pro Arg Cys Thr Glu Gly Gln Ser Asn Trp Ser Thr Cys Arg Ser  
 35 40 45  
 Val Thr Lys Ser Ala Glu Ser Thr Ser Pro  
 50 55

<210> 493  
 <211> 863



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 493

nacgcgttcc aacctcgtca aaacggctat cgcaggaaat gaccccaact ggggtcgc  
 60  
 cctcgcggcg atcggatgtg ttcctgagaa tatagctccc ttcgatcccg accaggtgga  
 120  
 tgtgtccatc aatgacattc agatctgtaa ggccgggggt atcggggagg accgcaacct  
 180  
 cgtcgatatg aggccacgag aggttcacat cgatattgag ctgcatgcgg gtgatgccga  
 240  
 agctgcggta tggactaatg atctgaccca ccaatacgtc gaagagaata gcgcgtatac  
 300  
 atcatgaccc ttgctcttga catccccctc aacgactccc agttctcggc tcagcggaaa  
 360  
 tctgaggtcc tggtagaagc gctgccttgg atcaggcggg ttcagggccg cactgtcgtc  
 420  
 gtgaaatatg gcggcaacgc gatggttgat cccggtctgc agcaggcctt cgccgacgac  
 480  
 attgtgttta tggcctctgt ggggattcgc cctattgtcg tccacggtgg tggccctcag  
 540  
 atcaatgccca tgcttcttga atccgctacc ccggtggagt tccgtaatgg tttgcgggtg  
 600  
 acatctccgg aggtcatgga gggtgtccgg atggtgctcg tcgggcaggg gggccgctcag  
 660  
 ctcgtaacc gaatcaacgc ctatgcgccg ctagcagctg gcatgtcagg cgaggacttt  
 720  
 ggcctttttt cggcccgga gtcgcgggta attgttgatg gcgagcaaat agacatgggt  
 780  
 ttagtgggag acatcgttga cgtcaacatc gatctcgta tctctatgct tgatcgcggg  
 840  
 cagattccgg tcattgcacc ggt  
 863

&lt;210&gt; 494

&lt;211&gt; 186

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 494

Met Thr Leu Ala Leu Asp Ile Pro Leu Asn Asp Ser Gln Phe Ser Ala  
 1 5 10 15  
 Gln Arg Lys Ser Glu Val Leu Val Glu Ala Leu Pro Trp Ile Arg Arg  
 20 25 30  
 Phe Gln Gly Arg Thr Val Val Val Lys Tyr Gly Gly Asn Ala Met Val  
 35 40 45  
 Asp Pro Gly Leu Gln Gln Ala Phe Ala Asp Asp Ile Val Phe Met Ala  
 50 55 60  
 Ser Val Gly Ile Arg Pro Ile Val Val His Gly Gly Gly Pro Gln Ile  
 65 70 75 80  
 Asn Ala Met Leu Ala Glu Ser Ala Thr Pro Val Glu Phe Arg Asn Gly  
 85 90 95  
 Leu Arg Val Thr Ser Pro Glu Val Met Glu Val Val Arg Met Val Leu

```

      100      105      110
Val Gly Gln Val Gly Arg Gln Leu Val Asn Arg Ile Asn Ala Tyr Ala
      115      120      125
Pro Leu Ala Ala Gly Met Ser Gly Glu Asp Phe Gly Leu Phe Ser Ala
      130      135      140
Arg Lys Ser Arg Val Ile Val Asp Gly Glu Gln Ile Asp Met Gly Leu
      145      150      155      160
Val Gly Asp Ile Val Asp Val Asn Ile Asp Leu Val Ile Ser Met Leu
      165      170      175
Asp Arg Gly Gln Ile Pro Val Ile Ala Pro
      180      185

```

&lt;210&gt; 495

&lt;211&gt; 514

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 495

```

gcgcgcgaca ccggtgcccc gattagcgtg ccagtgggtg acgtcactaa gggtcacgtc
60
tggaatgtga caggtgacgt tcttaacgcc ngatccctcc acaatcgagg tgacnntgag
120
cgttgccga tccaccggga tccccggcc ttcgatgacc ttgagccga gaccgagatg
180
ctggagaccg gtattaaggt ccttgacttg ctgactcctt acgtcaaggg cggcaagatt
240
ggcctctttg gcggcgctgg tgtgggtaag acggtgctca ttcaggagat gatttaccgt
300
atcgcccaca acttcggcgg tacttcgggtt ttcgcgggtg tcggtgagcg taccgcgag
360
ggtaacgacc tcatcaacga gatggacgag gccggtgtgc tcaaagacac cgccctggta
420
ttcgccaga tggacgagcc cccgggcacg cggtacgagc tgtcgcgctg gcagccctgc
480
ggcccatgcc tggtaactg ctgtgggacc ttgg
514

```

&lt;210&gt; 496

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 496

```

Ala Arg Asp Thr Gly Ala Pro Ile Ser Val Pro Val Gly Asp Val Thr
1      5      10      15
Lys Gly His Val Trp Asn Val Thr Gly Asp Val Leu Asn Ala Xaa Ser
      20      25      30
Leu His Asn Arg Gly Asp Xaa Glu Arg Trp Pro Ile His Arg Asp Pro
      35      40      45
Pro Ala Phe Asp Asp Leu Glu Pro Glu Thr Glu Met Leu Glu Thr Gly
      50      55      60
Ile Lys Val Leu Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
      65      70      75      80
Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu

```

Met	Asn	Glu	Glu	Lys	Thr	Gln	Pro	His	Lys	Arg	Asp	Thr	Arg	Trp	Arg
1				5					10					15	
Gly	Glu	Thr	Gln	Gln	Ser	Ser	Phe	Leu	Ser	Val	Asp	Ser	Glu	Gln	Arg
			20					25					30		
Arg	Gly	Ala	Pro	Ser	Phe	Val	Phe	Ser	Ser	Ser	Gly	Glu	Arg	Met	Asp

```

      35          40          45
Cys Leu His Ala Ser Cys His Thr Pro Ala Val Ile Pro Ala Arg Ala
  50          55          60
Pro Ser Ala Glu Ala Glu Leu Cys Ser Ala Gln Ala Trp Asp Leu Pro
  65          70          75          80
Arg Gln Ala Pro Val Gly Gly Ala Ala Pro Gly Lys Glu Ala Thr Ala
      85          90          95
Ser Leu Asn Ile Leu Arg Cys Lys Val Val Ala Pro Arg Gly Val Ser
      100          105          110
Val Lys Thr Gly Thr Arg Met Ala Gly Pro Ala Arg Leu Phe Pro His
      115          120          125
Leu Ser Ala Ser Glu Ala Ser Leu Glu Asp Ser Gly Pro Arg Met Ser
      130          135          140
Pro Arg Thr Ser Gln Ser Ala Ser Ser Ser Tyr Phe Cys Cys Ser Leu
      145          150          155          160
Gly Pro Asp Leu Ala Lys Val Ser Gln Arg Gly Gly Pro Arg Ser Glu
      165          170          175
Leu Ser Ser Cys Arg Gly Pro Arg Asp Gly Leu Gly Cys Lys Leu
      180          185          190

```

<210> 499  
 <211> 444  
 <212> DNA  
 <213> Homo sapiens

```

<400> 499
acgcgtgaag ggtgggcagt gttgagctga gtgagccctc ctccctgcaa tgctggagcc
60
ctgccttctg cctgaccctc tggcttccta agcagtctat acgtgagaag ccctttcttc
120
aagtgaagac ttctgagctc actacgagag cactggagct ggaacctctc tgggttcaaa
180
tcttcaactg gggggttga ggaggttact tcacttctca aaacctcaat ttccttatct
240
gcaaaatggg gtaataggag cccctcttca tcaatgcttg gagggaaatgc ctggcacagt
300
agggcagtta ccgtcatgga gaacagaaaag gcccagagct atcctggatg tggtgagaat
360
gggtcctgga tctgcctgc tcggcctttt cattctcttc ttcacctaca ggctcccaca
420
aagggcctct gaaaacacag ggtg
444

```

<210> 500  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

```

<400> 500
Met Thr Val Thr Ala Leu Leu Cys Gln Ala Phe Pro Pro Ser Ile Asp
  1          5          10          15
Glu Glu Gly Leu Leu Leu Pro His Phe Ala Asp Lys Glu Ile Glu Val
      20          25          30
Leu Arg Ser Glu Val Thr Ser Ser Asn Pro Pro Val Glu Asp Leu Asn

```

```

      35              40              45
Pro Glu Arg Phe Gln Leu Gln Cys Ser Arg Ser Glu Leu Arg Ser Phe
   50              55              60
His Leu Lys Lys Gly Leu Leu Thr Tyr Arg Leu Leu Arg Lys Pro Glu
  65              70              75              80
Gly Gln Ala Glu Gly Arg Ala Pro Ala Leu Gln Gly Gly Gly Leu Thr
      85              90              95
Gln Leu Asn Thr Ala His Pro Ser Arg
      100              105

```

<210> 501  
 <211> 800  
 <212> DNA  
 <213> Homo sapiens

```

<400> 501
agatctgata cgagaagtgg ctgctcaggg aaatgactac tccatggctt tcttaactca
 60
ggtactcctt attcaatgag aggcctgagg tgagaccgcg catgcggcgc gtggatcgca
 120
tggtgttagt gcacactagc aaggggctta ggtctccagc tgaggtcaga tgcacacttg
 180
gaccttgtag tggggagtaa cacacatctc tgtgttcagc gaaccatcca ggagctgttt
 240
gaagttttatt ctcccatgga tgatgctggc ttcccggtea aagctgagga gtttgtggtg
 300
ctttctcagg aaccttctgt caccgaaacc attgcaccca aaattgcaag acctttcata
 360
gaggccctca agagtattga gtatctggag gaggatgccc agaagtccgc acaggagggg
 420
gtgctgggac cacacactga tgctctgtca tcagactctg agaacatgcc gtgtgatgaa
 480
gaaccatccc aattagagga gctagctgac ttcattggagc agcttacacc aattgaaaaa
 540
tatgctttta attacctgga atcttgaggc agggcctgag agagcacgct gcgccgtact
 600
tccagcagct gcggcagacc acggctccac gcctgctgca gttccctgag ctgaggctgg
 660
tgcagttcga ctcaggtatg cggcagttgg gggcgtggcc cgtgcggggag ctgcactggc
 720
cctggatgat gaggcgctct tgatgtgatt cgtttcccag ggaagttgga agcttttagct
 780
atcttgcttc agaaactgaa
 800

```

<210> 502  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

```

<400> 502
Met Asp Asp Ala Gly Phe Pro Val Lys Ala Glu Glu Phe Val Val Leu
 1              5              10              15
Ser Gln Glu Pro Ser Val Thr Glu Thr Ile Ala Pro Lys Ile Ala Arg

```

20 25 30  
 Pro Phe Ile Glu Ala Leu Lys Ser Ile Glu Tyr Leu Glu Glu Asp Ala  
 35 40 45  
 Gln Lys Ser Ala Gln Glu Gly Val Leu Gly Pro His Thr Asp Ala Leu  
 50 55 60  
 Ser Ser Asp Ser Glu Asn Met Pro Cys Asp Glu Glu Pro Ser Gln Leu  
 65 70 75 80  
 Glu Glu Leu Ala Asp Phe Met Glu Gln Leu Thr Pro Ile Glu Lys Tyr  
 85 90 95  
 Ala Leu Asn Tyr Leu Glu Ser  
 100

<210> 503  
 <211> 538  
 <212> DNA  
 <213> Homo sapiens

<400> 503  
 nnacgcgttg tcgtctctcc gatcattgat tttgttgat tctgcaatga tgtaaaggaa  
 60  
 gatgatgaca cggagaagtt taaagaagcc attgtgaaat ttcattaggct gtttgggatg  
 120  
 ccagaggaag agaaactcgt caactattac tcttcagct attggaaggg gaagggtcccc  
 180  
 cgtcaggggtt ggatgtacct cagcattaac cacctttgct tttattcttt tcttatggga  
 240  
 agggaaagcga aactgggtcat ccgggtgggta gacatcactc agcttgagaa gaatgcccc  
 300  
 ctgcttctgc ctgatgtgat caaagtgagc acacgggtcca gtgagcattt cttctctgta  
 360  
 ttctcaaca tcaacgagac cttcaagta atggagcagc ttgccaacat agccatgagg  
 420  
 caactcttag acaatgaggg atttgaacaa gatcgatccc tgcccaaact caaaaggaaa  
 480  
 tctcctaaaa aagtgtctgc tctaaaacgt gatcttgatg cctgggcccct tcacgcgt  
 538

<210> 504  
 <211> 179  
 <212> PRT  
 <213> Homo sapiens

<400> 504  
 Xaa Arg Val Val Val Ser Pro Ile Ile Asp Phe Val Val Phe Cys Asn  
 1 5 10 15  
 Asp Val Lys Glu Asp Asp Asp Thr Glu Lys Phe Lys Glu Ala Ile Val  
 20 25 30  
 Lys Phe His Arg Leu Phe Gly Met Pro Glu Glu Glu Lys Leu Val Asn  
 35 40 45  
 Tyr Tyr Ser Cys Ser Tyr Trp Lys Gly Lys Val Pro Arg Gln Gly Trp  
 50 55 60  
 Met Tyr Leu Ser Ile Asn His Leu Cys Phe Tyr Ser Phe Leu Met Gly  
 65 70 75 80  
 Arg Glu Ala Lys Leu Val Ile Arg Trp Val Asp Ile Thr Gln Leu Glu

```

      85              90              95
Lys Asn Ala Pro Leu Leu Leu Pro Asp Val Ile Lys Val Ser Thr Arg
      100              105              110
Ser Ser Glu His Phe Phe Ser Val Phe Leu Asn Ile Asn Glu Thr Phe
      115              120              125
Lys Leu Met Glu Gln Leu Ala Asn Ile Ala Met Arg Gln Leu Leu Asp
      130              135              140
Asn Glu Gly Phe Glu Gln Asp Arg Ser Leu Pro Lys Leu Lys Arg Lys
145              150              155              160
Ser Pro Lys Lys Val Ser Ala Leu Lys Arg Asp Leu Asp Ala Trp Ala
      165              170              175
Leu His Ala

```

<210> 505  
 <211> 381  
 <212> DNA  
 <213> Homo sapiens

```

<400> 505
gtgcacgaca ccgaacggta cgaacgtatc tcccaggcac gtcgagagga acagcaggcc
60
atgctcggct acgaacgtc aagaacctgt cgcacgacct tgctcaccgg gcagctggac
120
gacccctcca cgactccttg cggacgctgc gacgtctgtg ctggcccggtg gtactcagtc
180
gaggtcgata agtcagccgc tgtgagagcc gtccaatccc tcaaccgggt gggagttccg
240
gtggaaccac gcgcgcctg gccgcagggt atggacgccc tccaggttgc gctcaagggt
300
cgcatcagtg ccgaggagat cgctgcagag ggccgcgtca tcgccagact ctccgatctg
360
ggttggggag gggcgctgcg c
381

```

<210> 506  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

```

<400> 506
Val His Asp Thr Glu Arg Tyr Glu Arg Ile Ser Gln Ala Arg Arg Glu
1      5      10      15
Glu Gln Gln Ala Met Leu Gly Tyr Asp Xaa Ser Arg Thr Cys Arg Met
20     25     30
Thr Leu Leu Thr Gly Gln Leu Asp Asp Pro Ser Thr Thr Pro Cys Gly
35     40     45
Arg Cys Asp Val Cys Ala Gly Pro Trp Tyr Ser Val Glu Val Asp Gln
50     55     60
Ser Ala Ala Val Arg Ala Val Gln Ser Leu Asn Arg Val Gly Val Pro
65     70     75     80
Val Glu Pro Arg Ala Ala Trp Pro Ala Gly Met Asp Ala Leu Gln Val
85     90     95
Ala Leu Lys Gly Arg Ile Ser Ala Glu Glu Ile Ala Ala Glu Gly Arg

```

100 105 110  
 Val Ile Ala Arg Leu Ser Asp Leu Gly Trp Gly Gly Ala Leu Arg  
 115 120 125

<210> 507  
 <211> 499  
 <212> DNA  
 <213> Homo sapiens

<400> 507  
 gccggcgtgt tcaacctcat ggtgtgggcc ttcattaccg acgtcatcga tgcccaggag  
 60  
 gtcatgtccg gggagcgtga agacgggtgc atctatggcg tgaactcctt cgcccgcaaa  
 120  
 cttgcccagg ccattgccgg tggaatcggc ggagccatgc tgacgatgat cggctaccag  
 180  
 tcctcctccc aagggtggtgc cgttcagtcg gagtcgcgcg tcaatcacct gtacacgctc  
 240  
 gccaccgcca tcccgacgat ctgctgcctc ggcgctgccc tgctcatgct gggctaccg  
 300  
 ctcacccgcg acaaggtggt cgccaacgcc gacgagttgg ctcgtcgcca cgcagtacag  
 360  
 gccgagcaaa actcctgacc cataacggag gcacatcatg gacacgctca tgcggatcac  
 420  
 cgaccacttg acaacctcgc cgggtatcca attgaaaatt gacaagcgat ggggtgcctc  
 480  
 cgtcacattt gtgacgct  
 499

<210> 508  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 508  
 Ala Gly Val Phe Asn Leu Met Val Trp Ala Phe Ile Thr Asp Val Ile  
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 Asp Ala Gln Glu Val Met Ser Gly Glu Arg Glu Asp Gly Val Ile Tyr  
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 Gly Val Asn Ser Phe Ala Arg Lys Leu Ala Gln Ala Ile Ala Gly Gly  
 35 40 45  
 Ile Gly Gly Ala Met Leu Thr Met Ile Gly Tyr Gln Ser Ser Ser Gln  
 50 55 60  
 Gly Gly Ala Val Gln Ser Glu Ser Val Val Asn His Leu Tyr Thr Leu  
 65 70 75 80  
 Ala Thr Ala Ile Pro Thr Ile Cys Cys Leu Gly Ala Ala Leu Leu Met  
 85 90 95  
 Leu Gly Tyr Pro Leu Thr Arg Asp Lys Val Val Ala Asn Ala Asp Glu  
 100 105 110  
 Leu Ala Arg His Ala Val Gln Ala Glu Gln Asn Ser  
 115 120 125

<210> 509  
 <211> 360



<212> DNA  
<213> Homo sapiens

<400> 509  
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 120  
 ttggatcata cggagaagat tgccaagttt gtacgcatca tggagcggga gctcaaccgg  
 180  
 cgtaagaagc tcttgctcga ctacggtgtt ggtacactag agctctaccg tcaggctagc  
 240  
 ggtcagcaag agccggccat cgtcatcctg ctggacagtt atgagtccat gaaggaagag  
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 360

<210> 510  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 510  
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 1 5 10 15  
 Tyr Leu Met Asp Phe Gly Thr Asn Gly Val Ala Pro Leu Gly Gln Leu  
 20 25 30  
 Pro Gln Val Ala Asp Thr Leu Leu Leu Asp His Thr Glu Lys Ile Ala  
 35 40 45  
 Lys Phe Val Arg Ile Met Glu Arg Glu Leu Asn Arg Arg Lys Lys Leu  
 50 55 60  
 Leu Ser Asp Tyr Gly Val Gly Thr Leu Glu Leu Tyr Arg Gln Ala Ser  
 65 70 75 80  
 Gly Gln Gln Glu Pro Ala Ile Val Ile Leu Leu Asp Ser Tyr Glu Ser  
 85 90 95  
 Met Lys Glu Glu Ala Tyr Glu Ala Glu Leu Phe Thr Leu Leu Val Arg  
 100 105 110  
 Ile Ser Arg Glu Gly Leu Ser Ile  
 115 120

<210> 511  
 <211> 361  
 <212> DNA  
 <213> Homo sapiens

<400> 511  
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 actgcgttcg gcgatgccgg catcgccag atcgggcgca agatgcagga cgatctcgac  
 120  
 gacgggatgg actggctggt caaggagggc atcgtcgaca agggccgggt gtgcatcgtc  
 180  
 ggggcctcct atggcggcta tgccgcgatg tggggcgaga tccgcaatcc cgaacgctat  
 240

cgctgcgcgg cgagcctggc ggggggttgcc gattaaggcc atgctcaaataaaccggcg  
 300  
 ctatctcgac aaggaggcgg gcaagcgctg gccgccccgn tcaaccggcg aaccgaatt  
 360  
 c  
 361

<210> 512  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<400> 512  
 Xaa Ala Asn Arg Gly Tyr Ala Val Leu Gln Pro Asn Phe Arg Gly Ser  
 1 5 10 15  
 Gly Gly Tyr Gly Thr Ala Phe Gly Asp Ala Gly Ile Gly Gln Ile Gly  
 20 25 30  
 Arg Lys Met Gln Asp Asp Leu Asp Asp Gly Met Asp Trp Leu Val Lys  
 35 40 45  
 Glu Gly Ile Val Asp Lys Gly Arg Val Cys Ile Val Gly Ala Ser Tyr  
 50 55 60  
 Gly Gly Tyr Ala Ala Met Trp Gly Ala Ile Arg Asn Pro Glu Arg Tyr  
 65 70 75 80  
 Arg Cys Ala Ala Ser Leu Ala Gly Val Ala Asp  
 85 90

<210> 513  
 <211> 369  
 <212> DNA  
 <213> Homo sapiens

<400> 513  
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 aataactgtg gtgtagatgg ttttggttta ggggttttgc tagaagataa gcaagtacgc  
 180  
 aaaatggtgt cttcttatgt ggggtgaaat gcactgtttg agaagcaatt attacaaggt  
 240  
 gagttggaag tcgagctcac tcctcaaggc actcttgccg aaaaactacg cgctggcggc  
 300  
 gcgggaattc ctgccttttt cacagcaacg ggtgtaggta cacctattgg tgagggtaaa  
 360  
 gacacgcgt  
 369

<210> 514  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 514  
 Xaa Cys Arg Leu Glu Asp Gly Met Thr Val Leu Ala Gly Gly Phe Gly

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      1           5           10           15
Leu Cys Gly Ile Pro Glu Asn Leu Ile Gln Glu Ile Lys Arg Arg Gln
      20           25           30
Thr Cys Asp Leu Thr Ile Val Ser Asn Asn Cys Gly Val Asp Gly Phe
      35           40           45
Gly Leu Gly Val Leu Leu Glu Asp Lys Gln Val Arg Lys Met Val Ser
      50           55           60
Ser Tyr Val Gly Glu Asn Ala Leu Phe Glu Lys Gln Leu Leu Gln Gly
      65           70           75           80
Glu Leu Glu Val Glu Leu Thr Pro Gln Gly Thr Leu Ala Glu Lys Leu
      85           90           95
Arg Ala Gly Gly Ala Gly Ile Pro Ala Phe Phe Thr Ala Thr Gly Val
      100           105           110
Gly Thr Pro Ile Gly Glu Gly Lys Asp Thr Arg
      115           120

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&lt;210&gt; 515

&lt;211&gt; 387

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 515

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60
tccgacgtgc aggactcgtc gctgaccgcg atggacgagc tgatcaccga gggcgtgaca
120
tccttcaagc tcttcgtggc ctacaagggc gtcttctctc cggacgacgg gcagatcctg
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240
gcgatcatcg acgtgctcgt gcagcaggcg ctcgaggccg ggaagaccac cccgtactac
300
cacggcatca gccggccgtg gcaggccgag gaggaggcca cccaccgcgc gatcatgatc
360
gccgacctga ccggtgcgcc gttgtac
387

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&lt;210&gt; 516

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 516

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Ala Trp Asp Glu Lys Ala Ala Gly Asn Cys Ala Ile Asp Tyr Gly Phe
      1           5           10           15
His Gln Ile Leu Ser Asp Val Gln Asp Ser Ser Leu Thr Ala Met Asp
      20           25           30
Glu Leu Ile Thr Glu Gly Val Thr Ser Phe Lys Leu Phe Val Ala Tyr
      35           40           45
Lys Gly Val Phe Leu Ser Asp Asp Gly Gln Ile Leu Arg Ala Phe Gln
      50           55           60
Lys Gly Ala Asp Asn Gly Ala Met Met Met Met His Ala Glu Asn Gly
      65           70           75           80
Ala Ile Ile Asp Val Leu Val Gln Gln Ala Leu Glu Ala Gly Lys Thr

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85 90 95  
 Thr Pro Tyr Tyr His Gly Ile Ser Arg Pro Trp Gln Ala Glu Glu Glu  
 100 105 110  
 Ala Thr His Arg Ala Ile Met Ile Ala Asp Leu Thr Gly Ala Pro Leu  
 115 120 125  
 Tyr

<210> 517  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<400> 517  
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 agaccccttc gggccaacag tggggagggg ctgccgtctg agccactgtt ccgacagggg  
 120  
 attcgcgagt tccgggggag ctggggactg agctcggggc ctctctgggct ggggctcttc  
 180  
 tccgaggttg gaggcagctt tagaaacttg agacccttag ctggagaggg cagaaggggt  
 240  
 ccctgagctt ccccaggaga aggggggcca atttgagct tgcttttcac ctgagatgag  
 300  
 gaatgggggt ggccaggccg agagcccagt ggggcatccc cagcaccat gaacatgcta  
 360  
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 377

<210> 518  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 518  
 Met Phe Met Gly Ala Gly Asp Ala Pro Leu Gly Ser Arg Pro Gly His  
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 Pro His Ser Ser Ser Gln Val Lys Ser Lys Leu Gln Ile Gly Pro Pro  
 20 25 30  
 Ser Pro Gly Glu Ala Gln Gly Pro Leu Leu Pro Ser Pro Ala Arg Gly  
 35 40 45  
 Leu Lys Phe Leu Lys Leu Pro Pro Thr Ser Glu Lys Ser Pro Ser Pro  
 50 55 60  
 Gly Gly Pro Gln Leu Ser Pro Gln Leu Pro Arg Asn Ser Arg Ile Pro  
 65 70 75 80  
 Cys Arg Asn Ser Gly Ser Asp Gly Ser Pro Ser Pro Leu Leu Ala Arg  
 85 90 95  
 Arg Gly Leu Gly Gly Gly Glu Leu Ser Pro Glu Gly Ala Gln Gly Leu  
 100 105 110  
 Pro Thr Ser Pro Ser Arg  
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<210> 519  
 <211> 311

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 519

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 agaatttaaa ttattataaa ggaacctttt ctgcaactct gaaaaatgtt agaatatcca  
 120  
 aagaaattga taattttcta ggaaaacatg acttaccaaa attaactcta gaaaagaatc  
 180  
 gatacacatc agtaacaaca gaagttgaga aagtagttaa catattgcc aacctggaat  
 240  
 tcatgattga attctttgag atctactgtg agtacatact ctgcctctgt tcagctgttc  
 300  
 cagaacttaa g  
 311

&lt;210&gt; 520

&lt;211&gt; 92

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 520

Met	Arg	Gly	Lys	Tyr	Gln	Ile	Leu	Lys	Asn	Leu	Asn	Tyr	Tyr	Lys	Gly
1			5					10					15		
Thr	Phe	Ser	Ala	Thr	Leu	Lys	Asn	Val	Arg	Ile	Ser	Lys	Glu	Ile	Asp
		20					25					30			
Asn	Phe	Leu	Gly	Lys	His	Asp	Leu	Pro	Lys	Leu	Thr	Leu	Glu	Lys	Asn
	35					40				45					
Arg	Tyr	Thr	Ser	Val	Thr	Thr	Glu	Val	Glu	Lys	Val	Val	Asn	Ile	Leu
	50				55				60						
Pro	Asn	Leu	Glu	Phe	Met	Ile	Glu	Phe	Phe	Glu	Ile	Tyr	Cys	Glu	Tyr
65				70				75						80	
Ile	Leu	Cys	Leu	Cys	Ser	Ala	Val	Pro	Glu	Leu	Lys				
			85					90							

&lt;210&gt; 521

&lt;211&gt; 352

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 521

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 180  
 ctgtgtaccg gccgtaccgg cgtgcgcccc gtggtggtag aaacttatgc caaggcgctc  
 240  
 aacgcccggc tcgtgccggg ggtgcgcgaa tacgggtcgc tgggctgctc cggcgacttg  
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 352

<210> 522  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 522  
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 1 5 10 15  
 Ala Arg Arg His Ile Pro Glu Glu Met Arg Ala Gln Leu Gln Leu Ser  
 20 25 30  
 Leu Val Arg Ser His Ala Ala Gly Thr Gly Pro Glu Val Glu Glu Glu  
 35 40 45  
 Val Ile Arg Ala Leu Met Leu Leu Arg Leu Ser Thr Leu Cys Thr Gly  
 50 55 60  
 Arg Thr Gly Val Arg Pro Val Val Val Glu Thr Tyr Ala Lys Ala Leu  
 65 70 75 80  
 Asn Ala Gly Ile Val Pro Gly Val Arg Glu Tyr Gly Ser Leu Gly Cys  
 85 90 95  
 Ser Gly Asp Leu Ala Pro Leu Ala His Cys Ala Leu Ala Leu Leu Gly  
 100 105 110  
 Glu Gly Glu Val Arg  
 115

<210> 523  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 523  
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 tcagagccac caagctgcgg caccatctaa ggagaacatg tcccctggag gtctgttag  
 120  
 aagctcctgg ttgagaaggc cctgaagctg ggtggcatca atgtccagcc tctgctgagc  
 180  
 atatctgttg aaaatgcttt gttgggagcc atgttctgaa gggcttcctt tcattctgag  
 240  
 gttgaaatgg ctgctcaggt gcctgtcact gtctggcatt ttcaggaaga ttcggagcaa  
 300  
 gaactccgct gattttctcc gtgtctgtgc aaccacaaca tagttcccag ggctcagatg  
 360  
 gtaagtcacg gtgaagttgc ggcggaattt attatttgag ctttggacag tgtttctgaa  
 420  
 cgaggaaaaa aacacgggtg gaaatttctc ccggaaccgc tgtgagccag ccagaatcac  
 480  
 ttggaaaatcg agtggaaatt ttgcatcttc tgctttcaaa tttgatggtg tgacagcaac  
 540  
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 600  
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 660  
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 693

<210> 524  
 <211> 193  
 <212> PRT  
 <213> Homo sapiens

<400> 524  
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 20 25 30  
 Val Thr Val Ala Val Thr Pro Ser Asn Leu Lys Ala Glu Asp Ala Lys  
 35 40 45  
 Phe Pro Leu Asp Phe Gln Val Ile Leu Ala Gly Ser Gln Arg Phe Arg  
 50 55 60  
 Glu Lys Phe Pro Pro Val Phe Phe Ser Ser Phe Arg Asn Thr Val Gln  
 65 70 75 80  
 Ser Ser Asn Asn Lys Phe Arg Arg Asn Phe Thr Met Thr Tyr His Leu  
 85 90 95  
 Ser Pro Gly Asn Tyr Val Val Val Ala Gln Thr Arg Arg Lys Ser Ala  
 100 105 110  
 Glu Phe Leu Leu Arg Ile Phe Leu Lys Met Pro Asp Ser Asp Arg His  
 115 120 125  
 Leu Ser Ser His Phe Asn Leu Arg Met Lys Gly Ser Pro Ser Glu His  
 130 135 140  
 Gly Ser Gln Gln Ser Ile Phe Asn Arg Tyr Ala Gln Gln Arg Leu Asp  
 145 150 155 160  
 Ile Asp Ala Thr Gln Leu Gln Gly Leu Leu Asn Gln Glu Leu Leu Thr  
 165 170 175  
 Gly Pro Pro Gly Asp Met Phe Ser Leu Asp Gly Ala Ala Ala Trp Trp  
 180 185 190  
 Leu

<210> 525  
 <211> 1101  
 <212> DNA  
 <213> Homo sapiens

<400> 525  
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 120  
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 180  
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 240  
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 420

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 1080  
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 1101

&lt;210&gt; 526

&lt;211&gt; 290

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 526

Met	Ala	Arg	Phe	Pro	Lys	Ala	Asp	Leu	Ala	Ala	Ala	Gly	Val	Met	Leu
1				5				10					15		
Leu	Cys	His	Phe	Phe	Thr	Asp	Gln	Phe	Gln	Phe	Ala	Asp	Gly	Lys	Pro
			20				25						30		
Gly	Asp	Gln	Ile	Leu	Asp	Trp	Gln	Tyr	Gly	Val	Thr	Gln	Ala	Phe	Pro
		35				40						45			
His	Thr	Glu	Glu	Glu	Val	Glu	Val	Asp	Ser	His	Ala	Tyr	Ser	His	Arg
	50					55				60					
Trp	Lys	Arg	Asn	Leu	Asp	Phe	Leu	Lys	Ala	Val	Asp	Thr	Asn	Arg	Ala
65				70					75					80	
Ser	Val	Gly	Gln	Asp	Ser	Leu	Glu	Pro	Arg	Ser	Phe	Thr	Asp	Leu	Leu
			85					90						95	
Leu	Asp	Asp	Gly	Gln	Asp	Asn	Asn	Thr	Gln	Ile	Glu	Glu	Asp	Thr	Asp
			100					105					110		
His	Asn	Tyr	Tyr	Ile	Ser	Arg	Ile	Tyr	Gly	Pro	Ser	Asp	Ser	Ala	Ser
	115					120						125			
Arg	Asp	Leu	Trp	Val	Asn	Ile	Asp	Gln	Met	Glu	Lys	Asp	Lys	Val	Lys
	130				135						140				
Ile	His	Gly	Ile	Leu	Ser	Asn	Thr	His	Arg	Gln	Ala	Ala	Arg	Val	Asn
145				150					155					160	
Leu	Ser	Phe	Asp	Phe	Pro	Phe	Tyr	Gly	His	Phe	Leu	Arg	Glu	Ile	Thr
			165					170					175		
Val	Ala	Thr	Gly	Gly	Phe	Ile	Tyr	Thr	Gly	Glu	Val	Val	His	Arg	Met



	180		185		190
Leu Thr Ala Thr Gln Tyr Ile	Ala Pro Leu Met Ala Asn Phe Asp Pro				
195	200		205		
Ser Val Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala					
210	215		220		
Leu Val Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu					
225	230		235		240
Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile					
245	250		255		
Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr					
260	265		270		
Asn His Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val Val Val His					
275	280		285		
Arg Ile					
290					

&lt;210&gt; 527

&lt;211&gt; 5343

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 527

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120
gcctcccag agctagacat cctctcctc gaggacagt agacggctta cgactgggag
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900
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960

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1080  
ggccgttgcc tgcagaactc caaacggctt ggcatcacca agtcaggctc actaaaaatc  
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1920  
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&lt;210&gt; 528

&lt;211&gt; 886

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 528

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 Leu Pro Glu Asp Ser Glu Thr Ala Tyr Asp Trp Glu Tyr Ala Gly Phe

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Asp	Met	Val	His 100	Arg	Pro	Pro	Ala	Met	Ser	Gln	Ala	Cys	Asn	Thr	Glu	
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Arg	Arg	Val	Thr	Cys 195	Arg	Gln	Leu	Thr	Asp	Gly	Ser	Phe	Leu	Asn		
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Cys 225	Ala	Arg	Thr	Asp 230	Cys	Pro	Pro	His	Leu	Ala	Val	Gly	Asp	Trp	Ser	
Lys	Cys	Ser	Val	Ser 245	Cys	Gly	Val	Gly	Ile	Gln	Arg	Arg	Lys	Gln	Val	
Cys	Gln	Arg	Leu	Ala 260	Ala	Lys	Gly	Arg	Arg	Ile	Pro	Leu	Ser	Glu	Met	
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Pro 465	Phe	Leu	Arg	Ala 470	Leu	Leu	Gly	His	Cys	Ser	Asn	Ser	Ala	Gly	Ser	
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&lt;210&gt; 529

&lt;211&gt; 4566

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 529

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&lt;210&gt; 530

&lt;211&gt; 802

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 530

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Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser Asp Pro Asp Gly Gly
 65           70           75           80
Pro Arg Asp Arg Asn Phe Leu Phe Val Gly Val Met Thr Ala Gln Lys
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Tyr Leu Gln Thr Arg Ala Val Ala Ala Tyr Arg Thr Trp Ser Lys Thr
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115           120           125
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130           135           140
Pro Gln Lys Lys Ser Phe Met Met Leu Lys Tyr Met His Asp His Tyr
145           150           155           160
Leu Asp Lys Tyr Glu Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile
165           170           175
Lys Gly Asp Arg Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu
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Pro Leu Phe Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly
195           200           205
Lys Leu Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly
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Glu Ile Val Leu Met Ser Lys Tyr Ser Asn Thr Glu Ile His Lys Glu
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Gln Arg Glu Glu Ile Leu Glu Trp Glu Phe Leu Thr Gly Lys Tyr Leu
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Tyr Ser Ala Val Asp Gly Gln Pro Pro Arg Arg Gly Met Asp Ser Ala
385           390           395           400
Gln Arg Glu Ala Leu Asp Asp Ile Val Met Gln Val Met Glu Met Ile

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```

      405      410      415
Asn Ala Asn Ala Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys Glu Ile
      420      425      430
Gln Tyr Gly Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr Ile
      435      440      445
Leu Asp Leu Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met Thr
      450      455      460
Val Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile
      465      470      475      480
Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys Arg
      485      490      495
Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser Leu Lys
      500      505      510
Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu His Lys Glu
      515      520      525
Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu Ser Gly Arg Phe
      530      535      540
Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu Lys Thr Cys Leu Ile
      545      550      555      560
Pro Asn Gln Asn Val Lys Leu Val Val Leu Leu Phe Asn Ser Asp Ser
      565      570      575
Asn Pro Asp Lys Ala Lys Gln Val Glu Leu Met Thr Asp Tyr Arg Ile
      580      585      590
Lys Tyr Pro Lys Ala Asp Met Gln Ile Leu Pro Val Ser Gly Glu Phe
      595      600      605
Ser Arg Ala Leu Ala Leu Glu Val Gly Ser Ser Gln Phe Asn Asn Glu
      610      615      620
Ser Leu Leu Phe Phe Cys Asp Val Asp Leu Val Phe Thr Thr Glu Phe
      625      630      635      640
Leu Gln Arg Cys Arg Ala Asn Thr Val Leu Gly Gln Gln Ile Tyr Phe
      645      650      655
Pro Ile Ile Phe Ser Gln Tyr Asp Pro Lys Ile Val Tyr Ser Gly Lys
      660      665      670
Val Pro Ser Asp Asn His Phe Ala Phe Thr Gln Lys Thr Gly Phe Trp
      675      680      685
Arg Asn Tyr Gly Phe Gly Ile Thr Cys Ile Tyr Lys Gly Asp Leu Val
      690      695      700
Arg Val Gly Gly Phe Asp Val Ser Ile Gln Gly Trp Gly Leu Glu Asp
      705      710      715      720
Val Asp Leu Phe Asn Lys Val Val Gln Ala Gly Leu Lys Thr Phe Arg
      725      730      735
Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe Cys Asp
      740      745      750
Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly Ser Lys Ala
      755      760      765
Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met Trp Leu Glu Lys
      770      775      780
Asn Asp Pro Ser Tyr Ser Lys Ser Ser Asn Asn Asn Gly Ser Val Arg
      785      790      795      800
Thr Ala

```

&lt;210&gt; 531

&lt;211&gt; 321

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 531

ngatgatgaa tccccccgca gcctcgtcaa tatggggggc ttcctacccc agcaaaaggc  
 60  
 acggcaatac gtctcgaaca aaggtctttt gtttcgaaat aacaaggggt tagagctaag  
 120  
 aggaagaagc gtgaaacgct gtaggaccag cgtttcgaac gcccccgagg tgaaccctcg  
 180  
 ggggcgctctg aatcaggcca gttgggcctg ggacgacagc ggttgacagc gcagcaatgg  
 240  
 cgcgtgcgga tcagccttga tcgattcacg ccaggcgccg agccactcgg cgtggccttc  
 300  
 gttccacacc tgctgggtgca g  
 321

&lt;210&gt; 532

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 532

Met	Gly	Gly	Phe	Leu	Pro	Gln	Gln	Lys	Ala	Arg	Gln	Tyr	Val	Ser	Asn
1				5					10					15	
Lys	Gly	Leu	Leu	Phe	Arg	Asn	Asn	Lys	Gly	Leu	Glu	Leu	Arg	Gly	Arg
			20				25						30		
Ser	Val	Lys	Arg	Cys	Arg	Thr	Ser	Val	Ser	Asn	Ala	Pro	Glu	Val	Asn
		35				40					45				
Pro	Arg	Gly	Arg	Leu	Asn	Gln	Ala	Ser	Trp	Ala	Trp	Asp	Asp	Ser	Gly
	50				55					60					
Cys	Ser	Gly	Ser	Asn	Gly	Ala	Cys	Gly	Ser	Ala	Leu	Ile	Asp	Ser	Arg
65				70					75				80		
Gln	Ala	Pro	Ser	His	Ser	Ala	Trp	Pro	Ser	Phe	His	Thr	Cys	Trp	Cys
			85					90					95		

&lt;210&gt; 533

&lt;211&gt; 335

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 533

nagtttccgg tgaaccgcgc cgcaatgcct cgtgacatcg acttcagcga agccaacagg  
 60  
 agcatcatcg acaacatggc aactgcctca atcccgtttt tccgaaccca caaaaactgg  
 120  
 gagacgtggc cgagtcaggc ccggcatttc attagccttt tacacccaaa agtcaccctc  
 180  
 accaaacattg acaacgtcct caacaaagat cacctgcgtt ggctacactt tcttttggag  
 240  
 ggtcgcctgg agccaaacgt gcgcctgatt gtccagggct actgttcgcc tggcaagctg  
 300  
 taccgcaagc ttgaggagct atatgccctt tctgc  
 335

<210> 534  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 534  
 Met Pro Arg Asp Ile Asp Phe Ser Glu Ala Asn Arg Ser Ile Ile Asp  
 1 5 10 15  
 Asn Met Ala Thr Ala Ser Ile Pro Leu Phe Arg Thr His Lys Asn Trp  
 20 25 30  
 Glu Thr Trp Ser Ser Gln Val Arg His Phe Ile Ser Leu Leu His Pro  
 35 40 45  
 Lys Val Thr Leu Thr Asn Ile Asp Asn Val Leu Asn Lys Asp His Leu  
 50 55 60  
 Arg Trp Leu His Phe Leu Leu Glu Gly Arg Leu Glu Pro Asn Val Arg  
 65 70 75 80  
 Leu Ile Val Gln Gly Tyr Cys Ser Pro Gly Lys Leu Tyr Arg Lys Leu  
 85 90 95  
 Glu Glu Leu Tyr Ala Pro Ser  
 100

<210> 535  
 <211> 402  
 <212> DNA  
 <213> Homo sapiens

<400> 535  
 acgcgtctct acagccggac taagcacagg ctcagccccg gtcgccatgc gccaggtc  
 60  
 gggtatcagc cgaggaatcc acggcgaaat gaccagtagc ggccctaata caactatgct  
 120  
 gccgagcagc agacgtcgag gtcgggtcat gaggatgccg acggccaccg cgaccgggta  
 180  
 taccacaaat gcaggaacaa ggctgatagc tagggctgac cacagagcca ggccgcctgc  
 240  
 cgaggaaaacg cccccacct ggtgactgcc agtatcagca ccgcgcagct caacgacgtc  
 300  
 aacagtctcg ggattgacca accgccacgt atgcagggcc atgtggggga gaatcacccc  
 360  
 caacgccaat gctgtcaccg agcctcgggc taggccgccg gc  
 402

<210> 536  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

<400> 536  
 Met Ala Leu His Thr Trp Arg Leu Val Asn Pro Glu Thr Val Asp Val  
 1 5 10 15  
 Val Glu Leu Arg Gly Ala Asp Thr Gly Ser His Gln Val Gly Val  
 20 25 30  
 Ser Ser Ala Gly Gly Leu Ala Leu Trp Ser Ala Leu Ala Ile Ser Leu

```

      35          40          45
Val Pro Ala Leu Trp Val Tyr Pro Val Ala Val Ala Val Gly Ile Leu
      50          55          60
Met Thr Arg Pro Arg Arg Leu Leu Leu Gly Ser Ile Val Val Leu Gly
      65          70          75          80
Pro Leu Leu Val Ile Ser Pro Trp Ile Pro Arg Leu Ile Thr Glu Pro
      85          90          95
Gly Arg Met Ala Thr Gly Ala Glu Pro Val Leu Ser Pro Ala Val Glu
      100          105          110
Thr Arg

```

<210> 537  
 <211> 404  
 <212> DNA  
 <213> Homo sapiens

```

<400> 537
gtgcacatcg gcggcaccga cttegacaaa caactctcgc tggctggcat gatgccgctg
60
ttcggctacg gcagccgcat gaagagcggc gcctacatgc ccaccagcca ccacatgaac
120
ctggcgacct ggcacaccat caactcgggtg tactcgcaaa aatcccagct ggccttgggc
180
agcatgcgct acgacatcga agacaccggc ggcacatgacc gcctgttcaa gctgatcgaa
240
cagcgtgctg ggcactggct tgccatggaa gtggaagaaa ccaagatcca gctcaccat
300
caagacagcc gccacgtgcc gctggaccgc atcgaagcgg gcctgagcgt agacctgagc
360
cgggcgctgt tcgaatcgtc catcgacaac ctgctcgaac gcgt
404

```

<210> 538  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

```

<400> 538
Met Met Pro Leu Phe Gly Tyr Gly Ser Arg Met Lys Ser Gly Ala Tyr
1          5          10          15
Met Pro Thr Ser His His Met Asn Leu Ala Thr Trp His Thr Ile Asn
20          25          30
Ser Val Tyr Ser Gln Lys Ser Gln Leu Ala Leu Gly Ser Met Arg Tyr
35          40          45
Asp Ile Glu Asp Thr Gly Gly Ile Asp Arg Leu Phe Lys Leu Ile Glu
50          55          60
Gln Arg Ala Gly His Trp Leu Ala Met Glu Val Glu Glu Thr Lys Ile
65          70          75          80
Gln Leu Thr His Gln Asp Ser Arg His Val Pro Leu Asp Arg Ile Glu
85          90          95
Ala Gly Leu Ser Val Asp Leu Ser Arg Ala Leu Phe Glu Ser Ser Ile
100          105          110
Asp Asn Leu Leu Glu Arg

```

115

<210> 539  
 <211> 534  
 <212> DNA  
 <213> Homo sapiens

<400> 539  
 nnacgcgtga aaaagaagaa aatgaaggaa agcgaggctg acagcgagggt gaagcatcaa  
 60  
 ccaattttca taaaagaaag attgaagctt tttgaaatac tgaagaaaga ccatcagctc  
 120  
 ttacttgcca tttatggaaa aaagggggat acaagcaaca tcatcacagt aagagtggct  
 180  
 gatgggcaaa cagtgcagg ggaagtctgg aaaacaacgc cttaccaagt ggctgctgaa  
 240  
 attagtcagg aactggctga aagcacggta atagccaaag tcaatgggtga actgtggggac  
 300  
 ctggaccgcc cattggaagg ggactcttct ctagagctgc ttacatttga taatgaggaa  
 360  
 gctcaagctg tgagtattttt aaaaccagac agccaaactt tgggtagtta tgttgtaaac  
 420  
 tacattatat aagaggccac atattgaatt cacgaatgtt gagttttttg ggggtttcta  
 480  
 agatttaaaa tttgattatt gatgtttaat aaatatttgc ctcatgaatg ttaa  
 534

<210> 540  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<400> 540  
 Xaa Arg Val Lys Lys Lys Lys Met Lys Glu Ser Glu Ala Asp Ser Glu  
 1 5 10 15  
 Val Lys His Gln Pro Ile Phe Ile Lys Glu Arg Leu Lys Leu Phe Glu  
 20 25 30  
 Ile Leu Lys Lys Asp His Gln Leu Leu Leu Ala Ile Tyr Gly Lys Lys  
 35 40 45  
 Gly Asp Thr Ser Asn Ile Ile Thr Val Arg Val Ala Asp Gly Gln Thr  
 50 55 60  
 Val Gln Gly Glu Val Trp Lys Thr Thr Pro Tyr Gln Val Ala Ala Glu  
 65 70 75 80  
 Ile Ser Gln Glu Leu Ala Glu Ser Thr Val Ile Ala Lys Val Asn Gly  
 85 90 95  
 Glu Leu Trp Asp Leu Asp Arg Pro Leu Glu Gly Asp Ser Ser Leu Glu  
 100 105 110  
 Leu Leu Thr Phe Asp Asn Glu Glu Ala Gln Ala Val Ser Ile Leu Lys  
 115 120 125  
 Pro Asp Ser Gln Thr Leu Gly Ser Tyr Val Val Asn Tyr Ile Ile  
 130 135 140

<210> 541  
 <211> 551

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 541

ggtaccgagc tgcgcgtgtg gtatgcggcc ttctatgcca agaagatgga caagcccatg  
 60  
 ctgaagcagg cgggctcttg cgtccacgct gcaggcacc cagaaaacag cgccccctg  
 120  
 gagtcggagc ccagccagtg ggcgtgtaaa gtgtgttctg ccaccttcct ggagctgcag  
 180  
 ctctcaatg gtaaggagga cgtgtgggga gccccagttg taaaactcct gtgtcgattt  
 240  
 ctctctgact tacgctgtca cctgtctgcg gctgtcgggg gtgtcccaga ctttgtctg  
 300  
 tctgccccat tgccccacaa tgtagtcgcc agaaccaagg ctttctcagg gtttaaagct  
 360  
 tctgggcagt cccgcttccc acccccgacc cctgcaggcc tcaactcctca ctctctctg  
 420  
 ttgggaagtt gcatttcagc tggggcctt gactctggag cactggcagg ggccaggggc  
 480  
 caggagccag ccgtggcatg tgttgtgcac tcttgccctt gttgtctcta cttgacagcc  
 540  
 ccctcacgcg t  
 551

&lt;210&gt; 542

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 542

Met	Asp	Lys	Pro	Met	Leu	Lys	Gln	Ala	Gly	Ser	Gly	Val	His	Ala	Ala
1				5					10					15	
Gly	Thr	Pro	Glu	Asn	Ser	Ala	Pro	Val	Glu	Ser	Glu	Pro	Ser	Gln	Trp
			20					25					30		
Ala	Cys	Lys	Val	Cys	Ser	Ala	Thr	Phe	Leu	Glu	Leu	Gln	Leu	Leu	Asn
		35					40					45			
Gly	Lys	Glu	Asp	Val	Trp	Gly	Ala	Pro	Val	Val	Lys	Leu	Leu	Cys	Arg
	50					55					60				
Phe	Leu	Ser	Asp	Leu	Arg	Cys	His	Leu	Ser	Ala	Ala	Val	Gly	Gly	Val
65					70				75					80	
Pro	Asp	Phe	Val	Leu	Ser	Ala	Pro	Leu	Pro	His	Asn	Val	Val	Ala	Arg
			85					90					95		
Thr	Lys	Ala	Phe	Ser	Gly	Phe	Lys	Ala	Ser	Gly	Gln	Ser	Arg	Phe	Pro
		100						105					110		
Pro	Pro	Thr	Pro	Ala	Gly	Leu	Thr	Pro	His	Ser	Ser	Trp	Leu	Gly	Ser
		115				120						125			
Cys	Ile	Ser	Ala	Gly	Arg	Leu	Asp	Ser	Gly	Ala	Leu	Ala	Gly	Ala	Arg
	130					135					140				
Gly	Gln	Glu	Pro	Ala	Val	Ala	Cys	Val	Val	His	Ser	Cys	Leu	Cys	Cys
145					150					155				160	
Leu	Tyr	Leu	Thr	Ala	Pro	Ser	Arg								
					165										



<210> 543  
 <211> 349  
 <212> DNA  
 <213> Homo sapiens

<400> 543  
 nnaaagccgg acatgaatac ccgcattgct ggcaaaactg tcctgaccat cattctggcc  
 60  
 ggggggcaaag gcagccgcct ggccccgatg accgatcagg tggccaaacc agccgtgccg  
 120  
 tttatgggga cgtaccgcct gattgacttt tcgctgtcca acattgtcca cagcggttg  
 180  
 caggagctct ggatcattga gcaaaacctg ccccatagct taaacgagca cctggtggg  
 240  
 gggcgctcct gggatctgga ccgcacccgc ggtggcctga aggtcatgcc gcccttttcc  
 300  
 ggccctgccg atgaggacgg tggcttttcc gaaggcaacg cacacgcgt  
 349

<210> 544  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 544  
 Xaa Lys Pro Asp Met Asn Thr Arg Ile Ala Gly Lys Thr Val Leu Thr  
 1 5 10 15  
 Ile Ile Leu Ala Gly Gly Lys Gly Ser Arg Leu Ala Pro Met Thr Asp  
 20 25 30  
 Gln Val Ala Lys Pro Ala Val Pro Phe Met Gly Thr Tyr Arg Leu Ile  
 35 40 45  
 Asp Phe Ser Leu Ser Asn Ile Val His Ser Gly Leu Gln Asp Val Trp  
 50 55 60  
 Ile Ile Glu Gln Asn Leu Pro His Ser Leu Asn Glu His Leu Ala Gly  
 65 70 75 80  
 Gly Arg Ser Trp Asp Leu Asp Arg Thr Arg Gly Gly Leu Lys Val Met  
 85 90 95  
 Pro Pro Phe Ser Gly Pro Ala Asp Glu Asp Gly Gly Phe Ser Glu Gly  
 100 105 110  
 Asn Ala His Ala  
 115

<210> 545  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<400> 545  
 catgatgcaa aaacagacat gcttatttca aaatataaaa gtgaaaaaga tcgttttagca  
 60  
 caagaaattg ttggtgtcat cacaggttct gcaatgccgg gtggttcagc aaaccgtatc  
 120  
 ccaaataaag caggctcaaa tccagaagggt tctattgcaa cgcgttttat tgcagaaaca  
 180

```
<210> 546
<211> 130
<212> PRT
<213> Homo sapiens
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```
<210> 547
<211> 306
<212> DNA
<213> Homo sapiens
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<210> 548

<211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 548  
 Met Asp Glu Ala Cys Ser Phe Arg Ile Ser Ser Val Leu Thr Thr Tyr  
 1 5 10 15  
 Gln Asp Ile Leu Gln Ser Ile Ser Met Tyr Val His Glu Ala Ser Asn  
 20 25 30  
 Ile Phe Cys Gly Ile Pro Ser Leu Ser Gly Ile Val Leu Gly Thr Val  
 35 40 45  
 Pro Ala Val Asn Lys Lys Asp Arg Ile Ser Val Phe Met Gly Leu Ser  
 50 55 60  
 Thr Lys Leu Phe Ser Asn Phe His Val Cys Val Tyr Lys Ser Ala Glu  
 65 70 75 80  
 Ala Phe Thr Lys Leu Xaa Xaa Xaa Xaa Xaa  
 85 90

<210> 549  
 <211> 780  
 <212> DNA  
 <213> Homo sapiens

<400> 549  
 nnacgcgtac ttccaacacc tatgctccag tatggaggac gggtaaagtc tcttgtaaat  
 60  
 gttttaatca tacacatatt gtctgtaagt atgaagagaa aggcataatca gaaatatctc  
 120  
 aattcagcga tttgaaatgt ttactttctg tttattgaaa atttttgttc tttttcacca  
 180  
 tggtattttt ttctctcgt gtagaatcgg acagtagcaa caccgagcca tggagtatgg  
 240  
 gacatgcgag ggaaacaatt ccacacagga gttgaaatca aaatgtgggc tategcttgt  
 300  
 tttgccacac agaggcagtg cagagaagaa atattgaagg gtttcacaga ccagctgcgt  
 360  
 aagatttcta aggatgcagg gatgcccatc cagggccagc catgcttctg caaatatgca  
 420  
 cagggggcag acagcgtaga gcccattgtc cggcatctca agaacacata ttctggccta  
 480  
 cagcttatta tcgtcatcct gccggggaag acaccagtgt atgcggaagt gaaacgtgta  
 540  
 ggagacacac ttttgggtat ggctacacaa tgtgttcaag tcaagaatgt aataaaaaca  
 600  
 tctctcaaaa ctctgtcaaa cttgtgccta aagataaatg ttaaaactcg agggatcaat  
 660  
 aatattcttg tacctcatca aagaccttct gtgttccagc aaccagtgat ctttttggga  
 720  
 gccgatgtca ctcatccacc tgctgggtgat ggaaagaagc cttctattgc tgctgttgta  
 780

<210> 550  
 <211> 192  
 <212> PRT

<213> Homo sapiens

<400> 550

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Asn Arg Thr Val Ala Thr Pro Ser His Gly Val Trp Asp Met Arg Gly
 1           5           10           15
Lys Gln Phe His Thr Gly Val Glu Ile Lys Met Trp Ala Ile Ala Cys
          20           25           30
Phe Ala Thr Gln Arg Gln Cys Arg Glu Glu Ile Leu Lys Gly Phe Thr
          35           40           45
Asp Gln Leu Arg Lys Ile Ser Lys Asp Ala Gly Met Pro Ile Gln Gly
          50           55           60
Gln Pro Cys Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro
          65           70           75           80
Met Phe Arg His Leu Lys Asn Thr Tyr Ser Gly Leu Gln Leu Ile Ile
          85           90           95
Val Ile Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val Lys Arg Val
          100          105          110
Gly Asp Thr Leu Leu Gly Met Ala Thr Gln Cys Val Gln Val Lys Asn
          115          120          125
Val Ile Lys Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys Ile
          130          135          140
Asn Val Lys Leu Gly Gly Ile Asn Asn Ile Leu Val Pro His Gln Arg
          145          150          155          160
Pro Ser Val Phe Gln Gln Pro Val Ile Phe Leu Gly Ala Asp Val Thr
          165          170          175
His Pro Pro Ala Gly Asp Gly Lys Lys Pro Ser Ile Ala Ala Val Val
          180          185          190

```

<210> 551

<211> 291

<212> DNA

<213> Homo sapiens

<400> 551

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nnggatccgg attatggggc tattgctaac aggtcaacgg ccatcaaggt gctcgttgcc
60
gtggcaccgc cagccccgga gcctactcgc gagccaccga cgaactccgc tccttccgag
120
gaaccgtcct cgtcgtaaat cgcaccggtc ccgccggccc cgacgactgc agtaccacg
180
actagttcgt cgtcggggccg ctgaccgatg cgcccatcgg cgggctcatc tggctggcgc
240
tagcggggggc ttcgatgtcc ccataccaca gcgtccgcta aattgccnc c
291

```

<210> 552

<211> 67

<212> PRT

<213> Homo sapiens

<400> 552

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Xaa Asp Pro Asp Tyr Gly Ala Ile Ala Asn Arg Ser Thr Ala Ile Lys
 1           5           10           15
Val Leu Val Ala Val Ala Pro Pro Ala Pro Glu Pro Thr Arg Glu Pro

```

20                      25                      30  
 Pro Thr Asn Ser Ala Pro Ser Glu Glu Pro Ser Ser Ser Ser Ile Ala  
                     35                      40                      45  
 Pro Val Pro Pro Ala Pro Thr Thr Ala Val Pro Thr Thr Ser Ser Ser  
                     50                      55                      60  
 Ser Gly Arg  
 65

<210> 553  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

<400> 553  
 ctagccgatg taggattagt aggttttccg agcgtgggta aatctacctt actctcaata  
 60  
 gtatctaaag ccaaaccgaa aattggtgca tatcatttca ctacaattaa acctaactta  
 120  
 ggtgttgttt ccacaaaaga tcaacgtagt tttgttatgg cagatttacc aggtttaatt  
 180  
 gaaggtgcat ctgatggcgt tggattagga catcaatttt taagacatgt agagagaaca  
 240  
 aaagttattg ttcacatgat tgatatgagc ggttctgaag gtagagaacc tattgaagat  
 300  
 tataaagtca ttaatcaaga attagctgcg tacgagcaac gtttagaaga tagacctcaa  
 360  
 atcgtagtag ctaacaagat ggatttacct gaatcacaag ataatttaaa cttgttttaa  
 420  
 gaagaaattg gcgaagatgt gccagttatt ccagtttcaa caataacgcg t  
 471

<210> 554  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 554  
 Leu Ala Asp Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr  
   1                      5                      10                      15  
 Leu Leu Ser Ile Val Ser Lys Ala Lys Pro Lys Ile Gly Ala Tyr His  
                     20                      25                      30  
 Phe Thr Thr Ile Lys Pro Asn Leu Gly Val Val Ser Thr Lys Asp Gln  
                     35                      40                      45  
 Arg Ser Phe Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala Ser  
                     50                      55                      60  
 Asp Gly Val Gly Leu Gly His Gln Phe Leu Arg His Val Glu Arg Thr  
 65                      70                      75                      80  
 Lys Val Ile Val His Met Ile Asp Met Ser Gly Ser Glu Gly Arg Glu  
                     85                      90                      95  
 Pro Ile Glu Asp Tyr Lys Val Ile Asn Gln Glu Leu Ala Ala Tyr Glu  
                     100                      105                      110  
 Gln Arg Leu Glu Asp Arg Pro Gln Ile Val Val Ala Asn Lys Met Asp  
                     115                      120                      125  
 Leu Pro Glu Ser Gln Asp Asn Leu Asn Leu Phe Lys Glu Glu Ile Gly

130 135 140  
 Glu Asp Val Pro Val Ile Pro Val Ser Thr Ile Thr Arg  
 145 150 155

<210> 555  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 555  
 tctagagatt gagaacaatt atggatacag aaatgggtga ttccgtcaaa tatattcgag  
 60  
 attcgaatc atgtgaggct cgcgtgctgg agatcttagc cagaaggccg tccatgatgg  
 120  
 tgcagatctt gcgtagcgac ggcttaatta acgaagacca gagattagtc agattatggc  
 180  
 ttaataaagt acctagaatt gtccgcctgc ttctccggct tagtgtgttc gtcgctgcgg  
 240  
 caataggtgc ccgtgcggta tgggcggcgg cttccggtaa tcccgatctt gttcacgcgt  
 300

<210> 556  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 556  
 Met Asp Thr Glu Met Val Asp Ser Val Lys Tyr Ile Arg Asp Ser Glu  
 1 5 10 15  
 Ser Cys Glu Ala Arg Val Leu Glu Ile Leu Ala Arg Arg Pro Ser Met  
 20 25 30  
 Met Val Gln Ile Leu Arg Gly Asp Gly Leu Ile Asn Glu Asp Gln Arg  
 35 40 45  
 Leu Val Arg Leu Trp Leu Asn Lys Val Pro Arg Ile Val Arg Leu Leu  
 50 55 60  
 Leu Arg Leu Ser Val Phe Val Ala Ala Ala Ile Gly Ala Arg Ala Val  
 65 70 75 80  
 Trp Ala Ala Ala Ser Gly Asn Pro Asp Leu Val His Ala  
 85 90

<210> 557  
 <211> 678  
 <212> DNA  
 <213> Homo sapiens

<400> 557  
 atcttcccgg tttatgagga gaatgcgctg cgtgtcgagt ttttcggcga cgaaattgag  
 60  
 gccctcacga cgatgcaccc gctcaccggg gaggtcatca gcgaggacga gcagggtctac  
 120  
 gtgttcccgg ctaccacta tgtagccggc ccggaacgta tggagcgggc catagcgtcc  
 180  
 atccagcagg agctcgagga gcgcctggcc gttctagagc gtgatgggaa actgttggag  
 240

gcccaacggt tacgtatgcg tactacctac gatatcgaga tgatgcagca ggtcgggtgcc  
 300  
 tgtgctggca tcgaaaacta ttcgcggcac atcgacggac gcgctcccgg ctcagccccg  
 360  
 aactgtctgc ttgactactt tccggaagat tttgtgctcg tcattgatga atccccacgtg  
 420  
 accgtcccgc agattggcgg gatgtatgag ggggacatga gccgcaagcg gacattggta  
 480  
 gaacatgggt tccgactgcc cagcgcgatg gacaaccgtc ctctcaaatt cgacgagttc  
 540  
 acccagcgga tcggccagac tgtctacctg tccgccacgc ccggttcgta cgagaccgaa  
 600  
 cgagctcacg gcgtcgtcga acaaatcatt cgtccgacag gtctgggtgga tccggagatt  
 660  
 atcgtcaagc ctacgcgt  
 678

<210> 558

<211> 226

<212> PRT

<213> Homo sapiens

<400> 558

Ile	Phe	Pro	Val	Tyr	Glu	Glu	Asn	Ala	Leu	Arg	Val	Glu	Phe	Phe	Gly
1				5					10				15		
Asp	Glu	Ile	Glu	Ala	Leu	Thr	Thr	Met	His	Pro	Leu	Thr	Gly	Glu	Val
			20					25					30		
Ile	Ser	Glu	Asp	Glu	Gln	Val	Tyr	Val	Phe	Pro	Ala	Thr	His	Tyr	Val
		35				40						45			
Ala	Gly	Pro	Glu	Arg	Met	Glu	Arg	Ala	Ile	Ala	Ser	Ile	Gln	Gln	Glu
	50					55					60				
Leu	Glu	Glu	Arg	Leu	Ala	Val	Leu	Glu	Arg	Asp	Gly	Lys	Leu	Leu	Glu
65					70					75				80	
Ala	Gln	Arg	Leu	Arg	Met	Arg	Thr	Thr	Tyr	Asp	Ile	Glu	Met	Met	Gln
			85						90					95	
Gln	Val	Gly	Ala	Cys	Ala	Gly	Ile	Glu	Asn	Tyr	Ser	Arg	His	Ile	Asp
		100						105					110		
Gly	Arg	Ala	Pro	Gly	Ser	Ala	Pro	Asn	Cys	Leu	Leu	Asp	Tyr	Phe	Pro
		115				120						125			
Glu	Asp	Phe	Val	Leu	Val	Ile	Asp	Glu	Ser	His	Val	Thr	Val	Pro	Gln
	130					135						140			
Ile	Gly	Gly	Met	Tyr	Glu	Gly	Asp	Met	Ser	Arg	Lys	Arg	Thr	Leu	Val
145					150					155				160	
Glu	His	Gly	Phe	Arg	Leu	Pro	Ser	Ala	Met	Asp	Asn	Arg	Pro	Leu	Lys
			165						170					175	
Phe	Asp	Glu	Phe	Thr	Gln	Arg	Ile	Gly	Gln	Thr	Val	Tyr	Leu	Ser	Ala
		180						185					190		
Thr	Pro	Gly	Ser	Tyr	Glu	Thr	Glu	Arg	Ala	His	Gly	Val	Val	Glu	Gln
		195				200						205			
Ile	Ile	Arg	Pro	Thr	Gly	Leu	Val	Asp	Pro	Glu	Ile	Ile	Val	Lys	Pro
	210					215					220				
Thr	Arg														
225															

<210> 559  
 <211> 335  
 <212> DNA  
 <213> Homo sapiens

<400> 559  
 ggatcctatg gagctcaagt tcaagaaaag aaactgtaaa catggagggt ttgtgataaa  
 60  
 tggaatgcag tcagagggaa ggaactgccn gcttaaagtg tcctatgctg cgctttccag  
 120  
 agcaatacag tacacagtgg agggcgctac catggagtct ctgggtgaaa gttaggatgg  
 180  
 tatggtggca ccagccaaac ttctcagggt tcataggcag acagcagctc tggagtggaa  
 240  
 ctaaagtgtg tccaggagct gaagccctta atcagctagg gctcacacag agtcaaggta  
 300  
 ggggtcaaaaa cattcagtct gggaccatat ctaga  
 335

<210> 560  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 560  
 Met Glu Cys Ser Gln Arg Glu Gly Thr Ala Xaa Leu Lys Cys Pro Met  
 1 5 10 15  
 Leu Arg Phe Pro Glu Gln Tyr Ser Thr Gln Trp Arg Ala Leu Pro Trp  
 20 25 30  
 Ser Leu Trp Val Lys Val Arg Met Val Trp Trp His Gln Pro Asn Phe  
 35 40 45  
 Ser Gly Phe Ile Gly Arg Gln Gln Leu Trp Ser Gly Thr Lys Val Tyr  
 50 55 60  
 Pro Gly Ala Glu Ala Leu Asn Gln Leu Gly Leu Thr Gln Ser Gln Gly  
 65 70 75 80  
 Arg Val Lys Asn Ile Gln Ser Gly Thr Ile Ser Arg  
 85 90

<210> 561  
 <211> 477  
 <212> DNA  
 <213> Homo sapiens

<400> 561  
 ngcgcgcccc ctccctccgat ggcggcgagg atccagccca agcctctgac ccgcaagccg  
 60  
 atcctgctgc agcgatgga ggggtcccag gaggtggtga atatggccgt gatcgtgccc  
 120  
 aaagaggagg gcgtcatcag cgtctccgag gacaggacag ttcgtgtttg gttaaagaga  
 180  
 gacagtggac agtattggcc aagcgtatac catgcaatgc cttgagttta tattgtcaga  
 240  
 agattataac aagatgactc ctgtgaaaaa ctatcaagcg catcagagca gagtgacgat  
 300



gatacctgttt gtcctggagc tggagtgggt gctgagcaca ggacaggaca agcaatttgc  
 360  
 ctggcactgc tctgagagtg ggcagcgcct gggagggttat cggaccagtg ctgtggcctc  
 420  
 aggcctgcaa tttgatgttg aaaccggca tgtgtttatc ggtgaccact caggcca  
 477

<210> 562  
 <211> 74  
 <212> PRT  
 <213> Homo sapiens

<400> 562  
 Xaa Ala Pro Pro Pro Pro Met Ala Ala Glu Ile Gln Pro Lys Pro Leu  
 1 5 10 15  
 Thr Arg Lys Pro Ile Leu Leu Gln Arg Met Glu Gly Ser Gln Glu Val  
 20 25 30  
 Val Asn Met Ala Val Ile Val Pro Lys Glu Glu Gly Val Ile Ser Val  
 35 40 45  
 Ser Glu Asp Arg Thr Val Arg Val Trp Leu Lys Arg Asp Ser Gly Gln  
 50 55 60  
 Tyr Trp Pro Ser Val Tyr His Ala Met Pro  
 65 70

<210> 563  
 <211> 403  
 <212> DNA  
 <213> Homo sapiens

<400> 563  
 ccatggcaga cagggagctg agcggcctgc ggacccaggt gcaccagagc atggtgcccc  
 60  
 tgctcctaca cctgaaggac caatgcccaa ctgtcgccac gggcaatgcc caccccaaga  
 120  
 aaaggaaggg aaaaggcctc aaccttgccc agggctggaa cccacaggag gccagggtag  
 180  
 ggggcagacg gatggcagca gcactgcctg agagttgggg gagctcccac ggggcagcaa  
 240  
 gtggcgggca gagggctctg ccatctgcac tggtttctgt gaccacagtt ggctgccccg  
 300  
 ctccccact gcaccactga cgaagcgaga ccctgcctca aaaaaaaaaa caaaaacaaa  
 360  
 aacaaaaaca aaactcaaac ttcacactgg agatctgtgc aat  
 403

<210> 564  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 564  
 Met Ala Asp Arg Glu Leu Ser Gly Leu Arg Thr Gln Val His Gln Ser  
 1 5 10 15  
 Met Val Pro Leu Leu Leu His Leu Lys Asp Gln Cys Pro Thr Val Ala

```

      20      25      30
Thr Gly Asn Ala His Pro Lys Lys Arg Lys Gly Lys Gly Leu Asn Leu
      35      40      45
Gly Gln Gly Trp Asn Pro Gln Glu Ala Arg Val Arg Gly Arg Arg Met
      50      55      60
Ala Ala Ala Leu Pro Glu Ser Trp Gly Ser Ser His Gly Ala Ala Ser
65      70      75      80
Gly Gly Gln Arg Val Trp Pro Ser Ala Leu Val Ser Val Thr Thr Val
      85      90      95
Gly Leu Pro Ala Pro Pro Leu His His
      100      105

```

<210> 565  
 <211> 311  
 <212> DNA  
 <213> Homo sapiens

```

<400> 565
nccctctccat ggagcagccc catcttcact cttcacctgg ggccaggcct tccacagcag
60
ccaccaccca gcgaccacag agaggctgcg cggaggacac aggagagagg gagcccacgg
120
gcacgatctc caccggcttt cccagctccc tgggtcagcc ccacgggacc tctcctctc
180
tctcccatat ctccaagcca gccttgcata tagtaagagc tgtgatcagg atggaaagag
240
gcttggggccg cacagacctg gacaatgtcc cagtgagggc tggaggtgct agaagggcac
300
aggaggcccc n
311

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<210> 566  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

```

<400> 566
Met Glu Gln Pro His Leu His Ser Ser Pro Gly Ala Arg Pro Ser Thr
1      5      10      15
Ala Ala Thr Thr Gln Arg Pro Gln Arg Gly Cys Ala Glu Asp Thr Gly
      20      25      30
Glu Arg Glu Pro Thr Gly Thr Ile Ser Thr Gly Phe Pro Ser Ser Leu
      35      40      45
Gly Gln Pro His Gly Thr Ser Pro Pro Leu Ser His Ile Ser Lys Pro
      50      55      60
Ala Leu His Ile Val Arg Ala Val Ile Arg Met Glu Arg Gly Leu Gly
65      70      75      80
Arg Thr Asp Leu Asp Asn Val Pro Val Arg Ala Gly Gly Ala Arg Arg
      85      90      95
Ala Gln Glu Ala Pro
      100

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<210> 567  
 <211> 929

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 567

atcacatcgg tcgctgaacc ccgacgagcc tcaccttgtc gaaatattca tccttgagat  
 60  
 cagccacagt gccgtcgacc tctacctcgg tgagggtcgc gggcgggtac caacagccga  
 120  
 cctcgtcctc ggctccactc atggcggcaa gtcccgctgc cagtccgggg atcgtcgggg  
 180  
 catgggcat gatgagcagg ttatccacat cgctcgatgat ttctccgatg cgccgacgca  
 240  
 cggatatcagt gccgcagtaa tagagggtc gcataaattc gaccggacaa tccagttgga  
 300  
 ggcagtccta ggtctggcgg gtgcgtaggg catcggagac cagagcatgt ccaacattgc  
 360  
 gcagtcctaa acgcgtgccg acctcacggg cctgacggcg cccacgctcg gtgagcggac  
 420  
 gtcctcgatc cccgcccggg gcatgggatg cgggctgtgc atgtctcatg aggaacagag  
 480  
 tgtgcatgga tccatcgctg cacttcgcgg tcgcccgggt tctacgatgt tggcatgccg  
 540  
 ttgacggatt tgggcattga tgaggcgcgt acctaccgcc cgaacgtccc tgaacccgat  
 600  
 ggtttcgact ctttttgggc cgagaccctc gatgagtatt cgggcgttcc ccaagatctg  
 660  
 acggcgggtgc ctttcgataa ccgtcaggct ctgatagata cctgggattt gtcgtgggtg  
 720  
 gggatatcaca actctcgggt gagcgggtga ttacatgcc cagccgctgt gaacggccca  
 780  
 ttcccccttg tcatcgagta cctcgggtac tcgagttcgc gtggtgtgcc gattggatca  
 840  
 gtcttcgctg ctgctggcta tgcacatata gtcgtcgatc cacgtggtca ggggtggggc  
 900  
 caccacacct tgacggaaaa ctgtccgga  
 929

&lt;210&gt; 568

&lt;211&gt; 71

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 568

Met	Pro	Leu	Thr	Asp	Leu	Gly	Ile	Asp	Glu	Ala	Arg	Thr	Tyr	Arg	Pro
1				5					10					15	
Asn	Val	Pro	Glu	Pro	Asp	Gly	Phe	Asp	Ser	Phe	Trp	Ala	Glu	Thr	Leu
		20						25					30		
Asp	Glu	Tyr	Ser	Gly	Val	Pro	Gln	Asp	Leu	Thr	Ala	Val	Pro	Phe	Asp
		35					40					45			
Asn	Arg	Gln	Ala	Leu	Ile	Asp	Thr	Trp	Asp	Leu	Ser	Trp	Val	Gly	Tyr
	50					55					60				
His	Asn	Ser	Arg	Val	Ser	Gly									
65					70										

<210> 569  
 <211> 371  
 <212> DNA  
 <213> Homo sapiens

<400> 569  
 ncgcaaactt caacggtgcc atctgccata ttccagggat gccagatttg gatggaaaat  
 60  
 accatatcac tctcgattca gaattcgtac ttgatttagt ggcctttaac aaaacgctac  
 120  
 ctgtcgatta cttaatggtc gaaggaacgg aacttgtgta ttcaaactg gaagaactac  
 180  
 ctgaatgccc atattatcca aaagatcaaa agccaatcgt gattgggaaa aacacaaaac  
 240  
 tcaaggaaca accaacagcc gttgctctct tctcggatgt tgataaacgg ccagagatta  
 300  
 aatcaaaaat cttagaccgc tatgataatg atattgaaat ccgtacttgg ggcgggtactt  
 360  
 cccatgtcta n  
 371

<210> 570  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 570  
 Met Pro Asp Leu Asp Gly Lys Tyr His Ile Thr Leu Asp Ser Glu Phe  
 1 5 10 15  
 Val Leu Asp Leu Val Ala Phe Asn Lys Thr Leu Pro Val Asp Tyr Leu  
 20 25 30  
 Met Val Glu Gly Thr Glu Leu Val Tyr Ser Asn Met Glu Glu Leu Pro  
 35 40 45  
 Glu Cys Pro Tyr Tyr Pro Lys Asp Gln Lys Pro Ile Val Ile Gly Lys  
 50 55 60  
 Asn Thr Lys Leu Lys Glu Gln Pro Thr Ala Val Ala Leu Phe Ser Asp  
 65 70 75 80  
 Val Asp Lys Arg Pro Glu Ile Lys Ser Lys Ile Leu Asp Arg Tyr Asp  
 85 90 95  
 Asn Asp Ile Glu Ile Arg Thr Trp Gly Gly Thr Ser His Val Xaa  
 100 105 110

<210> 571  
 <211> 407  
 <212> DNA  
 <213> Homo sapiens

<400> 571  
 nacgcgtatc ttcgctggtc cacaccagac gtggcattaa acgacgtcac aagaacgaca  
 60  
 ccgggccttg acgggcccac gcacgaagag gccaaagacac tgaccgagac tactgtttcc  
 120  
 gttcccacct ccttcgccga cctcggcgctc cgagaagata tctgccaggc gctggaaggg  
 180

gtgggaattg tctccccgtt cccgatccag gccatgtcga tcccgattgc cgtcgagggc  
 240  
 acggatctta ttgggcaggc gcgtactggc actggcaaaa cactcgcctt cggcatcacc  
 300  
 atcttgagc gcataccct gcccggtgac gaaggttggg aagaactcac caccaaaggc  
 360  
 aagccccaa gcactcgtga tgtgcccta cccgggagct aggtcgg  
 407

<210> 572  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 572  
 Leu Thr Glu Thr Thr Val Ser Val Pro Thr Ser Phe Ala Asp Leu Gly  
 1 5 10 15  
 Val Arg Glu Asp Ile Cys Gln Ala Leu Glu Gly Val Gly Ile Val Ser  
 20 25 30  
 Pro Phe Pro Ile Gln Ala Met Ser Ile Pro Ile Ala Val Glu Gly Thr  
 35 40 45  
 Asp Leu Ile Gly Gln Ala Arg Thr Gly Thr Gly Lys Thr Leu Ala Phe  
 50 55 60  
 Gly Ile Thr Ile Leu Gln Arg Ile Thr Leu Pro Gly Asp Glu Gly Trp  
 65 70 75 80  
 Glu Glu Leu Thr Thr Lys Gly Lys Pro Pro Ser Thr Arg Asp Val Pro  
 85 90 95  
 Leu Pro Gly Ser  
 100

<210> 573  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<400> 573  
 acgcgtctac cgtaggatcc atgaccttcc gcaagaccga ccaccacaag aacgccattg  
 60  
 actacgaggt cgccggacta atgtggctcg ctgctgccc gccagatggg gccggcatcg  
 120  
 tcgaggtgct cgaccacggc aagggtatggc tcaccgaacc cgaattgtcc actgggcacc  
 180  
 ccaccgcga ggcagccgag gactttggcc gccgactggc tcacaccac gcagccgggg  
 240  
 cctcacacct gggggctgca cctgacgggt ttgttcccga cgatgggtat atcgcccggtg  
 300  
 ctcccctgcc actgccgtcc gaaccaatct cctcctgggg agagttttac gctcagtgcc  
 360  
 gcatcgaacc atatatggac agtctcgacg ctg  
 393

<210> 574  
 <211> 124  
 <212> PRT

<213> Homo sapiens

<400> 574

```

Met Thr Phe Arg Lys Thr Asp His His Lys Asn Ala Ile Asp Tyr Glu
 1           5           10           15
Val Ala Gly Leu Met Trp Leu Ala Ala Ala Arg Pro Asp Gly Ala Gly
      20           25           30
Ile Val Glu Val Leu Asp His Gly Lys Gly Trp Leu Thr Glu Pro Glu
      35           40           45
Leu Ser Thr Gly His Pro Thr Arg Glu Ala Ala Glu Asp Phe Gly Arg
      50           55           60
Arg Leu Ala His Thr His Ala Ala Gly Ala Ser His Leu Gly Ala Ala
      65           70           75           80
Pro Asp Gly Phe Val Pro Asp Asp Gly Tyr Ile Gly Arg Ala Pro Leu
      85           90           95
Pro Leu Pro Ser Glu Pro Ile Ser Ser Trp Gly Glu Phe Tyr Ala Gln
      100          105          110
Cys Arg Ile Glu Pro Tyr Met Asp Ser Leu Asp Ala
      115          120

```

<210> 575

<211> 372

<212> DNA

<213> Homo sapiens

<400> 575

```

nntatccatg cagacatggg accaggggtct ctgagggcag gaagcaaagt gggtgagggg
60
gatgggacaa gatgccctgg tgctaaggcc tctggagctg gagctgggta tagggatgat
120
accaggcacc ctgagtcact cgcacctcac aatggggccg cttctgggag ccagtgggct
180
tatggggctg gcaatgtgct gggttatgag gatggatcag aacttccagg gcctcagggg
240
actgggggtca gaacagccta tggagaaagg tcaaggggcc ttgggcctag gagtacaggg
300
ccaggggggtg aggcaggctt tagagatggt tcaggaggcc tccaaggaat gggatcagca
360
gatggggcccgt
372

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<210> 576

<211> 124

<212> PRT

<213> Homo sapiens

<400> 576

```

Xaa Ile His Ala Asp Met Gly Pro Gly Ser Leu Arg Ala Gly Ser Lys
 1           5           10           15
Val Gly Glu Gly Asp Gly Thr Arg Cys Pro Gly Ala Lys Ala Ser Gly
      20           25           30
Ala Gly Ala Gly Tyr Arg Asp Asp Thr Arg His Pro Glu Ser Leu Ala
      35           40           45
Pro His Asn Gly Ala Ala Ser Gly Ser Gln Trp Ala Tyr Gly Ala Gly

```

```

      50              55              60
Asn Val Leu Gly Tyr Glu Asp Gly Ser Glu Leu Pro Gly Pro Gln Gly
65              70              75              80
Thr Gly Val Arg Thr Ala Tyr Gly Glu Arg Ser Arg Gly Leu Gly Pro
      85              90              95
Arg Ser Thr Gly Pro Gly Gly Glu Ala Gly Phe Arg Asp Gly Ser Gly
      100              105              110
Gly Leu Gln Gly Met Gly Ser Ala Asp Gly Pro Gly
      115              120

```

<210> 577  
 <211> 432  
 <212> DNA  
 <213> Homo sapiens

```

<400> 577
nagcgcaatg tcatgatgtc ggatttgtca atgtcggatt tctcatccca gccatcaccc
60
ccgcagcggc gggcgcggtat gaccagcggc cagcgccgtg aacagctcat cagcgtggcc
120
cgctgcctct tcgcagacaa tggcatggca gggacctccg tcgaggagat cgccgctacc
180
gcgggagtct ccaaaccggt catctacgag catttcgggt ccaaggatgg gctgtacgcc
240
gtcgtcgtag accgcgaggt acgccaccta caagattccc tcaacgccgc catgaccgcg
300
ccaaagcaag gcccgaaacg caccctggag tcagcggtag tggccctgct ggactacatc
360
gacgaccgtc cagacgggtt tcggatcatc tcgcgagact cctcggtcggt ttcagccacc
420
ggttcgtacg cg
432

```

<210> 578  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

```

<400> 578
Met Thr Ser Gly Gln Arg Arg Glu Gln Leu Ile Ser Val Ala Arg Arg
1              5              10              15
Leu Phe Ala Asp Asn Gly Met Ala Gly Thr Ser Val Glu Glu Ile Ala
      20              25              30
Ala Thr Ala Gly Val Ser Lys Pro Val Ile Tyr Glu His Phe Gly Ser
      35              40              45
Lys Asp Gly Leu Tyr Ala Val Val Val Asp Arg Glu Val Arg His Leu
50              55              60
Gln Asp Ser Leu Asn Ala Ala Met Thr Arg Pro Lys Gln Gly Pro Lys
65              70              75              80
Arg Thr Leu Glu Ser Ala Val Leu Ala Leu Leu Asp Tyr Ile Asp Asp
      85              90              95
Arg Pro Asp Gly Phe Arg Ile Ile Ser Arg Asp Ser Ser Val Gly Ser
      100              105              110
Ala Thr Gly Ser Tyr Ala

```

115

<210> 579  
 <211> 320  
 <212> DNA  
 <213> Homo sapiens

<400> 579  
 ggccccaac actccgacct cagctgggtcc agcatgctgg gcaccgtgct gctgctggcc  
 60  
 ctgctcccag ggatcaccac cttacccagc gggccacctg ctccccgtt ccccgcgcg  
 120  
 cccggcccct ggtgcgcag accctcttc agcctgaagc tgtccgacac agaggacgtc  
 180  
 ttctctgcc gcgcggggcc gctcgaggtc cgggcccaga gccgcgtgtt cgtgcaggcg  
 240  
 gccttgcccc gtcctcccc gcgctggggc ctggccctgc accgctgctc agtgacgccg  
 300  
 tcctcacgcc cggccccggg  
 320

<210> 580  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 580  
 Met Leu Gly Thr Val Leu Leu Leu Ala Leu Leu Pro Gly Ile Thr Thr  
 1 5 10 15  
 Leu Pro Ser Gly Pro Pro Ala Pro Pro Phe Pro Ala Ala Pro Gly Pro  
 20 25 30  
 Trp Leu Arg Arg Pro Leu Phe Ser Leu Lys Leu Ser Asp Thr Glu Asp  
 35 40 45  
 Val Phe Pro Arg Arg Ala Gly Pro Leu Glu Val Pro Ala Asp Ser Arg  
 50 55 60  
 Val Phe Val Gln Ala Ala Leu Ala Arg Pro Ser Pro Arg Trp Gly Leu  
 65 70 75 80  
 Ala Leu His Arg Cys Ser Val Thr Pro Ser Ser Arg Pro Ala Pro  
 85 90 95

<210> 581  
 <211> 419  
 <212> DNA  
 <213> Homo sapiens

<400> 581  
 nacgacggca accattcgct gtggaaggag ctgaacggcc agctcgacgt gcagtttttc  
 60  
 cacgtcggca tgggcttcaa gacgccagta cgcattgcaca gcgtcgaccc caagaccgc  
 120  
 gaagcccgcg aggtgcattt ccgcccgtcg ctgttcaact atgccaagac cacggtggac  
 180  
 accaagcagc tgaccggcga cctgggtttc tccggtttca agctgttcaa ggcgcggaa  
 240



ctggatcgcc atgacgtgct gtcgtttctc ggcgccagtt acttccgtgc ggtggacgca  
 300  
 acccgccagt acggcctctc cgcacgcggc ctggcgattg atacctacgc gaaaaaacgc  
 360  
 gaggaattcc ccgacttcac gcagttctgg ttcgaaacce cgagcaagga cccacgcgt  
 419

<210> 582  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens

<400> 582  
 Xaa Asp Gly Asn His Ser Leu Trp Lys Glu Leu Asn Gly Gln Leu Asp  
 1 5 10 15  
 Val Gln Phe Phe His Val Gly Met Gly Phe Lys Thr Pro Val Arg Met  
 20 25 30  
 His Ser Val Asp Pro Lys Thr Arg Glu Ala Arg Glu Val His Phe Arg  
 35 40 45  
 Pro Ser Leu Phe Asn Tyr Ala Lys Thr Thr Val Asp Thr Lys Gln Leu  
 50 55 60  
 Thr Gly Asp Leu Gly Phe Ser Gly Phe Lys Leu Phe Lys Ala Pro Glu  
 65 70 75 80  
 Leu Asp Arg His Asp Val Leu Ser Phe Leu Gly Ala Ser Tyr Phe Arg  
 85 90 95  
 Ala Val Asp Ala Thr Arg Gln Tyr Gly Leu Ser Ala Arg Gly Leu Ala  
 100 105 110  
 Ile Asp Thr Tyr Ala Lys Lys Arg Glu Glu Phe Pro Asp Phe Thr Gln  
 115 120 125  
 Phe Trp Phe Glu Thr Pro Ser Lys Asp Pro Arg  
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<210> 583  
 <211> 407  
 <212> DNA  
 <213> Homo sapiens

<400> 583  
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 120  
 tatagctatg cgaatttgga gcatgctgat catgatgtca agacgatgaa cgaactcatc  
 180  
 cgtgactttg agcttactcg tatctcccat acgcgagcca cactcccat ggacaagctt  
 240  
 gtgtttttga acaagcatca cttgacaaat aagctggcgc tcgccacgac gtgtgagcag  
 300  
 accaaacaag acctattgtc gcgtatccgg ccgatcacta cctcgtggta cggcgattat  
 360  
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 407

<210> 584

<211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 584  
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 Val Asn Leu Val Ala Leu Thr Gly Tyr Ser Tyr Ala Asn Leu Glu His  
 35 40 45  
 Ala Asp His Asp Val Lys Thr Met Asn Glu Leu Ile Arg Asp Phe Glu  
 50 55 60  
 Leu Thr Arg Ile Ser His Thr Arg Ala Thr Leu Pro Met Asp Lys Leu  
 65 70 75 80  
 Val Phe Leu Asn Lys His His Leu Thr Asn Lys Leu Ala Leu Ala Thr  
 85 90 95  
 Thr Cys Glu Gln Thr Lys Gln Asp Leu Leu Ser Arg Ile Arg Pro Ile  
 100 105 110  
 Thr Thr Ser Trp Tyr Gly Asp Tyr Ser Asp Asp Tyr Ile Leu Arg Val  
 115 120 125  
 Val Thr Leu Gly Pro Gln Arg  
 130 135

<210> 585  
 <211> 502  
 <212> DNA  
 <213> Homo sapiens

<400> 585  
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 cgggctcggg accgacattt cggtgtcgac gaataccagg acgtttctcc gctgcagcat  
 180  
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 240  
 caggccattc actcttatgc aggcgcacga gctgactacc tcctcgactt cggtgccgat  
 300  
 catcctggcg ctaaacgcat cgatttggtt cgcaactacc gctccactcc cgagatcggt  
 360  
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 502

<210> 586  
 <211> 167  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 586

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Ile Asp Leu Asp Asp Ile Leu Leu Cys Ala Val Gly Leu Leu Val Gln
           20           25           30
His Arg Asp Ile Thr Glu Glu Ile Arg Ala Arg Tyr Arg His Phe Val
           35           40           45
Val Asp Glu Tyr Gln Asp Val Ser Pro Leu Gln His Arg Leu Leu Glu
           50           55           60
Leu Trp Phe Gly Asp Arg Asn Asp Val Cys Val Val Gly Asp Pro His
65           70           75           80
Gln Ala Ile His Ser Tyr Ala Gly Ala Arg Ala Asp Tyr Leu Leu Asp
           85           90           95
Phe Val Ala Asp His Pro Gly Ala Lys Arg Ile Asp Leu Val Arg Asn
           100          105          110
Tyr Arg Ser Thr Pro Glu Ile Val Gln Leu Ala Asn Glu Val Leu Val
           115          120          125
Asn Arg Met Thr Pro Glu Glu Ala Leu Glu His Gly Arg Gly Val Thr
           130          135          140
Leu Val Ser Arg Gly Arg Ser Gly Pro Glu Pro Ile Tyr Gln Ala Leu
145          150          155          160
Gly Asp Asp Ala Ser Glu Ala
           165

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&lt;210&gt; 587

&lt;211&gt; 746

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 587

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240
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720

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<210> 588

<211> 248

<212> PRT

<213> Homo sapiens

<400> 588

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20 25 30  
Ser Pro Cys Gln His Gly Gly Arg Cys Leu Gln Arg Ser Asp Pro Ala  
35 40 45  
Leu Tyr Gly Gly Val Gln Ala Ala Phe Pro Gly Ala Phe Ser Phe Arg  
50 55 60  
His Ala Ala Gly Phe Leu Cys His Cys Pro Pro Gly Phe Glu Gly Ala  
65 70 75 80  
Asp Cys Gly Val Glu Val Asp Glu Cys Ala Ser Arg Pro Cys Leu Asn  
85 90 95  
Gly Gly His Cys Gln Asp Leu Pro Asn Gly Phe Gln Cys His Cys Pro  
100 105 110  
Asp Gly Tyr Ala Gly Pro Thr Cys Glu Glu Asp Val Asp Glu Cys Leu  
115 120 125  
Ser Asp Pro Cys Leu His Gly Gly Thr Cys Ser Asp Thr Val Ala Gly  
130 135 140  
Tyr Ile Cys Arg Cys Pro Glu Thr Trp Gly Gly Arg Asp Cys Ser Val  
145 150 155 160  
Gln Leu Thr Gly Cys Gln Gly His Thr Cys Pro Leu Ala Ala Thr Cys  
165 170 175  
Ile Pro Ile Phe Glu Ser Gly Val His Ser Tyr Val Cys His Cys Pro  
180 185 190  
Pro Gly Thr His Gly Pro Phe Cys Gly Gln Asn Thr Thr Phe Ser Val  
195 200 205  
Met Ala Gly Ser Pro Ile Gln Ala Ser Val Pro Ala Gly Gly Pro Leu  
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225 230 235 240  
Thr Arg Asn Asp Thr Lys Glu Ser  
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<210> 589

<211> 381

<212> DNA

<213> Homo sapiens

<400> 589

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180

cagctaccat attctcaggc ggctcctcca gtgcaaactc cccttccagg ggcaccacca  
 240  
 cccaacagt tacagtatgg acaacagcaa ccaatgggtt ctacacagat ggccccaggc  
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 360  
 caaacagcaa tgtcctccgg a  
 381

<210> 590  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

<400> 590  
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 20 25 30  
 Gly Ile Gln Pro Ser Pro Val Asn Val Val Gly Val Thr Ser Ala Leu  
 35 40 45  
 Gly Gln Gln Pro Ser Ile Ser Ser Leu Ala Gln Pro Gln Leu Pro Tyr  
 50 55 60  
 Ser Gln Ala Ala Pro Pro Val Gln Thr Pro Leu Pro Gly Ala Pro Pro  
 65 70 75 80  
 Pro Gln Gln Leu Gln Tyr Gly Gln Gln Gln Pro Met Val Ser Thr Gln  
 85 90 95  
 Met Ala Pro Gly His Val Lys Ser Val Thr Gln Asn Pro Ala Ser Glu  
 100 105 110  
 Tyr Val Gln Gln Gln Pro Ile Leu Gln Thr Ala Met Ser Ser Gly  
 115 120 125

<210> 591  
 <211> 684  
 <212> DNA  
 <213> Homo sapiens

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cttgtgacgg cagtgcagat atcacattaa aaggagggca ttcattgggtg ttgggttctgg  
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 684

<210> 592  
 <211> 133  
 <212> PRT  
 <213> Homo sapiens

<400> 592  
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 20 25 30  
 Ser Glu Leu Leu Asp Ser Ile Lys Arg Asp Ser Ile Arg Val Leu Phe  
 35 40 45  
 His Val Gln Gly Pro Gly Glu Lys Ser Val Ser Lys Xaa Lys Ala Arg  
 50 55 60  
 Leu Arg Gln Glu Ala Glu Ala Leu Ala Gln Arg Met Gln Phe Glu His  
 65 70 75 80  
 Ala Glu Ala Pro Gly Leu Asp Ala Pro Glu Ile Leu Gly Glu Glu Val  
 85 90 95  
 Asp Val Ala Leu Ala Thr Ala Pro Val Arg Asn Glu Gln Lys Leu Gly  
 100 105 110  
 Arg Asn Glu Leu Cys Tyr Cys Gly Ser Gly Lys Lys Tyr Lys His Cys  
 115 120 125  
 His Gly Gln Ile Ser  
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<210> 593  
 <211> 615  
 <212> DNA  
 <213> Homo sapiens

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 420

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<210> 594  
 <211> 205  
 <212> PRT  
 <213> Homo sapiens

<400> 594  
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 20 25 30  
 Pro Leu Arg Ala Ala Arg Phe Thr Asp Thr Ile Pro Ala Pro Leu Gly  
 35 40 45  
 Gln Pro Arg Trp Ser Thr Ala Thr Ile Gln Thr Pro Val Ile Pro Thr  
 50 55 60  
 Thr Arg Gly Arg Phe Val Ile Gly Pro Val Met Met Arg Thr Ile Asp  
 65 70 75 80  
 Pro Phe Gly Met Ala Arg His His Thr Asp Leu Gly Gln Val Ala Glu  
 85 90 95  
 Val Ile Val Thr Pro Arg Ile Val Asp Leu Gly Ala Ser Gly Glu Leu  
 100 105 110  
 Gly Gly Gln Gly Phe Asp Thr Arg Ser Ser Ala Ile His Ala Gly Arg  
 115 120 125  
 Arg Gly Pro Asp Asp Ala Met Val Arg Asp Trp His Thr Gly Asp Ser  
 130 135 140  
 Val Arg Arg Ile His Trp Arg Ser Thr Ala His Arg Gly Asp Leu Met  
 145 150 155 160  
 Val Arg Cys Glu Glu Gln Ala Trp Asn Pro Ser Val Val Ile Val Leu  
 165 170 175  
 Asp Ser Arg Ala Arg Arg His Ala Gly Thr Gly Pro Asp Ala Ser Phe  
 180 185 190  
 Glu Trp Ala Val Asn Ala Val Ala Ser Ile Ser Thr Arg  
 195 200 205

<210> 595  
 <211> 303  
 <212> DNA  
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 180

cggagcaagg ctcagaaaaa tgtcccagcc aaaaacatgg tacatgcctg tcatacagga  
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 303

<210> 596  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<400> 596  
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 20 25 30  
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 35 40 45  
 Ser Ala Leu Arg Ser Pro Glu Gln Gly Ser Glu Lys Cys Pro Ser Gln  
 50 55 60  
 Lys His Gly Thr Cys Leu Ser Ser Gly Lys Ser Ser Lys Ser Gly Trp  
 65 70 75 80  
 Asp Gln Gly Pro Arg Asp Leu Val  
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<210> 597  
 <211> 2709  
 <212> DNA  
 <213> Homo sapiens

<400> 597  
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 240  
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780  
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1080  
ctaggagca tctctgtaaa cacagtggct ggggaaaccc ttcctagtct cacttgattc  
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 2700  
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<210> 598

<211> 240

<212> PRT

<213> Homo sapiens

<400> 598

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Glu	Cys	Gly	Lys	Ser	Phe	Gly	Asp	Leu	Val	Ser	Arg	Arg	Lys	His	Met	35	40	45	
Arg	Ile	His	Ile	Val	Lys	Lys	Pro	Val	Glu	Cys	Arg	Gln	Cys	Gly	Lys	50	55	60	
Thr	Phe	Arg	Asn	Gln	Ser	Ile	Leu	Lys	Thr	His	Met	Asn	Ser	His	Thr	65	70	75	80
Gly	Glu	Lys	Pro	Tyr	Gly	Cys	Asp	Leu	Cys	Gly	Lys	Ala	Phe	Ser	Ala	85	90	95	
Ser	Ser	Asn	Leu	Thr	Ala	His	Arg	Lys	Ile	His	Thr	Gln	Glu	Arg	Arg	100	105	110	
Tyr	Glu	Cys	Ala	Ala	Cys	Gly	Lys	Val	Phe	Gly	Asp	Tyr	Leu	Ser	Arg	115	120	125	
Arg	Arg	His	Met	Ser	Val	His	Leu	Val	Lys	Lys	Arg	Val	Glu	Cys	Arg	130	135	140	
His	Cys	Gly	Lys	Ala	Phe	Arg	Asn	Gln	Ser	Thr	Leu	Lys	Thr	His	Met	145	150	155	160
Arg	Ser	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asp	His	Cys	Gly	Lys	165	170	175	
Ala	Phe	Ser	Ile	Gly	Ser	Asn	Leu	Asn	Val	His	Arg	Arg	Ile	His	Thr	180	185	190	
Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Leu	Val	Cys	Gly	Lys	Ala	Phe	Ser	Asp	195	200	205	
His	Ser	Ser	Leu	Arg	Ser	His	Val	Lys	Thr	His	Arg	Gly	Glu	Lys	Leu	210	215	220	
Phe	Xaa	Cys	His	Pro	Cys	Gly	Lys	Gly	Ser	Ser	Glu	Arg	Ala	Xaa	Leu	225	230	235	240

<210> 599  
 <211> 340  
 <212> DNA  
 <213> Homo sapiens

<400> 599  
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 120  
 caggcatgtt tgccggggccg catcccttgc acttgcatgc cgtggcctat cggccgaggg  
 180  
 gcaggcctgc agttggagcc gtgcgtgggt gtcccgcgcg aggagcgtgt tggcagacta  
 240  
 tggggctcgt cggaggacga ggatgtgagt ggcgatggct ttgcgcgact gggcgatttc  
 300  
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 340

<210> 600  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 600  
 Met Pro Trp Thr Ile Trp Ser Thr Ile Ala Gly Trp Asn Thr Pro Ser  
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 Arg Ala Lys Pro Ser Pro Leu Thr Ser Ser Ser Asp Glu Pro His  
 20 25 30  
 Ser Leu Pro Thr Arg Ser Ser Arg Gly Thr Pro Thr His Gly Ser Asn  
 35 40 45  
 Cys Arg Pro Ala Pro Arg Pro Ile Gly His Gly Leu Gln Val Gln Gly  
 50 55 60  
 Met Arg Pro Gly Lys His Ala Trp Ala Lys Arg Cys Arg Leu Arg Cys  
 65 70 75 80  
 Thr Ala Thr Pro Ser Thr Cys Ala Met Thr Pro Asn Lys Arg Ser Asp  
 85 90 95  
 Thr Thr Glu Arg Ser His His Asp Val Lys Ser Arg Glu Ala Arg  
 100 105 110

<210> 601  
 <211> 421  
 <212> DNA  
 <213> Homo sapiens

<400> 601  
 gccggcgga ggcacatctc gctcaacgtc ggctgcgcgc gcctgacttc gcgtctttct  
 60  
 ccgcgctcca ccattttgat ggacggcgct ccgctggcgg tcgcgcctta cggccagccg  
 120  
 cagctgtcga tggccccgct gtctatcggt aatctgcaat cgggtggacgt ggtgcgcggc  
 180  
 ggccggcgcg tcgcgtacgg gccgcagaac gtcggcgggc tgatcaactt cgttaccgga  
 240

gacattccca aaacgtttgg cgggtgccgcc agcgtacaaa cccaggggtgc cagccacggc  
 300  
 ggccctgaaga ccttgaccag cgcctccgtg ggcggcaccg cagacaacgg cctcggcgcc  
 360  
 gagctgctct actccggcct gcacggccag ggctaccgag acaacaacga caacaccgac  
 420  
 n  
 421

<210> 602

<211> 140

<212> PRT

<213> Homo sapiens

<400> 602

Ala	Gly	Gly	Ser	Asp	Ile	Ser	Leu	Asn	Val	Gly	Val	Arg	Gly	Leu	Thr
1			5					10					15		
Ser	Arg	Leu	Ser	Pro	Arg	Ser	Thr	Ile	Leu	Met	Asp	Gly	Val	Pro	Leu
	20						25					30			
Ala	Val	Ala	Pro	Tyr	Gly	Gln	Pro	Gln	Leu	Ser	Met	Ala	Pro	Leu	Ser
	35					40					45				
Ile	Gly	Asn	Leu	Gln	Ser	Val	Asp	Val	Val	Arg	Gly	Gly	Gly	Ala	Val
	50				55					60					
Arg	Tyr	Gly	Pro	Gln	Asn	Val	Gly	Gly	Val	Ile	Asn	Phe	Val	Thr	Arg
65				70					75				80		
Asp	Ile	Pro	Lys	Thr	Phe	Gly	Gly	Ala	Ala	Ser	Val	Gln	Thr	Gln	Gly
			85					90				95			
Ala	Ser	His	Gly	Gly	Leu	Lys	Thr	Leu	Thr	Ser	Ala	Ser	Val	Gly	Gly
		100					105					110			
Thr	Ala	Asp	Asn	Gly	Leu	Gly	Ala	Glu	Leu	Leu	Tyr	Ser	Gly	Leu	His
	115					120						125			
Gly	Gln	Gly	Tyr	Arg	Asp	Asn	Asn	Asp	Asn	Thr	Asp				
	130					135					140				

<210> 603

<211> 309

<212> DNA

<213> Homo sapiens

<400> 603

nagggcggca tgcacgaaag cttgcgcaaa cgctcgctgg aaggcttgga caagatcggc  
 60  
 ttcgacggcc tggccatcgg cggctctgtcg gtgggcgagc ccaagcacga gatgatcaag  
 120  
 gtgctggatt acctgccggg cctgatgccg gctgacaaac ctcgttacct tatgggcggt  
 180  
 ggcaaacggg aagacctcgt agagggtgtg cgccgcgggtg tggacatggt cgattgcgtg  
 240  
 atgccaaccc gtaatgcccg caatgggcat ctgttcacg atacaggcgt gctgaagatc  
 300  
 cgtaacgag  
 309

<210> 604

<211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 604  
 Xaa Gly Gly Met His Glu Ser Leu Arg Lys Arg Ser Leu Glu Gly Leu  
 1 5 10 15  
 Asp Lys Ile Gly Phe Asp Gly Leu Ala Ile Gly Gly Leu Ser Val Gly  
 20 25 30  
 Glu Pro Lys His Glu Met Ile Lys Val Leu Asp Tyr Leu Pro Gly Leu  
 35 40 45  
 Met Pro Ala Asp Lys Pro Arg Tyr Leu Met Gly Val Gly Lys Pro Glu  
 50 55 60  
 Asp Leu Val Glu Gly Val Arg Arg Gly Val Asp Met Phe Asp Cys Val  
 65 70 75 80  
 Met Pro Thr Arg Asn Ala Arg Asn Gly His Leu Phe Ile Asp Thr Gly  
 85 90 95  
 Val Leu Lys Ile Arg Asn Ala  
 100

<210> 605  
 <211> 428  
 <212> DNA  
 <213> Homo sapiens

<400> 605  
 acgcgttcac gatagggtag ttgcctatatt caacgcggtc ggtattttcc tgcacaacaa  
 60  
 actggcccaa ggctgggcta tagtcagggtg catagtactt ggtgaagtag cgtacgtccg  
 120  
 caccacatc acatttcagt accttggtta tcttcaatcg gaaaaaaga ttggagtaaa  
 180  
 tggttagttt tggtaatggc aacgccgttt gactggaaga gttttggaag gtaatgaccg  
 240  
 attcccagtg caaaggtccc catgctacat cctgcgacaa tgaggccggt agcacgttta  
 300  
 ttgcctcgct gctttgccga acgccaacct ctgtaccgat acgctgatac tgattgttga  
 360  
 tggatataggc ttgcgccagg taggtataat tggtaattc gtccatggca atgcgcagtg  
 420  
 aagtcttg  
 428

<210> 606  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 606  
 Met Asp Glu Leu Thr Asn Tyr Thr Tyr Leu Ala Gln Ala Tyr Thr Ile  
 1 5 10 15  
 Asn Asn Gln Tyr Gln Arg Ile Gly Thr Glu Val Gly Val Arg Gln Ser  
 20 25 30  
 Ser Glu Ala Ile Asn Val Leu Thr Ala Ser Leu Ser Gln Asp Val Ala

```

      35              40              45
Trp Gly Pro Leu His Trp Glu Ser Val Ile Thr Phe Gln Asn Ser Ser
  50              55              60
Ser Gln Thr Ala Leu Pro Leu Pro Lys Leu Asn Ile Tyr Ser Asn Leu
  65              70              75              80
Phe Phe Arg Leu Lys Ile Ala Lys Val Leu Lys Cys Asp Val Gly Ala
      85              90              95
Asp Val Arg Tyr Phe Thr Lys Tyr Tyr Ala Pro Asp Tyr Ser Pro Ala
      100              105              110
Leu Gly Gln Phe Val Val Gln Glu Asn Thr Asp Arg Val Glu Ile Gly
      115              120              125
Asn Tyr Pro Ile Val Asn Ala
      130              135

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<210> 607  
 <211> 366  
 <212> DNA  
 <213> Homo sapiens

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<400> 607
gatcacgatg aattgtgggc gtacacgtac gagaatgtga tggcgctaaa cttgccgcct
  60
gacattgtgt gtaaaggatt ctttagaaaa ttggaaaacg tagtgaccgg agtcaatttg
  120
gttttcaacg gcaaacatta tcaaattgta aagaagagg atgacctatt caaattgacc
  180
aaaagcaatt gttacaagtt gagcaacata aaatttaaca attggaaata cttgtacttg
  240
acaacgcacg gtgtgtacaa cgtgttcacc aacagctttc attcgagctg tccatttttg
  300
ttgggcacca cgttgccgca gacattcaag aagcccaccg acgaaaagta tttgcccgag
  360
gacgcg
  366

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<210> 608  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

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<400> 608
Asp His Asp Glu Leu Trp Ala Tyr Thr Tyr Glu Asn Val Met Ala Leu
  1              5              10              15
Asn Leu Pro Pro Asp Ile Val Cys Lys Gly Phe Phe Arg Lys Leu Glu
      20              25              30
Asn Val Val Thr Gly Val Asn Leu Val Phe Asn Gly Lys His Tyr Gln
      35              40              45
Ile Val Lys Lys Glu Asp Asp Leu Phe Lys Leu Thr Lys Ser Asn Cys
      50              55              60
Tyr Lys Leu Ser Asn Ile Lys Phe Asn Asn Trp Lys Tyr Leu Tyr Leu
  65              70              75              80
Thr Thr His Gly Val Tyr Asn Val Phe Thr Asn Ser Phe His Ser Ser
      85              90              95
Cys Pro Phe Leu Leu Gly Thr Thr Leu Pro Gln Thr Phe Lys Lys Pro

```

100                      105                      110  
 Thr Asp Glu Lys Tyr Leu Pro Glu Asp Ala  
 115                      120

<210> 609  
 <211> 291  
 <212> DNA  
 <213> Homo sapiens

<400> 609  
 nacgcgttat gacacggcct cctccaaggt cagtgtcatc gagtcacgta actcgtcggg  
 60  
 tgggtcgggtt ggaacgagtc cgtcatgagc ccggtcgcca tggacgactc cagcagtcgg  
 120  
 taccacagcct ggaagcagga ccccccacgcg acggaatcgc cggcttccaa gtcgtcgccc  
 180  
 ccgaagcctc aaacttcccc cgccccgtac gccgggcccgg ctccgaagac accggccaca  
 240  
 cctggaccat ctggggcggg ggcgccgccc tgggtggtggc ggggtggagcc g  
 291

<210> 610  
 <211> 69  
 <212> PRT  
 <213> Homo sapiens

<400> 610  
 Met Ser Pro Val Ala Met Asp Asp Ser Ser Ser Pro Tyr Pro Ala Trp  
 1                      5                      10                      15  
 Lys Gln Asp Pro His Ala Thr Glu Ser Pro Ala Ser Lys Ser Ser Pro  
 20                      25                      30  
 Pro Lys Pro Gln Thr Ser Pro Ala Pro Tyr Ala Gly Pro Ala Pro Lys  
 35                      40                      45  
 Thr Pro Ala Thr Pro Gly Pro Ser Gly Ala Gly Ala Pro Pro Trp Trp  
 50                      55                      60  
 Trp Arg Val Glu Pro  
 65

<210> 611  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<400> 611  
 nnnatcttgt gtcgattttc ggtcgcatac actatggggg agtattgtat aatgcggcgg  
 60  
 tgtaccaag tagagaggtg ttcgatgccca cacagtccgg aagaaaagaa gcaagcactg  
 120  
 acgcgcatca ggcgcaccaa aggtcaggta gcgactcttg agcaagcgct tgatgcaggc  
 180  
 gcgaatgtc ctgcaattct tcagcagctt gcggccggtt gtggcgagc caacggattg  
 240  
 atggcaacgg ttctggagag ctatctgcgg gaagagtttc ccagtagcga aatcaggagc  
 300

gattcgcaga acaagtcctat tgacgagacc atctctatcg tccgctccta tctgcggttag  
 360  
 aggcaccagg gtgtcctcgg tgagggaataa ttt  
 393

<210> 612  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 612  
 Xaa Ile Leu Cys Arg Phe Ser Val Ala Tyr Thr Met Gly Glu Tyr Cys  
 1 5 10 15  
 Ile Met Arg Arg Cys Thr Gln Val Glu Arg Cys Ser Met Pro His Ser  
 20 25 30  
 Pro Glu Glu Lys Lys Gln Ala Leu Thr Arg Ile Arg Arg Ile Lys Gly  
 35 40 45  
 Gln Val Ala Thr Leu Glu Gln Ala Leu Asp Ala Gly Ala Lys Cys Pro  
 50 55 60  
 Ala Ile Leu Gln Gln Leu Ala Ala Val Arg Gly Ala Val Asn Gly Leu  
 65 70 75 80  
 Met Ala Thr Val Leu Glu Ser Tyr Leu Arg Glu Glu Phe Pro Ser Ser  
 85 90 95  
 Glu Ile Arg Ser Asp Ser Gln Asn Lys Ser Ile Asp Glu Thr Ile Ser  
 100 105 110  
 Ile Val Arg Ser Tyr Leu Arg  
 115

<210> 613  
 <211> 567  
 <212> DNA  
 <213> Homo sapiens

<400> 613  
 gaaaatgctc ctggcgccctc aggggaaggctc cttctcaaag aaaaggatgg ggctgaatcg  
 60  
 ctggaaacgg ttcacaagga agccgagtcc caagcctact tttggctcctg acagtgtgga  
 120  
 aacttgata aagagagtgg agaaagcctc agagtttgca gtgtcaaag cattttttac  
 180  
 tagaaattca gatttaccta gaagtccttg gggccaaatc acagatttga aaacatctga  
 240  
 gcaaatagag gatcatgatg aaatctatgc agaagctcag gagctgggtca atgactgggt  
 300  
 agacacaaaa cttaagcaag aattagcaag tgaggaagaa ggtgatgcta aaaacactgt  
 360  
 gtcaagtgtc actattatgc cggaagccaa tggccatttg aaatatgaca agtttgatga  
 420  
 tttatgtggc tatttgaggg aagaagagga agtaccacc gttcaaaaat ttatagacca  
 480  
 tctgtccat aaaaatgtgg tagattctgc aatgatggaa gatcttgga ggaaggaaaa  
 540  
 ccaagacaag aagcagcaga aggatcc  
 567



<210> 614  
 <211> 187  
 <212> PRT  
 <213> Homo sapiens

<400> 614  
 Met Leu Leu Ala Pro Gln Gly Arg Ser Phe Ser Lys Lys Arg Met Gly  
 1 5 10 15  
 Leu Asn Arg Trp Lys Arg Phe Thr Arg Lys Pro Ser Pro Lys Pro Thr  
 20 25 30  
 Phe Gly Pro Asp Ser Val Glu His Trp Ile Lys Arg Val Glu Lys Ala  
 35 40 45  
 Ser Glu Phe Ala Val Ser Asn Ala Phe Phe Thr Arg Asn Ser Asp Leu  
 50 55 60  
 Pro Arg Ser Pro Trp Gly Gln Ile Thr Asp Leu Lys Thr Ser Glu Gln  
 65 70 75 80  
 Ile Glu Asp His Asp Glu Ile Tyr Ala Glu Ala Gln Glu Leu Val Asn  
 85 90 95  
 Asp Trp Leu Asp Thr Lys Leu Lys Gln Glu Leu Ala Ser Glu Glu Glu  
 100 105 110  
 Gly Asp Ala Lys Asn Thr Val Ser Ser Val Thr Ile Met Pro Glu Ala  
 115 120 125  
 Asn Gly His Leu Lys Tyr Asp Lys Phe Asp Asp Leu Cys Gly Tyr Leu  
 130 135 140  
 Glu Glu Glu Glu Glu Ser Thr Thr Val Gln Lys Phe Ile Asp His Leu  
 145 150 155 160  
 Leu His Lys Asn Val Asp Ser Ala Met Met Glu Asp Leu Gly Arg  
 165 170 175  
 Lys Glu Asn Gln Asp Lys Lys Gln Gln Lys Asp  
 180 185

<210> 615  
 <211> 685  
 <212> DNA  
 <213> Homo sapiens

<400> 615  
 nnacgcgtgc tgcctaagt gacggattcc atgtcgggtc gagtcgggtc ggggccgatg  
 60  
 ggccatgaac gggccctagc gagggccgga ctgggccccc tggccggatg cgacgaggcg  
 120  
 gggcggggcg cgtgtgcagg gccattggta gccgcagctg tcattcttga tgatcgaga  
 180  
 tccggcagga ttgcggggct agcagattcc aagacactat ctgcggccaa gagagaggcc  
 240  
 ctgtttaacg tcatcatgga taaagctttg gcagtgtcgt gggtagtgtt agaagccgac  
 300  
 gaatgcgacg gggtggggat gcaggaggca gatatcagcg gcttgaggcg tgccgtggtg  
 360  
 aggcgtgggag ttgaaccggg ctacgtgctg tcggacgggt tcccggtcga cggactgacg  
 420  
 gttccccgatg tgggaatgtg gaagggcgat tcagtgtgtg cgtgtgtggc agctgcctcc  
 480

atcgtggcca aagtggccag ggatcgcatc atgatcgcta tggacgccga gattcctggt  
 540  
 tacgattttg cgggtgcacaa ggggtacgcg acagccttac accagcgctcg tctgaaggag  
 600  
 ttaggaccgt ctcgtcagca ccggatgagc tacgccaatg tgcgacgagc ggctaggctt  
 660  
 cattcatcat gagtgcgcaa gatct  
 685

<210> 616  
 <211> 213  
 <212> PRT  
 <213> Homo sapiens

<400> 616  
 Met Ser Val Arg Val Gly Ser Gly Pro Met Gly His Glu Arg Ala Leu  
 1 5 10 15  
 Ala Arg Ala Gly Leu Gly Pro Val Ala Gly Cys Asp Glu Ala Gly Arg  
 20 25 30  
 Gly Ala Cys Ala Gly Pro Leu Val Ala Ala Val Ile Leu Asp Asp  
 35 40 45  
 Arg Arg Ser Gly Arg Ile Ala Gly Leu Ala Asp Ser Lys Thr Leu Ser  
 50 55 60  
 Ala Ala Lys Arg Glu Ala Leu Phe Asn Val Ile Met Asp Lys Ala Leu  
 65 70 75 80  
 Ala Val Ser Trp Val Arg Val Glu Ala Asp Glu Cys Asp Arg Leu Gly  
 85 90 95  
 Met Gln Glu Ala Asp Ile Ser Gly Leu Arg Arg Ala Val Val Arg Leu  
 100 105 110  
 Gly Val Glu Pro Gly Tyr Val Leu Ser Asp Gly Phe Pro Val Asp Gly  
 115 120 125  
 Leu Thr Val Pro Asp Leu Gly Met Trp Lys Gly Asp Ser Val Cys Ala  
 130 135 140  
 Cys Val Ala Ala Ala Ser Ile Val Ala Lys Val Ala Arg Asp Arg Ile  
 145 150 155 160  
 Met Ile Ala Met Asp Ala Glu Ile Pro Gly Tyr Asp Phe Ala Val His  
 165 170 175  
 Lys Gly Tyr Ala Thr Ala Leu His Gln Arg Arg Leu Lys Glu Leu Gly  
 180 185 190  
 Pro Ser Arg Gln His Arg Met Ser Tyr Ala Asn Val Arg Arg Ala Ala  
 195 200 205  
 Arg Leu His Ser Ser  
 210

<210> 617  
 <211> 337  
 <212> DNA  
 <213> Homo sapiens

<400> 617  
 nncacctgtt tggctcgggg cactcgcgga tcatgggtcga ggaaatgtgg ccgcgctacg  
 60  
 gctcggtttcc cggcttcaac cccatcgctcg agctgtcgct gtcgttccac aacctcgctcg  
 120

tcggcgccaa cggccagcgc caggccatgt tcctcgaaaa cgtttccggc cttcccggag  
 180  
 cgaatcctcc gaaacttcga cctgtcccaa caagactctg cactcgtgat ttcacaaagc  
 240  
 gctgcaacgt cgtgccaatc gagatggccg aggagtcca gcgtcgcggc gtccgcgtcg  
 300  
 tctcgatcat ctgctggcg cactcgcagg cgtcgac  
 337

<210> 618

<211> 112

<212> PRT

<213> Homo sapiens

<400> 618

Xaa	Thr	Cys	Leu	Ala	Arg	Gly	Thr	Arg	Gly	Ser	Trp	Ser	Arg	Lys	Cys
1				5					10					15	
Gly	Arg	Ala	Thr	Ala	Arg	Phe	Pro	Ala	Ser	Thr	Pro	Ser	Ser	Ser	Cys
			20					25					30		
Arg	Cys	Arg	Ser	Thr	Thr	Ser	Ser	Ser	Ala	Pro	Thr	Ala	Ser	Ala	Arg
			35					40				45			
Pro	Cys	Ser	Ser	Lys	Thr	Phe	Pro	Ala	Phe	Pro	Glu	Arg	Ile	Leu	Arg
			50			55					60				
Asn	Phe	Asp	Leu	Ser	Gln	Asp	Ser	Ala	Leu	Val	Ile	Ser	Ser	Ser	
65					70				75					80	
Ala	Ala	Thr	Ser	Cys	Gln	Ser	Arg	Trp	Pro	Arg	Ser	Ser	Ser	Val	Ala
				85					90					95	
Ala	Ser	Ala	Ser	Ser	Arg	Ser	Ser	Arg	Trp	Arg	Thr	Arg	Arg	Arg	Arg
			100					105						110	

<210> 619

<211> 425

<212> DNA

<213> Homo sapiens

<400> 619

acgcgttttt tatgccgatc ttatgctcta acctagaaac aatatcagct acaaacctaa  
 60  
 tagctataag ataatatcgc aaagcatcaa taggagtttt gatcatttcc gcatacctaa  
 120  
 gttttatagc atctttgtca gaaggcaaac ctgccaaacc agatgaatcg atgccactct  
 180  
 caaacttgct caaatgttca attaaatcat ccaagttgtg gccatgctta ccgcttcag  
 240  
 attttgaatg aatcattact ttaattgatt tttcaatcgc taaatggaat tcccagcaag  
 300  
 caatagaagc ccgctcattt ttaaagctca gtatgtcact aatgcctttt tcgaagtggc  
 360  
 tccatattcc ctgcgccata ttagaagctg actggttgga atggcttgcc atgttcaa  
 420  
 ctaga  
 425

<210> 620

<211> 137  
 <212> PRT  
 <213> Homo sapiens

<400> 620  
 Met Ala Ser His Ser Asn Gln Ser Ala Ser Asn Met Ala Gln Gly Ile  
 1 5 10 15  
 Trp Ser His Phe Glu Lys Gly Ile Ser Asp Ile Leu Ser Phe Lys Asn  
 20 25 30  
 Glu Arg Ala Ser Ile Ala Cys Trp Glu Phe His Leu Ala Ile Glu Lys  
 35 40 45  
 Ser Ile Lys Val Met Ile His Ser Lys Ser Gly Ser Gly Lys His Gly  
 50 55 60  
 His Asn Leu Asp Asp Leu Ile Glu His Leu Ser Lys Phe Glu Ser Gly  
 65 70 75 80  
 Ile Asp Ser Ser Gly Leu Ala Gly Leu Pro Ser Asp Lys Asp Ala Ile  
 85 90 95  
 Lys Leu Arg Tyr Ala Glu Met Ile Lys Thr Pro Ile Asp Ala Phe Glu  
 100 105 110  
 Tyr Tyr Leu Ile Ala Ile Arg Phe Val Ala Asp Ile Val Ser Arg Leu  
 115 120 125  
 Glu His Lys Ile Gly Ile Lys Asn Ala  
 130 135

<210> 621  
 <211> 453  
 <212> DNA  
 <213> Homo sapiens

<400> 621  
 cccggcaagg gagccatctt gacgaatatg tccttgtggt ggttcgacca attggccgac  
 60  
 atcgtcgata accatctcgt gagcgtggat gtccccgccg aggtcgcagg gcgcgccatg  
 120  
 gtcgttgagg aactcgacat gttcccggtc gaatgcgtcg tgcgggggcta cctcaccggt  
 180  
 tcagggtggg ccgaatatca gcgcaaccag gccgtgtgcg gaatccgcct tcccgagggg  
 240  
 ctgcagaatg ggtcccggct cgaagagccc attttcaccc cggcaattaa ggccccgcag  
 300  
 ggagaacatg acgagaacat cgactatcta cgcttgtag aactcgtcgg tccngatgn  
 360  
 tcagcgcagc tgcattgacct ttcgctgcgg gtctaccagc gtgcagagga gatcgtcgg  
 420  
 aagcagggca tcctcctggc ggataccaag ctt  
 453

<210> 622  
 <211> 151  
 <212> PRT  
 <213> Homo sapiens

<400> 622  
 Pro Gly Lys Gly Ala Ile Leu Thr Asn Met Ser Leu Trp Trp Phe Asp

```

1           5           10           15
Gln Leu Ala Asp Ile Val Asp Asn His Leu Val Ser Val Asp Val Pro
20           25           30
Ala Glu Val Ala Gly Arg Ala Met Val Val Glu Glu Leu Asp Met Phe
35           40           45
Pro Val Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Trp Ala
50           55           60
Glu Tyr Gln Arg Asn Gln Ala Val Cys Gly Ile Arg Leu Pro Glu Gly
65           70           75           80
Leu Gln Asn Gly Ser Arg Leu Glu Glu Pro Ile Phe Thr Pro Ala Ile
85           90           95
Lys Ala Pro Gln Gly Glu His Asp Glu Asn Ile Asp Tyr Leu Arg Leu
100          105          110
Val Glu Leu Val Gly Pro Xaa Xaa Ser Ala Gln Leu His Asp Leu Ser
115          120          125
Leu Arg Val Tyr Gln Arg Ala Glu Glu Ile Ala Arg Lys Arg Gly Ile
130          135          140
Leu Leu Ala Asp Thr Lys Leu
145          150

```

&lt;210&gt; 623

&lt;211&gt; 345

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 623

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acgcgtccag tatgtccacg gaggacatgc ttgacctcga ctcgaacgtc tcctactacg
60
cgaggaacta tcaggccgcg caatcagttg tggcgaaatt cgacgcgggc accattgccc
120
aagccgaaga cctgccacct gacgacaccc acacgggggc ggaactggta aagagcgtgg
180
tcaacagcat cacctgtgtg tcacccctgt acatcgaaga tttcaccacc atagagatcc
240
aggggctggg actgcactgt gtcaggctct gggcgctgg gctgctcgcc ctgtcactgc
300
ccagcgcacc catgcgggca caccctcgct acgcccata tggcg
345

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&lt;210&gt; 624

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 624

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Met Ser Thr Glu Asp Met Leu Asp Leu Asp Ser Asn Val Ser Tyr Tyr
1           5           10           15
Ala Arg Asn Tyr Gln Ala Ala Gln Ser Val Val Ala Lys Phe Asp Ala
20           25           30
Gly Thr Ile Ala Gln Ala Glu Asp Leu Pro Pro Asp Asp Thr His Thr
35           40           45
Gly Ala Glu Leu Val Lys Ser Val Val Asn Ser Ile Thr Cys Val Ser
50           55           60
Pro Leu Tyr Ile Glu Asp Phe Thr Thr Ile Glu Ile Gln Gly Leu Gly

```

```

65          70          75          80
Leu His Cys Val Arg Leu Trp Ala Pro Gly Leu Leu Ala Leu Ser Leu
          85          90          95
Pro Ser Ala Pro Met Arg Ala His Pro Arg Tyr Ala Ala Tyr Gly
          100          105          110

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<210> 625  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

```

<400> 625
ggtacccagc atgatgctgc tagacatttg ctgaatgcat agatgatttt tccagggcct
60
gtaatttaca gggagagcaa tggaggccca gagacaagat gattcagctc ctccactctg
120
ttcaggatca tatcctaagg accaacaatgt ctgtctacct ttacactgag cccccacca
180
gccaaccacc tcccatgaga gacaggctct ccttgctga gcttggaccc aggccccctc
240
tctgctgagc tcagaacaca tgcttgactg tgatgtaaca ggggtggcagc cccacagca
300
ttgcatctgc cccataactca gtgtggggag ataggacgc
339

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<210> 626  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

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<400> 626
Met Gly Gln Met Gln Cys Cys Gly Gly Cys His Pro Val Thr Ser Gln
 1          5          10          15
Ser Ser Met Cys Ser Glu Leu Ser Arg Glu Gly Ala Trp Val Gln Ala
 20          25          30
Gln Ala Gly Arg Ala Cys Leu Ser Trp Glu Val Val Gly Trp Val Gly
 35          40          45
Ala Gln Cys Lys Gly Arg Gln Thr Cys Trp Ser Leu Gly Tyr Asp Pro
 50          55          60
Glu Gln Ser Gly Gly Ala Glu Ser Ser Cys Leu Trp Ala Ser Ile Ala
65          70          75          80
Leu Pro Val Asn Tyr Arg Pro Trp Lys Asn His Leu Cys Ile Gln Gln
 85          90          95
Met Ser Ser Ser Ile Met Leu Gly Thr
          100          105

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<210> 627  
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Ile Ala Cys Gly Ile Trp Phe Ser Asn Val Ser Gly Gly Ile Ala Trp
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Leu Pro Leu Ala Leu Leu Thr Leu Ala Ser Leu Phe Leu Gly Phe His
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Phe Val Ala Ala Ile Gly Gly Ala Asp Met Pro Val Val Ile Ser Met
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gagagaggtc gtaaggaagt gtcgtgtcgc tcatgactct cttctattag ttgggtaaca  
6660

gtggcctcat gtttgtgtct gtgtgtacac agagccctta ggttctgctc tgtttctttg  
 6720  
 ccaggtgaat gtttgtggca tgcgctgctg tccgcgcccc tctgtcctgc gcagggttca  
 6780  
 gctgtgcggc gccctgattt cctccatgca cacagaacct ccttgtgtct gtttctctgt  
 6840  
 tcctctgtgg ctgactcaat aaacttttcc ctctgaaaaa aaaaaaaaaa aaaaaaaaaa  
 6900  
 aaaaaaaaaa aaaaaaag  
 6918

<210> 636

<211> 619

<212> PRT

<213> Homo sapiens

<400> 636

Xaa	Pro	Asn	Arg	Gln	Pro	Ile	Gly	Ile	Val	Leu	Thr	Val	Leu	Gly	Val
1				5					10				15		
Val	Val	Leu	Asp	Phe	Ser	Ala	Asp	Ala	Thr	Glu	Gly	Pro	Ile	Arg	Ala
		20					25						30		
Tyr	Leu	Leu	Asp	Val	Val	Asp	Ser	Glu	Glu	Gln	Asp	Met	Ala	Leu	Asn
		35					40					45			
Ile	His	Ala	Phe	Ser	Ala	Gly	Leu	Gly	Gly	Ala	Ile	Gly	Tyr	Val	Leu
	50					55					60				
Gly	Gly	Leu	Asp	Trp	Thr	Gln	Thr	Phe	Leu	Gly	Ser	Trp	Phe	Arg	Thr
65					70					75				80	
Gln	Asn	Gln	Val	Leu	Phe	Phe	Phe	Ala	Ala	Ile	Ile	Phe	Thr	Val	Ser
			85						90					95	
Val	Ala	Leu	His	Leu	Phe	Ser	Ile	Asp	Glu	Glu	Gln	Tyr	Ser	Pro	Gln
		100						105					110		
Gln	Glu	Arg	Ser	Ala	Glu	Glu	Pro	Gly	Ala	Leu	Asp	Gly	Gly	Glu	Pro
		115					120					125			
His	Gly	Val	Pro	Ala	Phe	Pro	Asp	Glu	Val	Gln	Ser	Glu	His	Glu	Leu
	130					135					140				
Ala	Leu	Asp	Tyr	Pro	Asp	Val	Asp	Ile	Met	Arg	Ser	Lys	Ser	Asp	Ser
145					150					155				160	
Ala	Leu	His	Val	Pro	Asp	Thr	Ala	Leu	Asp	Leu	Glu	Pro	Glu	Leu	Leu
			165						170					175	
Phe	Leu	His	Asp	Ile	Glu	Pro	Ser	Ile	Phe	His	Asp	Ala	Ser	Tyr	Pro
		180						185					190		
Ala	Thr	Pro	Arg	Ser	Thr	Ser	Gln	Glu	Leu	Ala	Lys	Thr	Lys	Leu	Pro
		195					200					205			
Arg	Leu	Ala	Thr	Phe	Leu	Lys	Glu	Ala	Ala	Lys	Glu	Asp	Glu	Thr	Leu
	210					215					220				
Leu	Asp	Asn	His	Leu	Asn	Glu	Ala	Lys	Val	Pro	Asn	Gly	Ser	Gly	Ser
225					230					235				240	
Pro	Thr	Lys	Asp	Ala	Leu	Gly	Gly	Tyr	Thr	Arg	Val	Asp	Thr	Lys	Pro
			245						250					255	
Ser	Ala	Thr	Ser	Ser	Ser	Met	Arg	Arg	Arg	Arg	His	Ala	Phe	Arg	Arg
		260						265					270		
Gln	Ala	Ser	Ser	Thr	Phe	Ser	Tyr	Tyr	Gly	Lys	Leu	Gly	Ser	His	Cys
		275					280					285			
Tyr	Arg	Tyr	Arg	Arg	Ala	Asn	Ala	Val	Val	Leu	Ile	Lys	Pro	Ser	Arg



```

      290              295              300
Ser Met Ser Asp Leu Tyr Asp Met Gln Lys Arg Gln Arg Gln His Arg
305              310              315              320
His Arg Asn Gln Ser Gly Ala Thr Thr Ser Ser Gly Asp Thr Glu Ser
      325              330              335
Glu Glu Gly Glu Gly Glu Thr Thr Val Arg Leu Leu Trp Leu Ser Met
      340              345              350
Leu Lys Met Pro Arg Glu Leu Met Arg Leu Cys Leu Cys His Leu Leu
      355              360              365
Thr Trp Phe Ser Val Ile Ala Glu Ala Val Phe Tyr Thr Asp Phe Met
370              375              380
Gly Gln Val Ile Phe Glu Gly Asp Pro Lys Ala Pro Ser Asn Ser Thr
385              390              395              400
Ala Trp Gln Ala Tyr Asn Ala Gly Val Lys Met Gly Cys Trp Gly Leu
      405              410              415
Val Ile Tyr Ala Ala Thr Gly Ala Ile Cys Ser Ala Leu Leu Gln Lys
      420              425              430
Tyr Leu Asp Asn Tyr Asp Leu Ser Val Arg Val Ile Tyr Val Leu Gly
      435              440              445
Thr Leu Gly Phe Ser Val Gly Thr Ala Val Met Ala Met Phe Pro Asn
450              455              460
Val Tyr Val Ala Met Val Thr Ile Ser Thr Met Gly Ile Val Ser Met
465              470              475              480
Ser Ile Ser Tyr Cys Pro Tyr Ala Leu Leu Gly Gln Tyr His Asp Ile
      485              490              495
Lys Gln Tyr Ile His His Ser Pro Gly Asn Ser Lys Arg Gly Phe Gly
      500              505              510
Ile Asp Cys Ala Ile Leu Ser Cys Gln Val Tyr Ile Ser Gln Ile Leu
515              520              525
Val Ala Ser Ala Leu Gly Gly Val Val Asp Ala Val Gly Thr Val Arg
530              535              540
Val Ile Pro Met Val Ala Ser Val Gly Ser Phe Leu Gly Phe Leu Thr
545              550              555              560
Ala Thr Phe Leu Val Ile Tyr Pro Asp Val Ser Glu Glu Ala Lys Glu
      565              570              575
Glu Gln Lys Gly Leu Ser Ser Pro Leu Ala Gly Glu Gly Arg Ala Gly
      580              585              590
Gly Asn Ser Glu Lys Pro Thr Val Leu Lys Leu Thr Arg Lys Glu Gly
595              600              605
Leu Gln Gly Pro Val Glu Thr Glu Ser Val Val
610              615

```

&lt;210&gt; 637

&lt;211&gt; 370

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 637

```

ngaaaaacag gatgaatccc gtatcattct taagcccgaa aagtactgaa tgcgtcttc
60
tctcgatcgg tgatgatctg gaaaggaaaa atcatcgtga ctactacatc acccgctact
120
acgcaaagac cgtcagttgg caggaaagtt gggtcctggt cccttaatcc atgggtgttt
180

```

tgtaggcctt tattattttt cggaatgggt cggtttattg cgattccagt attcctcact  
 240  
 gtgccgaata tcattaatat cggaatccaa gccgcggtgg tggcgattat ggccttcggt  
 300  
 atgaccttcg tcacgtttac ctccggcatt gatttgtctg tgggttcggt cgcagctctt  
 360  
 tcagccatgg  
 370

<210> 638  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 638  
 Met Ile Trp Lys Gly Lys Ile Ile Val Thr Thr Thr Ser Pro Ala Thr  
 1 5 10 15  
 Thr Gln Arg Pro Ser Val Gly Arg Lys Val Gly Ser Trp Ser Leu Asn  
 20 25 30  
 Pro Trp Cys Phe Cys Arg Pro Leu Leu Phe Phe Gly Met Val Arg Phe  
 35 40 45  
 Ile Ala Ile Pro Val Phe Leu Thr Val Pro Asn Ile Ile Asn Ile Gly  
 50 55 60  
 Ile Gln Ala Ala Val Val Ala Ile Met Ala Phe Gly Met Thr Phe Val  
 65 70 75 80  
 Ile Val Thr Ser Gly Ile Asp Leu Ser Val Gly Ser Val Ala Ala Leu  
 85 90 95  
 Ser Ala Met

<210> 639  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

<400> 639  
 nacgcgtcga tgggcaacta catcttcagt cgggatgccc tggtcgaggc actcttcgca  
 60  
 gactcccagt ccgtgagtc gcgtcatgac atgggtggcg acatcatccc gagattcgtc  
 120  
 gaggcgggg acgcgcaggt ctacgacttc tgtgacaacc aggtgcccgg aaccaccgag  
 180  
 aaggatcggg actactggcg ggacgtggga actatcgatg cctaccacga cgcgcacatg  
 240  
 gacctcgtgt cgggtggaacc ggagttcaac ctctacaacc ccgactggcc gatctggagc  
 300  
 atccaggaac aggcaccggg agcgaaattt  
 330

<210> 640  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 640

Xaa Ala Ser Met Gly Asn Tyr Ile Phe Ser Arg Asp Ala Leu Val Glu  
 1 5 10 15  
 Ala Leu Phe Ala Asp Ser Gln Ser Ala Glu Ser Arg His Asp Met Gly  
 20 25 30  
 Gly Asp Ile Ile Pro Arg Phe Val Glu Ala Gly Asp Ala Gln Val Tyr  
 35 40 45  
 Asp Phe Cys Asp Asn Gln Val Pro Gly Thr Thr Glu Lys Asp Arg Asp  
 50 55 60  
 Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Tyr His Asp Ala His Met  
 65 70 75 80  
 Asp Leu Val Ser Val Glu Pro Glu Phe Asn Leu Tyr Asn Pro Asp Trp  
 85 90 95  
 Pro Ile Trp Ser Ile Gln Glu Gln Ala Pro Gly Ala Lys Phe  
 100 105 110

&lt;210&gt; 641

&lt;211&gt; 491

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 641

cgcgtgaccg gcgcggagaa cgtgcgcaag atcctcatgg gcgagcacca cctcgtgagc  
 60  
 accgagtggc ctgcgagcac ccgcatgttg ctggggcccca acacggtgtc caattccatt  
 120  
 ggcgacatcc accgcaacaa gcgcaaggtc ttctccaaga tcttcagcca cgaggccctg  
 180  
 gagagttacc tgccaagat ccagctggtg atccaggaca cactgcgcgc ctggagcagc  
 240  
 caccgagagg ccatcaacgt gtaccaggag gcgcagaagc tgaccttcg catggccatc  
 300  
 cgggtgctgc tgggcttcag catccctgag gaggaccttg ggcacctctt tgaggtctac  
 360  
 cagcagtttg tggacaatgt cttctccctg cctgtcgacc tgcccttcag tggctaccgg  
 420  
 cggggcattc aggctcggca gatcctgcag aaggggctgg agaaggccat ccgggagaag  
 480  
 ctgcagtga c  
 491

&lt;210&gt; 642

&lt;211&gt; 163

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 642

Arg Val Thr Gly Ala Glu Asn Val Arg Lys Ile Leu Met Gly Glu His  
 1 5 10 15  
 His Leu Val Ser Thr Glu Trp Pro Arg Ser Thr Arg Met Leu Leu Gly  
 20 25 30  
 Pro Asn Thr Val Ser Asn Ser Ile Gly Asp Ile His Arg Asn Lys Arg  
 35 40 45  
 Lys Val Phe Ser Lys Ile Phe Ser His Glu Ala Leu Glu Ser Tyr Leu

```

      50      55      60
Pro Lys Ile Gln Leu Val Ile Gln Asp Thr Leu Arg Ala Trp Ser Ser
65      70      75      80
His Pro Glu Ala Ile Asn Val Tyr Gln Glu Ala Gln Lys Leu Thr Phe
      85      90      95
Arg Met Ala Ile Arg Val Leu Leu Gly Phe Ser Ile Pro Glu Glu Asp
      100      105      110
Leu Gly His Leu Phe Glu Val Tyr Gln Gln Phe Val Asp Asn Val Phe
      115      120      125
Ser Leu Pro Val Asp Leu Pro Phe Ser Gly Tyr Arg Arg Gly Ile Gln
      130      135      140
Ala Arg Gln Ile Leu Gln Lys Gly Leu Glu Lys Ala Ile Arg Glu Lys
145      150      155      160
Leu Gln Cys

```

<210> 643  
 <211> 628  
 <212> DNA  
 <213> Homo sapiens

```

<400> 643
nagatctttg acatctacgt ggtcaccgct gactacctgc ccctaggggc tgagcaggat
60
gccatcacgc tgcgggaagg ccagtatgtg gaggtcctgg atgcagccca cccactgcgc
120
tggcttgtcc gcaccaagcc caccaagtcc agcccctcac ggcagggctg ggtgtcacca
180
gcctacctgg acaggaggct caagctgtca cctgagtggg gggccgctga ggcccctgag
240
ttccctgggg aggctgtgtc tgaagacgaa tacaaggcaa ggctgagctc tgtgatccag
300
gagctgctga gttctgagca ggccttcgtg gaggagctgc agttcctgca gagccaccac
360
ctgcagcacc tggagcgctg cccccacgtg cccatagctg tggccggcca gaaggcagtc
420
atcttccgca atgtgcggga catcggccgc ttccacagca gcttcctgca ggagttgcag
480
cagtgcgaca cggacgacga cgtggccatg tgcttcatca agaaccaggc ggcctttgag
540
cagtacctgg agttcctggt gggacgtgtg caggctgagt cggtggtcgt cagcacggcc
600
atccaggagt tctacaagaa atacgcgt
628

```

<210> 644  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

```

<400> 644
Xaa Ile Phe Asp Ile Tyr Val Val Thr Ala Asp Tyr Leu Pro Leu Gly
1      5      10      15
Ala Glu Gln Asp Ala Ile Thr Leu Arg Glu Gly Gln Tyr Val Glu Val

```

20					25					30					
Leu	Asp	Ala	Ala	His	Pro	Leu	Arg	Trp	Leu	Val	Arg	Thr	Lys	Pro	Thr
35					40					45					
Lys	Ser	Ser	Pro	Ser	Arg	Gln	Gly	Trp	Val	Ser	Pro	Ala	Tyr	Leu	Asp
50					55					60					
Arg	Arg	Leu	Lys	Leu	Ser	Pro	Glu	Trp	Gly	Ala	Ala	Glu	Ala	Pro	Glu
65					70					75					
Phe	Pro	Gly	Glu	Ala	Val	Ser	Glu	Asp	Glu	Tyr	Lys	Ala	Arg	Leu	Ser
85					90					95					
Ser	Val	Ile	Gln	Glu	Leu	Leu	Ser	Ser	Glu	Gln	Ala	Phe	Val	Glu	Glu
100					105					110					
Leu	Gln	Phe	Leu	Gln	Ser	His	His	Leu	Gln	His	Leu	Glu	Arg	Cys	Pro
115					120					125					
His	Val	Pro	Ile	Ala	Val	Ala	Gly	Gln	Lys	Ala	Val	Ile	Phe	Arg	Asn
130					135					140					
Val	Arg	Asp	Ile	Gly	Arg	Phe	His	Ser	Ser	Phe	Leu	Gln	Glu	Leu	Gln
145					150					155					
Gln	Cys	Asp	Thr	Asp	Asp	Val	Ala	Met	Cys	Phe	Ile	Lys	Asn	Gln	Gln
165					170					175					
Ala	Ala	Phe	Glu	Gln	Tyr	Leu	Glu	Phe	Leu	Val	Gly	Arg	Val	Gln	Ala
180					185					190					
Glu	Ser	Val	Val	Val	Ser	Thr	Ala	Ile	Gln	Glu	Phe	Tyr	Lys	Lys	Tyr
195					200					205					
Ala															

```
<210> 645
<211> 417
<212> DNA
<213> Homo sapiens
```

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<400> 645
atccataggc attgccagag tattcacttc ctgttgaggg cacacagggg agaggcctgt
60
gaggggaagg gcatcaatgc agggctgggg tgtgggaagg tctgcagggc tggcaatggg
120
caagctcagg aatggtgggg gagacagttg gagccacggc agggacaatg gagctcagaa
180
ggtcctctg tcatcccttt tggaacccat tgatctggaa aatttggggc agtgtccttt
240
tcgtaggta ctggaggcac tggcttgaca tactacagcc ctcccaggag gcccagaagg
300
tagatgttat aactaccccc attttccaga tgaagaaact gagcctctgg gatctgcgga
360
agctcccaga gctggagcag ttagtccctg ggccttacac tcacagcaca gtttccc
417
```

```
<210> 646
<211> 95
<212> PRT
<213> Homo sapiens
```

<400> 646  
Met Val Gly Glu Thr Val Gly Ala Thr Ala Gly Thr Met Glu Leu Arg

```

1           5           10           15
Arg Ser Leu Cys His Pro Phe Trp Asn Pro Leu Ile Trp Lys Ile Trp
      20           25           30
Gly Ser Val Leu Phe Arg Arg Tyr Trp Arg His Trp Leu Asp Ile Leu
      35           40           45
Gln Pro Ser Gln Glu Ala Gln Lys Val Asp Val Ile Thr Thr Pro Ile
      50           55           60
Phe Gln Met Lys Lys Leu Ser Leu Trp Asp Leu Arg Lys Leu Pro Glu
65           70           75           80
Leu Glu Gln Leu Val Pro Gly Pro Tyr Thr His Ser Thr Val Ser
      85           90           95

```

&lt;210&gt; 647

&lt;211&gt; 421

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 647

```

acgcggtttcg gttcttgagc gttccacca attcagcggg ggtgagcggc cctgtgcat
60
cgcgcagcag ggtgatcaga taggcgatat ccgcctcggt cagttgcacg gtgtcggtat
120
cggtagccat gcgtggcgaa ctcccttggc atgggaaaat cgggtgaggc caacgggcac
180
agcaacagga cgtgtccctt gcggcacgtg gcaacacgtc agtatagcgc gttccgccc
240
ggatttccgt tgaatgaagg caagaagtcg ggacgcgcat cacctgctac cgctcggtgg
300
tacgatagcc gcggcgccac caggttggtt acattccaaa cgcaacgcag gaacccgcat
360
gaacagcggt ttctgcaaca aacccttat gacgctgggt ctcgggcatt tcagtgtcga
420
c
421

```

&lt;210&gt; 648

&lt;211&gt; 90

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 648

```

Met Gly Lys Ser Gly Glu Ala Asn Gly His Ser Asn Arg Thr Cys Pro
1           5           10           15
Leu Arg His Val Ala Thr Arg Gln Tyr Ser Ala Phe Pro Pro Gly Phe
      20           25           30
Pro Leu Asn Glu Gly Lys Lys Ser Gly Thr His Pro Pro Ala Thr Ala
      35           40           45
Arg Trp Tyr Asp Ser Arg Gly Ala Thr Arg Leu Ala Thr Phe Gln Thr
      50           55           60
Gln Arg Arg Asn Pro His Glu Gln Arg Phe Ser Gln Gln Thr Pro Tyr
65           70           75           80
Asp Ala Gly Ser Arg Ala Phe Gln Cys Arg
      85           90

```

<210> 649  
 <211> 563  
 <212> DNA  
 <213> Homo sapiens

<400> 649  
 cgcaacatgc ataaacacat gtgtctctcc gagactcagc tacttccttt gccctctctg  
 60  
 gacctcagtg tccaggcttg tgcatttagg ggctcagggt tgggctctgt gcctatgagc  
 120  
 cagtctatgt gtgcactgtc tgtctgtctg tccgtctgcc agcaaccttc aaggccccag  
 180  
 gaggggaagg caccaatgga aggtgggggc agggaaggag gtagcgttga caagttccaa  
 240  
 tgtctggctt tccctcctgg aaacccccgag ctggggctgg ccccccttc ccttcctgtc  
 300  
 tctctcgtc aagcacgtcc cttctaagag cccctctctg cagacgcccc cagtggaacc  
 360  
 aagcctagat tcgtgccaa gaaggccgac attttttaga cttgccacgt taaaggggcc  
 420  
 tgcacaggca cgcactcaaa tccccccctc catgtcctcc gcctgtgcac attcaggcaa  
 480  
 cccgaaacac acaaagacac ggttggacac agcggccacc tgtgcacaca ggaggtagca  
 540  
 catggagcgc atctgacccc ggg  
 563

<210> 650  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 650  
 Met His Lys His Met Cys Ser Ser Glu Thr Gln Leu Leu Pro Leu Pro  
 1 5 10 15  
 Ser Leu Asp Leu Ser Val Gln Ala Cys Ala Phe Arg Gly Ser Gly Leu  
 20 25 30  
 Gly Ser Val Pro Met Ser Gln Ser Met Cys Ala Leu Ser Val Cys Leu  
 35 40 45  
 Ser Val Cys Gln Gln Pro Ser Arg Pro Gln Glu Gly Lys Ala Pro Met  
 50 55 60  
 Glu Gly Gly Gly Arg Glu Gly Gly Ser Val Asp Lys Phe Gln Cys Leu  
 65 70 75 80  
 Ala Phe Pro Pro Gly Asn Pro Glu Leu Gly Leu Ala Pro Pro Ser Leu  
 85 90 95  
 Pro Val Ser Leu Ala Gln Ala Arg Pro Phe  
 100 105

<210> 651  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 651

gaattcttca acaagctctc ctgctctagg atcaaggata gacctatata aggtccaaac  
60  
cataatggag tccatggggt caaagttatc tcctggagct cagcagttga tggatatggt  
120  
taggtgtcag cagcgggaatt gtattcccat tggagagcag cttcagtcgg tgttgggcaa  
180  
ttctggatac aagcatatga ttggactaca atcctcatct accttaggaa ccttaaacia  
240  
gtcgtctccc acaccttttc cttttagaac tggattgaca tctgggaacg tgactgaaaa  
300  
cttacaagcg tacattgata aaagtacaca actgcctggt ggagagaatt c  
351

&lt;210&gt; 652

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 652

Met	Glu	Ser	Met	Gly	Ser	Lys	Leu	Ser	Pro	Gly	Ala	Gln	Gln	Leu	Met
1				5				10					15		
Asp	Met	Val	Arg	Cys	Gln	Gln	Arg	Asn	Cys	Ile	Pro	Ile	Gly	Glu	Gln
		20					25				30				
Leu	Gln	Ser	Val	Leu	Gly	Asn	Ser	Gly	Tyr	Lys	His	Met	Ile	Gly	Leu
		35				40					45				
Gln	Ser	Ser	Ser	Thr	Leu	Gly	Thr	Leu	Asn	Lys	Ser	Ser	Ser	Thr	Pro
	50				55			60							
Phe	Pro	Phe	Arg	Thr	Gly	Leu	Thr	Ser	Gly	Asn	Val	Thr	Glu	Asn	Leu
65				70				75					80		
Gln	Ala	Tyr	Ile	Asp	Lys	Ser	Thr	Gln	Leu	Pro	Gly	Gly	Glu	Asn	
			85					90					95		

&lt;210&gt; 653

&lt;211&gt; 399

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 653

nnccccgggtg gggctggggt ggggccagca tcagaggagg acatgaccaa gctgtgcaac  
60  
caccggcgga aagctgttgc tatggcaact ctgtaccgca gcatggagac cacctgtctca  
120  
cactcttctc ctggagaggg agcgagcccc caaatgttcc acactgtgtc cccaggggccc  
180  
ccctctgccc gccctccctg tcgagttcct cctacaactc cacttaatgg gggtcctggc  
240  
tcccttcccc cagaaccacc ctacgtttcc caggcctttc ccactctagc aggccttggg  
300  
gggtcttttc cccaaggct tgctgacca gtcccttctg ggggcagtag cagcccccg  
360  
ttctcccaa ggggcaatgc cccctctcca gcccaccc  
399

&lt;210&gt; 654



<211> 133  
 <212> PRT  
 <213> Homo sapiens

<400> 654  
 Xaa Pro Gly Gly Ala Gly Val Gly Pro Ala Ser Glu Glu Asp Met Thr  
 1 5 10 15  
 Lys Leu Cys Asn His Arg Arg Lys Ala Val Ala Met Ala Thr Leu Tyr  
 20 25 30  
 Arg Ser Met Glu Thr Thr Cys Ser His Ser Ser Pro Gly Glu Gly Ala  
 35 40 45  
 Ser Pro Gln Met Phe His Thr Val Ser Pro Gly Pro Pro Ser Ala Arg  
 50 55 60  
 Pro Pro Cys Arg Val Pro Pro Thr Thr Pro Leu Asn Gly Gly Pro Gly  
 65 70 75 80  
 Ser Leu Pro Pro Glu Pro Pro Ser Val Ser Gln Ala Phe Pro Thr Leu  
 85 90 95  
 Ala Gly Pro Gly Gly Leu Phe Pro Pro Arg Leu Ala Asp Pro Val Pro  
 100 105 110  
 Ser Gly Gly Ser Ser Ser Pro Arg Phe Leu Pro Arg Gly Asn Ala Pro  
 115 120 125  
 Ser Pro Ala Pro Pro  
 130

<210> 655  
 <211> 368  
 <212> DNA  
 <213> Homo sapiens

<400> 655  
 tgaaggaaat tctctatggc ttgtgttcat catgtagaac agcccatgag gagaatagga  
 60  
 gatgaggtgg gaagtgcact gggatctggg ggaagaagcc cggggttcaa gactcagcta  
 120  
 ctgactgcat ggtgtcaaag gattcgggca tcctctctga ggctgagtct tcagatgaca  
 180  
 gtgagaacag ggacacctgc cctgcccttc tcacggggcg tgtgggcacc catgagcatg  
 240  
 cttgacaaat gcaaggtgcc atacaaacag gaactgcaca atctcaccgc ccggcctact  
 300  
 cagcattggt atttttacct ttacatctat atgaagatgt agttccattc cttttaactg  
 360  
 ttgttttc  
 368

<210> 656  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 656  
 Met Ala Cys Val His His Val Glu Gln Pro Met Arg Arg Ile Gly Asp  
 1 5 10 15  
 Glu Val Gly Ser Ala Leu Gly Ser Gly Gly Arg Ser Pro Gly Phe Lys

```

      20      25      30
Thr Gln Leu Leu Thr Ala Trp Cys Gln Arg Ile Arg Ala Ser Ser Leu
      35      40      45
Arg Leu Ser Leu Gln Met Thr Val Arg Thr Gly Thr Pro Ala Leu Pro
      50      55      60
Phe Ser Arg Gly Val Trp Ala Pro Met Ser Met Leu Asp Lys Cys Lys
      65      70      75      80
Val Pro Tyr Lys Gln Glu Leu His Asn Leu Thr Ala Arg Pro Thr Gln
      85      90      95
His Cys Tyr Phe Tyr Leu Tyr Ile Tyr Met Lys Met
      100      105

```

<210> 657  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

```

<400> 657
gtcgaccacg gcatgaaaaa gccggggatg atcctcatca acaaccctg gggcgagtcc
60
aacgaggcgg gcttcaagcg cgccctcgaa gagcgtggca tggccaacgc cgggtgctgag
120
cgtattcagg acagcgacct ggacgtggtg ccgcaattga cccgcctga aaaacgccgg
180
tgccgacacc ttgctgatgg tcggcaacgt cggcccttcg gcacaggtgg tcaagtcctt
240
ggaccgcatg gggtgggacg tgcctgtggt gtctcactgg gggccggccg gnggtcgctt
300
tggcgagctg gcggggccta acgcttctcg
330

```

<210> 658  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens

```

<400> 658
Met Lys Lys Pro Gly Met Ile Leu Ile Asn Asn Pro Trp Gly Glu Ser
1      5      10      15
Asn Glu Ala Gly Phe Lys Arg Ala Leu Glu Glu Arg Gly Met Ala Asn
      20      25      30
Ala Gly Val Glu Arg Ile Gln Asp Ser Asp Leu Asp Val Val Pro Gln
      35      40      45
Leu Thr Pro Pro Glu Lys Arg Arg Cys Arg His Leu Ala Asp Gly Arg
      50      55      60
Gln Arg Arg Pro Phe Gly Thr Gly Gly Gln Val Pro Gly Pro His Gly
      65      70      75      80
Leu Gly Arg Ala Cys Gly Val Ser Leu Gly Ala Gly Arg Xaa Ser Leu
      85      90      95
Trp Arg Ala Gly Gly Ala
      100

```

<210> 659  
 <211> 1505

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 659

gccaggatca tgtccaccac cacatgccaa gtggtggcgt tcctcctgtc catcctgggg  
60  
ctggccggct gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac  
120  
aaccctgtca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt gaggcagagt  
180  
tcaggcttca ccgaatgcag gccctatttc accatcctgg gacttcagc catgctgcag  
240  
gcagtgcgag ccctgatgat cgtaggcatc gtctctgggtg ccattggcct cctggtatcc  
300  
atctttgccc tgaaatgcat ccgcattggc agcatggagg actctgcaa agccaacatg  
360  
acactgacct ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct  
420  
gtgtttgcc aatgctgggt gactaacttc tggatgtcca cagctaacat gtacaccggc  
480  
atgggtggga tggtcagac tgttcagacc aggtacacat ttggtgcggc tctgttcgtg  
540  
ggctgggtcg ctggaggcct cacactaatt ggggtgtgta tgatgtgcat cgctgcccg  
600  
ggctggcac cagaagaaac caactacaaa gccgtttctt atcatgcctc aggccacagt  
660  
gttgcctaca agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac  
720  
aagaagatat acgatggagg tgcccgacac gaggacgagg tacaatctta tccttccaag  
780  
cacgactatg tgtaatgtc taagacctct cagcacgggc ggaagaaact cccggagagc  
840  
tcacccaaaa aacaaggaga tcccatctag atttcttctt gcttttgact cacagctgga  
900  
agttagaaaa gcctcgattt catctttgga gaggccaagt ggtcttagcc tcagtctctg  
960  
tctctaaata ttccaccata aaacagctga gttatttatg aattagaagc tatagctcac  
1020  
attttcaatc ctctatttct ttttttaaata ataactttct actctgatga gagaatgtgg  
1080  
ttttaatctc tctctcacat tttgatgatt tagacagact cccctcttct ctcctagtca  
1140  
ataaacccat tgatgatcta tttcccagct tatccccaag aaaacttttg aaaggaaaga  
1200  
gtagacccaa agatgttatt ttctgctgtt tgaattttgt ctccccacc ccaacttggc  
1260  
tagtaataaa cacttactga agaagaagca ataagagaaa gatatttgta atctctccag  
1320  
cccatgatct cggtttttctt aactgtgat cttaaaagt accaaaccaa agtcattttc  
1380  
agtttgaggc aaccaaacct ttctactgct gttgacatct tcttattaca gcaacacct  
1440  
tctaggagtt tcctgagctc tccactggag tctctccctt ctgtcgtctt ctcgcagcgg  
1500

tacccc  
1505

<210> 660  
<211> 261  
<212> PRT  
<213> Homo sapiens

<400> 660  
Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu  
1 5 10 15  
Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr  
20 25 30  
Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly  
35 40 45  
Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg  
50 55 60  
Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg  
65 70 75 80  
Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val  
85 90 95  
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser  
100 105 110  
Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser  
115 120 125  
Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val  
130 135 140  
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly  
145 150 155 160  
Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe  
165 170 175  
Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met  
180 185 190  
Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala  
195 200 205  
Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly  
210 215 220  
Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile  
225 230 235 240  
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser  
245 250 255  
Lys His Asp Tyr Val  
260

<210> 661  
<211> 451  
<212> DNA  
<213> Homo sapiens

<400> 661  
nnacgcgtgt agtttggtga tcggcgcgga actcgccgag tctgatctcg aggagcttcc  
60  
cccatggagc agattttaac cttgcttgcc ggaggcggtg acgacgagcc agagtggcat  
120

gacaaggcat tatgtgcccc gactgatccg gaggcattct tccctgaaaa ggggtggatcc  
 180  
 acccgtgagg ccaagcgcac ctgtgagtcc tgtgagggtcc gccaggagtg cttgggagtac  
 240  
 gcccttgcca atgacgagag gtccggaatc tggggcggat tgtccgagat ggagaggcgt  
 300  
 cggctgcgca agcgggcgtg acctgacgtc ggagcgcggt tattgacacg gcccggtaaa  
 360  
 atgccctgtc tgccccggat ggctgtctgc acgatgcggc atatgcatg atcgagacg  
 420  
 tgggtgtgcat cccgtgtctc atgacgtcga c  
 451

<210> 662

<211> 85

<212> PRT

<213> Homo sapiens

<400> 662

Met	Asp	Glu	Ile	Leu	Thr	Leu	Leu	Ala	Gly	Gly	Gly	Asp	Asp	Glu	Pro
1				5					10					15	
Glu	Trp	His	Asp	Lys	Ala	Leu	Cys	Ala	Gln	Thr	Asp	Pro	Glu	Ala	Phe
			20					25					30		
Phe	Pro	Glu	Lys	Gly	Gly	Ser	Thr	Arg	Glu	Ala	Lys	Arg	Ile	Cys	Glu
			35				40					45			
Ser	Cys	Glu	Val	Arg	Gln	Glu	Cys	Leu	Glu	Tyr	Ala	Leu	Ala	Asn	Asp
	50				55					60					
Glu	Arg	Phe	Gly	Ile	Trp	Gly	Gly	Leu	Ser	Glu	Met	Glu	Arg	Arg	Arg
65				70					75				80		
Leu	Arg	Lys	Arg	Ala											
				85											

<210> 663

<211> 552

<212> DNA

<213> Homo sapiens

<400> 663

ctcgagcgtc tcgacgccga cgccgcccag ggagccaagg aagacctctc gcagcgcgac  
 60  
 ccctacgacg tgcctcgtct agggggcgggt cccgcegggt ccgcgggcgc cgtgtacgag  
 120  
 gctcgtaagg gcattcgcac cgccatgggt ggggtctcgga tcggcgggcca ggtactcgat  
 180  
 accgaggcca tcgacaacct catctcgggt ccgcacacca ccggtccgag tctggccgac  
 240  
 gccctccgca gccacgtcaa cgactacaac attgacgtta ttgagcgtca gaccgccagc  
 300  
 gccatagaga ccaccggcgg tatgaccacc gtgcatctga ccgacggcga cctgcgggag  
 360  
 cgctcagtca tcgtggccac cgggtgccgc tggcgcaacc ttggcggtacc tggcgaggag  
 420  
 gaataccgca ccaaggggtg gacctactgc ccgactgag atggcccgtt attcacaggc  
 480

aaaaagggtgg ccgctcgtcgg aggtggaaac tccggtattg aggccgctat cgacctcgcc  
 540  
 ggcgtcgtcg ac  
 552

<210> 664  
 <211> 184  
 <212> PRT  
 <213> Homo sapiens

<400> 664  
 Leu Glu Arg Leu Asp Ala Asp Ala Ala Gln Gly Ala Lys Glu Asp Leu  
 1 5 10 15  
 Ser Gln Arg Asp Pro Tyr Asp Val Leu Val Val Gly Ala Gly Pro Ala  
 20 25 30  
 Gly Ala Ala Ala Val Tyr Ala Ala Arg Lys Gly Ile Arg Thr Ala  
 35 40 45  
 Met Val Gly Ser Arg Ile Gly Gly Gln Val Leu Asp Thr Glu Ala Ile  
 50 55 60  
 Asp Asn Leu Ile Ser Val Pro His Thr Thr Gly Pro Arg Leu Ala Asp  
 65 70 75 80  
 Ala Leu Arg Ser His Val Asn Asp Tyr Asn Ile Asp Val Ile Glu Arg  
 85 90 95  
 Gln Thr Ala Ser Ala Ile Glu Thr Thr Gly Gly Met Thr Thr Val His  
 100 105 110  
 Leu Thr Asp Gly Asp Leu Arg Ala Arg Ser Val Ile Val Ala Thr Gly  
 115 120 125  
 Ala Arg Trp Arg Asn Leu Gly Val Pro Gly Glu Glu Glu Tyr Arg Thr  
 130 135 140  
 Lys Gly Val Thr Tyr Cys Pro His Cys Asp Gly Pro Leu Phe Thr Gly  
 145 150 155 160  
 Lys Lys Val Ala Val Val Gly Gly Gly Asn Ser Gly Ile Glu Ala Ala  
 165 170 175  
 Ile Asp Leu Ala Gly Val Val Asp  
 180

<210> 665  
 <211> 352  
 <212> DNA  
 <213> Homo sapiens

<400> 665  
 acgcgtacag ttcgccgtcg aggttgaaca ccacgatcgg tgtaccggtc acttcgtcga  
 60  
 acacgctctt catttcgccc ggcagcagtt cggcgccggc gcagacaaag gtccaggcct  
 120  
 cgctcacgcg gtggccccgg ccagcggcct ttccaggatc tcgaaacgca ggtcgtcgcg  
 180  
 cttgggggatg ccgaatcggt cgtcgccata cgggaacggc ttcttgatgc cggtgcgag  
 240  
 gtacccgagg cgctcgtaga agcgatcaga tcgcgcgcac gtcgatcact gtcattctga  
 300  
 ttaccggcac gttccattcg cgcgcggcgt gggcttcggc ggcgtccatc aa  
 352

<210> 666  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 666  
 Met Glu Arg Ala Gly Asn Ala Asp Asp Ser Asp Arg Arg Ala Arg Asp  
 1 5 10 15  
 Leu Ile Ala Ser Thr Ser Ala Ala Ala Thr Cys Ala Pro Ala Ser Arg  
 20 25 30  
 Ser Arg Ser Arg Met Ala Thr Asn Asp Ser Ala Ser Pro Ser Ala Thr  
 35 40 45  
 Thr Cys Val Ser Arg Ser Trp Lys Ser Arg Trp Pro Gly Pro Pro Arg  
 50 55 60  
 Glu Arg Gly Leu Asp Leu Cys Leu Arg Arg Arg Thr Ala Ala Gly  
 65 70 75 80  
 Arg Asn Glu Glu Arg Val Arg Arg Ser Asp Arg Tyr Thr Asp Arg Gly  
 85 90 95  
 Val Gln Pro Arg Arg Arg Thr Val Arg  
 100 105

<210> 667  
 <211> 391  
 <212> DNA  
 <213> Homo sapiens

<400> 667  
 nacgcgtacg aatcgggtgtt gcgtcgcaac ccaggggagg ccgagttcca ccaggtgtg  
 60  
 cgggagatct ttgaatctct cggcccgggtg ctcgacaaga atccgcagta cgtggaggca  
 120  
 gccgtgttgt cgcgcattctg cgaaccggaa cgccagatca ttttccgggt gccgtgggtt  
 180  
 gacgacgagg gcaagatccg tatcaaccgt ggcttccgcg ttgaatatc gtcggtactg  
 240  
 gggccgtata aggggtggatt gcgattccac ccctcgggtg acttaggaac gattaagttc  
 300  
 cttggttttg agcagatctt caaaaatgct ctgactggca tgccgatcgg tggcgcgaaag  
 360  
 ggtgggtcgg actttgatcc ccatgacgcg t  
 391

<210> 668  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 668  
 Xaa Ala Tyr Glu Ser Val Leu Arg Arg Asn Pro Gly Glu Ala Glu Phe  
 1 5 10 15  
 His Gln Ala Val Arg Glu Ile Phe Glu Ser Leu Gly Pro Val Leu Asp  
 20 25 30  
 Lys Asn Pro Gln Tyr Val Glu Ala Ala Val Leu Ser Arg Ile Cys Glu

```

      35          40          45
Pro Glu Arg Gln Ile Ile Phe Arg Val Pro Trp Val Asp Asp Glu Gly
  50          55          60
Lys Ile Arg Ile Asn Arg Gly Phe Arg Val Glu Tyr Ser Ser Val Leu
  65          70          75          80
Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Tyr Leu Gly
      85          90          95
Thr Ile Lys Phe Leu Gly Phe Glu Gln Ile Phe Lys Asn Ala Leu Thr
      100          105          110
Gly Met Pro Ile Gly Gly Ala Lys Gly Gly Ser Asp Phe Asp Pro His
      115          120          125
Asp Ala
      130

```

<210> 669  
 <211> 707  
 <212> DNA  
 <213> Homo sapiens

```

<400> 669
nngagtcgct tccccgtcta agtcatcgct ggtggtgctg gcatggccgt caacaaggga
60
attgagaaca cccttgctgc cttcgccac gcggtcgagg tgggatgcac ctacctgaa
120
actgacgttc acgcgaccag cgacggggtg ctagtggcct tccacgatcc gatactcgat
180
cgcgtcactg aatcaggcgg agtcatcgcc gccatgccgt ggcacaaggc caaacaagcc
240
aagggttggtg gcgaaccgat cccacacctta gatgagattt tcgacgcctt tcccgcgcg
300
ttcatcaata tcgacatcaa gcatgatggc gccaccatgc cgctcatcga cgttctttcc
360
cgtcaccggg cttggagtcg ggtttgcgc gggtcgttca gcagtaaagc catccagacc
420
ttccgtcgcc tgggtcaggg acgcactgcg actgcagtgg ggtcgggtgg agtcnnggt
480
gggctgtcat cagccctcat agcatgcaga tggcacagtc ccatgggaat gcgtaccagg
540
tgccgcaccg cttgaccgg tnatggggtg ccccttgatga caccgacctt cattaaagct
600
gcccatcgtc aggggcgagc tgttcatgtc tggacgggta atgagatctc tgaggctcga
660
gaactgatgg atatgggggt cgacggcatc gtcacagatc gtccgga
707

```

<210> 670  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

```

<400> 670
Met Ala Val Asn Lys Gly Ile Glu Asn Thr Leu Ala Ala Phe Gly His
1          5          10          15
Ala Val Glu Val Gly Cys Thr Tyr Leu Glu Thr Asp Val His Ala Thr

```



```

      20      25      30
Ser Asp Gly Val Leu Val Ala Phe His Asp Pro Ile Leu Asp Arg Val
      35      40      45
Thr Glu Ser Gly Gly Val Ile Ala Ala Met Pro Trp His Lys Val Lys
      50      55      60
Gln Ala Lys Val Gly Gly Glu Pro Ile Pro Thr Leu Asp Glu Ile Phe
      65      70      75      80
Asp Ala Phe Pro Asp Ala Phe Ile Asn Ile Asp Ile Lys His Asp Gly
      85      90      95
Ala Thr Met Pro Leu Ile Asp Val Leu Ser Arg His Arg Ala Trp Ser
      100      105      110
Arg Val Cys Val Gly Ser Phe Ser Ser Lys Arg Ile Gln Thr Phe Arg
      115      120      125
Arg Leu Val Gln Gly Arg Thr Ala Thr Ala Val Gly Ser Val Gly Val
      130      135      140
Xaa Ala Gly Leu Ser Ser Ala Leu Ile Ala Cys Arg Trp His Ser Pro
      145      150      155      160
Met Gly Met Arg Thr Arg Cys Arg Thr Ala
      165      170

```

&lt;210&gt; 671

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 671

```

acgcgtgggc cttcgggttg atgggatcag aaggggacgg gacctgtaga aaggggcctg
60
cagctcagag catggggcgg ccttggtctca ctacgcctgc agctgtgaat tcgttctccg
120
gtgctggaga gggatctggt tatctccatt ctcttgcttc cacgtggaaa ggaaggacgt
180
gcgctctcat cctacgtggt ttgagaaatc gcattgtccc cagctctgcg ggaggatctg
240
gggacgcagt ggggaaccag acaggcagtt ggaggtctag tgcgcgccag aagccagttc
300
ccaccagggg tgccatttgc tgggcgcctt agggagctgc gtgggcatcc agaggagtga
360
gtcgcctcct gctctgctca gtgcccactt ccccgggcag ggcaggcggtt attaacgtag
420
agggagaaca cccatgcaca caac
444

```

&lt;210&gt; 672

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 672

```

Met Gly Ser Glu Gly Asp Gly Thr Cys Arg Lys Gly Pro Ala Ala Gln
1      5      10      15
Ser Met Gly Arg Pro Trp Leu Thr Thr Pro Ala Ala Val Asn Ser Phe
      20      25      30
Ser Gly Ala Gly Glu Gly Ser Gly Tyr Leu His Ser Leu Val Ser Thr

```

```

      35          40          45
Trp Lys Gly Arg Thr Cys Ala Leu Ile Leu Arg Val Leu Arg Asn Arg
  50          55          60
Ile Val Pro Ser Ser Ala Gly Gly Ser Gly Asp Ala Val Gly Asn Gln
  65          70          75          80
Thr Gly Ser Trp Arg Ser Ser Ala Arg Gln Lys Pro Val Pro Thr Gln
      85          90          95
Gly Ala Ile Cys Trp Ala Pro
      100

```

&lt;210&gt; 673

&lt;211&gt; 452

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 673

```

acgcgtccct gcagaaatcc tctcggccta ggatcatccgc aagatgtggc agggcatgca
  60
ccgtgaaagc cttcaagtct gccgcagcaa gaccgcacgc ctgctgaaat tcgcagttgt
 120
gccgcgggtcc ctgatgcgga caaactcggc caccacgatc agcctgacgc ttgcggacca
 180
acgttcaaat actgtgcact tgaaacgtcc gggccgcac acctgggtga ctttgtgcga
 240
ccgacattac ttatgttcac gctctttcag ttcttgtcaa taccgtatct ttcgtcgacg
 300
tctccatcag aaaaatgtcg gtgttaccgc accgcagacg atgcgtaccc ttgcgctgac
 360
gatggaggcc ttgaaaagtg cattagccac tactggggcga atctacggca aaaagctgtt
 420
actaggcggt gattggggag gcccgtagtg gc
 452

```

&lt;210&gt; 674

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 674

```

Met Trp Gln Gly Met His Arg Glu Ser Leu Gln Val Cys Arg Ser Lys
  1          5          10          15
Thr Ala Arg Leu Leu Lys Phe Ala Val Val Pro Arg Ser Leu Met Arg
      20          25          30
Thr Asn Ser Ala Thr Thr Ile Ser Leu Thr Leu Ala Asp Gln Arg Ser
      35          40          45
Asn Thr Val His Leu Lys Arg Pro Gly Arg Ile Thr Trp Val Thr Leu
      50          55          60
Cys Asp Arg His Tyr Leu Cys Ser Arg Ser Phe Ser Ser Cys Gln Tyr
      65          70          75          80
Arg Ile Phe Arg Arg Arg Leu His Gln Lys Asn Val Gly Val Thr Ala
      85          90          95
Pro Gln Thr Met Arg Thr Leu Ala Leu Thr Met Glu Ala Leu Lys Ser
      100          105          110
Ala Leu Ala Thr Thr Gly Arg Ile Tyr Gly Lys Lys Leu Leu Leu Gly

```

115  
Gly Asp Trp Gly Gly Pro  
130

120

125

&lt;210&gt; 675

&lt;211&gt; 8564

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 675

atgtcgggct ccacacagct tgtggcacag acgtggaggg ccactgagcc ccgctacccg  
60  
ccccacagcc ttctctaccc agtgcagatc gcccgagcgc acacggacgt cgggctcctg  
120  
gagtaccagc accactcccg cgactatgcc tcccacctgt cggcgggctc catcatccag  
180  
ccccagcggc ggaggccctc cctgctgtct gagttccagc cggggaatga acgggtcccag  
240  
gagctccacc tgcggccaga gtcccaactca tacctgcccg agctggggaa gtcagagatg  
300  
gagttcattg aaagcaagcg ccctcggcta gagctgctgc ctgaccccct gctgcgaccg  
360  
tcacccctgc tggccacggg ccagcctgcg ggatctgaag acctcaccaa ggaccgtagc  
420  
ctgacgggca agctggaacc ggtgtctccc cccagccccc cgcacactga ccctgagctg  
480  
gagctggtgc cgccacggct gtccaaggag gagctgatcc agaacatgga ccgctgtagc  
540  
cgagagatca ccatggtaga gcagcagatc tctaagctga agaagaagca gcaacagctg  
600  
gaggaggagg ctgccaagcc gcccgagcct gagaagcccg tgtcaccgcc gcccatcgag  
660  
tcgaagcacc gcagcctggt gcagatcatc tacgacgaga accggaagaa ggctgaagct  
720  
gcacatcgga ttctggaagg cctggggccc caggtggagc tgccgctgta caaccagccc  
780  
tccgacaccc ggcagtatca tgagaacatc aaaataaacc aggcgatgctg gaagaagcta  
840  
atcttgctact tcaagaggag gaatcacgct cggaaacaat gggagcagaa gttctgccag  
900  
cgctatgacc agctcatgga ggcctgggaa aaaaagggtg agcgcatcga gaacaacccc  
960  
cggcggcggg ccaaggagag caaggcgcgc gactactacg aaaagcagtt ccctgagatc  
1020  
cgcaagcagc gcgagctgca ggagcgcagc cagggcaggg tgggccagcg gggcagtggg  
1080  
ctgtccatgt cggccgcccc cagcagcac gaggtgtcag agatcatcga tggcctctca  
1140  
gagcaggaga acctggagaa gcagatgcgc cagctggccc tgatcccgcc catgctgtac  
1200  
gacgctgacc agcagcgcac caagttcatc aacatgaacg ggcttatggc cgaccccatg  
1260  
aagggtgtaca aagaccgcca ggtcatgaac atgtggagtg agcaggagaa ggagaccttc  
1320

cgggagaagt tcatgcagca tcccaagaac tttggcctga tcgcatcatt cctggagagg  
1380  
aagacagtgg ctgagtgcgt cctctattac tacctgacta agaagaatga gaactataag  
1440  
agcctggtga gacggagcta tcggcgccgc ggcaagagcc agcagcagca acaacagcag  
1500  
cagcagcagc agcagcagca gcagcagcag cagcccatgc cccgcagcag ccaggaggag  
1560  
aaagatgaga aggagaagga aaaggaggcg gagaaggagg aggagaagcc ggaggtggag  
1620  
aacgacaagg aagacctcct caaggagaag acagacgaca cctcagggga ggacaacgac  
1680  
gagaaggagg ctgtggcctc caaaggccgc aaaactgcc aagccaggg aagacgcaa  
1740  
ggccgcacat cccgctcaat ggctaagag gccaacagcg aggaggccat cccccccag  
1800  
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Thr	His	Thr	Asp	Val	Gly	Leu	Leu	Glu	Tyr	Gln	His	His	Ser	Arg	Asp
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 Lys Pro Ala His Glu Gly Leu Val Ala Thr Val Lys Glu Ala Gly Arg  
                                  1410                      1415                      1420  
 Ser Ile His Glu Ile Pro Arg Glu Glu Leu Arg His Thr Pro Glu Leu  
                                  1425                      1430                      1435                      1440  
 Pro Leu Ala Pro Arg Pro Leu Lys Glu Gly Ser Ile Thr Gln Gly Thr  
                                  1445                      1450                      1455  
 Pro Leu Lys Tyr Asp Thr Gly Ala Ser Thr Thr Gly Ser Lys Lys His

1460 1465 1470  
 Asp Val Arg Ser Leu Ile Gly Ser Pro Gly Arg Thr Phe Pro Pro Val  
 1475 1480 1485  
 His Pro Leu Asp Val Met Ala Asp Ala Arg Ala Leu Glu Arg Ala Cys  
 1490 1495 1500  
 Tyr Glu Glu Ser Leu Lys Ser Arg Pro Gly Thr Ala Ser Ser Ser Gly  
 1505 1510 1515 1520  
 Gly Ser Ile Ala Arg Gly Ala Pro Val Ile Val Pro Glu Leu Gly Lys  
 1525 1530 1535  
 Pro Arg Gln Ser Pro Leu Thr Tyr Glu Asp His Gly Ala Pro Phe Ala  
 1540 1545 1550  
 Gly His Leu Pro Arg Gly Ser Pro Val Thr Thr Arg Glu Pro Thr Pro  
 1555 1560 1565  
 Arg Leu Gln Glu Gly Ser Leu Ser Ser Ser Lys Ala Ser Gln Asp Arg  
 1570 1575 1580  
 Lys Leu Thr Ser Thr Pro Arg Glu Ile Ala Lys Ser Pro His Ser Thr  
 1585 1590 1595 1600  
 Val Pro Glu His His Pro His Pro Ile Ser Pro Tyr Glu His Leu Leu  
 1605 1610 1615  
 Arg Gly Val Ser Gly Val Asp Leu Tyr Arg Ser His Ile Pro Leu Ala  
 1620 1625 1630  
 Phe Asp Pro Thr Ser Ile Pro Arg Gly Ile Pro Leu Asp Ala Ala Ala  
 1635 1640 1645  
 Ala Tyr Tyr Leu Pro Arg His Leu Ala Pro Asn Pro Thr Tyr Pro His  
 1650 1655 1660  
 Leu Tyr Pro Pro Tyr Leu Ile Arg Gly Tyr Pro Asp Thr Ala Ala Leu  
 1665 1670 1675 1680  
 Glu Asn Arg Gln Thr Ile Ile Asn Asp Tyr Ile Thr Ser Gln Gln Met  
 1685 1690 1695  
 His His Asn Thr Ala Thr Ala Met Ala Gln Arg Ala Asp Met Leu Arg  
 1700 1705 1710  
 Gly Leu Ser Pro Arg Glu Ser Ser Leu Ala Leu Asn Tyr Ala Ala Gly  
 1715 1720 1725  
 Pro Arg Gly Ile Ile Asp Leu Ser Gln Val Pro His Leu Pro Val Leu  
 1730 1735 1740  
 Val Pro Pro Thr Pro Gly Thr Pro Ala Thr Ala Met Asp Arg Leu Ala  
 1745 1750 1755 1760  
 Tyr Leu Pro Thr Ala Pro Gln Pro Phe Ser Ser Arg His Ser Ser Ser  
 1765 1770 1775  
 Pro Leu Ser Pro Gly Gly Pro Thr His Leu Thr Lys Pro Thr Thr Thr  
 1780 1785 1790  
 Ser Ser Ser Glu Arg Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp  
 1795 1800 1805  
 Arg Glu Arg Glu Lys Ser Ile Leu Thr Ser Thr Thr Thr Val Glu His  
 1810 1815 1820  
 Ala Pro Ile Trp Arg Pro Gly Thr Glu Gln Ser Ser Gly Ser Ser Gly  
 1825 1830 1835 1840  
 Ser Ser Gly Gly Gly Gly Ser Ser Ser Arg Pro Ala Ser His Ser  
 1845 1850 1855  
 His Ala His Gln His Ser Pro Ile Ser Pro Arg Thr Gln Asp Ala Leu  
 1860 1865 1870  
 Gln Gln Arg Pro Ser Val Leu His Asn Thr Gly Met Lys Gly Ile Ile  
 1875 1880 1885  
 Thr Ala Val Glu Pro Ser Thr Pro Thr Val Leu Arg Ser Thr Ser Thr

1890	1895	1900
Ser Ser Pro Val Arg	Pro Ala Ala Thr Phe	Pro Pro Ala Thr His Cys
1905	1910	1915
Pro Leu Gly Gly Thr	Leu Asp Gly Val Tyr	Pro Thr Leu Met Glu Pro
1925	1930	1935
Val Leu Leu Pro Lys	Glu Ala Pro Arg Val Ala Arg	Pro Glu Arg Pro
1940	1945	1950
Arg Ala Asp Thr Gly	His Ala Phe Leu Ala Lys	Pro Pro Ala Arg Ser
1955	1960	1965
Gly Leu Glu Pro Ala	Ser Ser Pro Ser Lys	Gly Ser Glu Pro Arg Pro
1970	1975	1980
Leu Val Pro Pro Val	Ser Gly His Ala Thr	Ile Ala Arg Thr Pro Ala
1985	1990	1995
Lys Asn Leu Ala Pro	His His Ala Ser	Pro Asp Pro Pro Ala Pro Pro
2005	2010	2015
Ala Ser Ala Ser Asp	Pro His Arg Glu Lys	Thr Gln Ser Lys Pro Phe
2020	2025	2030
Ser Ile Gln Glu Leu	Glu Leu Arg Ser Leu	Gly Tyr His Gly Ser Ser
2035	2040	2045
Tyr Ser Pro Glu Gly	Val Glu Pro Val Ser	Pro Val Ser Ser Pro Ser
2050	2055	2060
Leu Thr His Asp Lys	Gly Leu Pro Lys His	Leu Glu Glu Leu Asp Lys
2065	2070	2075
Ser His Leu Glu Gly	Glu Leu Arg Pro Lys	Gln Pro Gly Pro Val Lys
2085	2090	2095
Leu Gly Gly Glu Ala	Ala His Leu Pro His	Leu Arg Pro Leu Pro Glu
2100	2105	2110
Ser Gln Pro Ser Ser	Ser Pro Leu Leu Gln	Thr Ala Pro Gly Val Lys
2115	2120	2125
Gly His Gln Arg Val	Val Thr Leu Ala Gln	His Ile Ser Glu Val Ile
2130	2135	2140
Thr Gln Asp Tyr Thr	Arg His His Pro Gln	Gln Leu Ser Ala Pro Leu
2145	2150	2155
Pro Ala Pro Leu Tyr	Ser Phe Pro Gly Ala	Ser Cys Pro Val Leu Asp
2165	2170	2175
Leu Arg Arg Pro Pro	Ser Asp Leu Tyr Leu	Pro Pro Pro Asp His Gly
2180	2185	2190
Ala Pro Ala Arg Gly	Ser Pro His Ser Glu	Gly Gly Lys Arg Ser Pro
2195	2200	2205
Glu Pro Asn Lys Thr	Ser Val Leu Gly Gly	Gly Glu Asp Gly Ile Glu
2210	2215	2220
Pro Val Ser Pro Pro	Glu Gly Met Thr Glu	Pro Gly His Ser Arg Ser
2225	2230	2235
Ala Val Tyr Pro Leu	Leu Tyr Arg Asp Gly	Glu Gln Thr Glu Pro Ser
2245	2250	2255
Arg Met Gly Ser Lys	Ser Pro Gly Asn Thr	Ser Gln Pro Pro Ala Phe
2260	2265	2270
Phe Ser Lys Leu Thr	Glu Ser Asn Ser Ala	Met Val Lys Ser Lys Lys
2275	2280	2285
Gln Glu Ile Asn Lys	Lys Leu Asn Thr His	Asn Arg Asn Glu Pro Glu
2290	2295	2300
Tyr Asn Ile Ser Gln	Pro Gly Thr Glu Ile	Phe Asn Met Pro Ala Ile
2305	2310	2315
Thr Gly Thr Gly Leu	Met Thr Tyr Arg Ser	Gln Ala Val Gln Glu His

2325                      2330                      2335  
 Ala Ser Thr Asn Met Gly Leu Glu Ala Ile Ile Arg Lys Ala Leu Met  
                          2340                      2345                      2350  
 Gly Lys Tyr Asp Gln Trp Glu Glu Ser Pro Pro Leu Ser Ala Asn Ala  
                          2355                      2360                      2365  
 Phe Asn Pro Leu Asn Ala Ser Ala Ser Leu Pro Ala Ala Met Pro Ile  
                          2370                      2375                      2380  
 Thr Ala Ala Asp Gly Arg Ser Asp His Thr Leu Thr Ser Pro Gly Gly  
 2385                      2390                      2395                      2400  
 Gly Gly Lys Ala Lys Val Ser Gly Arg Pro Ser Ser Arg Lys Ala Lys  
                          2405                      2410                      2415  
 Ser Pro Ala Pro Gly Leu Ala Ser Gly Asp Arg Pro Pro Ser Val Ser  
                          2420                      2425                      2430  
 Ser Val His Ser Glu Gly Asp Cys Asn Arg Arg Thr Pro Leu Thr Asn  
                          2435                      2440                      2445  
 Arg Val Trp Glu Asp Arg Pro Ser Ser Ala Gly Ser Thr Pro Phe Pro  
                          2450                      2455                      2460  
 Tyr Asn Pro Leu Ile Met Arg Leu Gln Ala Gly Val Met Ala Ser Pro  
 2465                      2470                      2475                      2480  
 Pro Pro Pro Gly Leu Pro Ala Gly Ser Gly Pro Leu Ala Gly Pro His  
                          2485                      2490                      2495  
 His Ala Trp Asp Glu Glu Pro Lys Pro Leu Leu Cys Ser Gln Tyr Glu  
                          2500                      2505                      2510  
 Thr Leu Ser Asp Ser Glu  
                          2515

<210> 677  
 <211> 345  
 <212> DNA  
 <213> Homo sapiens

<400> 677  
 gtaatgcaag gtgaacgccc aatggctgcg cagaacaaga gcattggtca gttcaccctt  
 60  
 gagggatatag ctccggcacc ccggtggtgtt ccacagattg aagttacttt cgatatcgat  
 120  
 gccaacggta tcttgaatgt gagcgcaaag gataaggcta ccggttaagga acagaagatt  
 180  
 cgcacgcaag cttcaagtgg tttagatcag gaagaaatcg acagaatgaa agctgaggca  
 240  
 gaacagaatg cagcagcagg caaggctgaa cgcgaaaaga ttgataagct gaaccaagct  
 300  
 gactcaatga tttccccccc cgaaaactcc tgaaagacaa cgatn  
 345

<210> 678  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 678  
 Val Met Gln Gly Glu Arg Pro Met Ala Ala Gln Asn Lys Ser Ile Gly  
 1                      5                      10                      15  
 Gln Phe Thr Leu Glu Gly Ile Ala Pro Ala Arg Arg Gly Val Pro Gln

```

      20      25      30
Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Ser
      35      40      45
Ala Lys Asp Lys Ala Thr Gly Lys Glu Gln Lys Ile Arg Ile Glu Ala
      50      55      60
Ser Ser Gly Leu Ser Gln Glu Glu Ile Asp Arg Met Lys Ala Glu Ala
65      70      75      80
Glu Gln Asn Ala Ala Ala Gly Lys Ala Glu Arg Glu Lys Ile Asp Lys
      85      90      95
Leu Asn Gln Ala Asp Ser Met Ile Ser Pro Pro Glu Asn Ser
      100      105      110

```

&lt;210&gt; 679

&lt;211&gt; 362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 679

```

acgcgtgacg tcaccgctcc atggggaaga tgacgactat ccctgtgaaa gtaaagcata
60
atgggaaaaa tgtacgttaa atgtgctaac gcgcagtatg atgtatctat gaatcttgag
120
gggtacaggcc tggatttcaa gcgtgccatt gctgacgtca cgcatgtgcc acccgaacgc
180
caaaaagtac tcatcaaggg aggattgcta aaagacgata cccattagg taaagtgggt
240
gcgcgtgcag gacagcagtt catggtgctg ggtgctgtgg gtgagctgcc caaggcccca
300
gaaaaacctg tgctgttcct ggaggatttg ccggaagacg agctcaacaa ggctaaggat
360
cc
362

```

&lt;210&gt; 680

&lt;211&gt; 100

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 680

```

Met Gly Lys Met Tyr Val Lys Cys Ala Asn Ala Gln Tyr Asp Val Ser
  1      5      10      15
Met Asn Leu Glu Gly Thr Gly Leu Asp Phe Lys Arg Ala Ile Ala Asp
      20      25      30
Val Thr His Val Pro Pro Glu Arg Gln Lys Val Leu Ile Lys Gly Gly
      35      40      45
Leu Leu Lys Asp Asp Thr Pro Leu Gly Lys Val Gly Ala Arg Ala Gly
      50      55      60
Gln Gln Phe Met Val Leu Gly Ala Val Gly Glu Leu Pro Lys Ala Pro
65      70      75      80
Glu Lys Pro Val Leu Phe Leu Glu Asp Leu Pro Glu Asp Glu Leu Asn
      85      90      95
Lys Ala Lys Asp
      100

```

<210> 681  
 <211> 357  
 <212> DNA  
 <213> Homo sapiens

<400> 681  
 acgcgtccaa atggacaaac gcttgatgat ttctaccatg aaattagagc aaaatatcca  
 60  
 gaacaattac tgatggcaga ctgttcaaca gtagaagaaa tgattcacgc tgatgaactc  
 120  
 gggttttgatt ttatcggaag tacttttagta ggatatacaa aacaaagtaa aggtgacaaa  
 180  
 atcgaagaaa atgactttga aatcttgaga acagtttttag aacgaattaa acatccacta  
 240  
 attgcagaag gcaatatcga tacacctgaa aagggtgaaac gtgtgcttga gttaggcgcg  
 300  
 tatagtgtcg ttgtaggggc agcgattact cgtccacaac tcatcacgaa aaaattt  
 357

<210> 682  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 682  
 Thr Arg Pro Asn Gly Gln Thr Leu Asp Asp Phe Tyr His Glu Ile Arg  
 1 5 10 15  
 Ala Lys Tyr Pro Glu Gln Leu Leu Met Ala Asp Cys Ser Thr Val Glu  
 20 25 30  
 Glu Met Ile His Ala Asp Glu Leu Gly Phe Asp Phe Ile Gly Ser Thr  
 35 40 45  
 Leu Val Gly Tyr Thr Lys Gln Ser Lys Gly Asp Lys Ile Glu Glu Asn  
 50 55 60  
 Asp Phe Glu Ile Leu Arg Thr Val Leu Glu Arg Ile Lys His Pro Leu  
 65 70 75 80  
 Ile Ala Glu Gly Asn Ile Asp Thr Pro Glu Lys Val Lys Arg Val Leu  
 85 90 95  
 Glu Leu Gly Ala Tyr Ser Val Val Val Gly Ser Ala Ile Thr Arg Pro  
 100 105 110  
 Gln Leu Ile Thr Lys Lys Phe  
 115

<210> 683  
 <211> 411  
 <212> DNA  
 <213> Homo sapiens

<400> 683  
 ntctccgacc gcgtggtaaa actggcgacc ttaattgctg aagatgagca agctgaaatg  
 60  
 aatattgttt tgcccgagc gtggttgcat gattgcgtca gttaccctaa aaaccatgta  
 120  
 ttaagagcac aaagtgcatt acatgcagca gataaagcga ttgtattttt gcgcagtatt  
 180



aattacccca aacaatactt attagcaatt catcatgcaa tttcagcgca cagtgtcagt  
 240  
 ggtaaaatac aggcaatgag tttagaagct caaatagtgc aagatgcaga tagattggat  
 300  
 gcgctagggg caattggcgt ggctcgttgc attcaagtaa gtagccagtt acagcgccca  
 360  
 ctatattctg aagttgaccc cttcagcgag acacgatctc tagtctgcat g  
 411

<210> 684

<211> 137

<212> PRT

<213> Homo sapiens

<400> 684

Xaa	Ser	Asp	Arg	Val	Val	Lys	Leu	Ala	Thr	Leu	Ile	Ala	Glu	Asp	Glu
1				5					10					15	
Gln	Ala	Glu	Met	Asn	Ile	Val	Leu	Pro	Ala	Ala	Trp	Leu	His	Asp	Cys
			20					25					30		
Val	Ser	Tyr	Pro	Lys	Asn	His	Val	Leu	Arg	Ala	Gln	Ser	Ala	Leu	His
		35					40					45			
Ala	Ala	Asp	Lys	Ala	Ile	Val	Phe	Leu	Arg	Ser	Ile	Asn	Tyr	Pro	Lys
		50				55					60				
Gln	Tyr	Leu	Leu	Ala	Ile	His	His	Ala	Ile	Ser	Ala	His	Ser	Val	Ser
65					70				75					80	
Gly	Lys	Ile	Gln	Ala	Met	Ser	Leu	Glu	Ala	Gln	Ile	Val	Gln	Asp	Ala
			85					90					95		
Asp	Arg	Leu	Asp	Ala	Leu	Gly	Ala	Ile	Gly	Val	Ala	Arg	Cys	Ile	Gln
		100					105						110		
Val	Ser	Ser	Gln	Leu	Gln	Arg	Pro	Leu	Tyr	Ser	Glu	Val	Asp	Pro	Phe
		115					120					125			
Ser	Glu	Thr	Arg	Ser	Leu	Val	Cys	Met							
		130				135									

<210> 685

<211> 417

<212> DNA

<213> Homo sapiens

<400> 685

acgcgttgcg ttgcggagtg aacccggaac gatggatgga ttgacactat tcggcctggt  
 60  
 cgccgtcact gcgatgctgg tctgctatgc catggaggac cgcagccact ggttcgtgct  
 120  
 gctgttcgcg gccgcttggc gctcggttcg gcctacggct tcctccaagg cgcttgccg  
 180  
 ttcggcttcg tcgaggcgat atgggcgctc gttgcctgcg gcgtggtgga cgatcaggcc  
 240  
 gcgatgaccg catcgtccgg cttaagcccg gaaacgaaac cgaccagtgc gctggtttga  
 300  
 tgggcggcgc gtcgctggat gcacagegtc tcgacgcgag cgtgatgatg gcctcagcgc  
 360  
 gtgcatgccg acgctgtcgc tcatcgcgct acgctcgacc acggcgcgcg gcaatag  
 417

<210> 686  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 686  
 Met Pro Trp Arg Thr Ala Ala Thr Gly Ser Cys Cys Cys Ser Arg Pro  
 1 5 10 15  
 Leu Gly Ala Arg Phe Gly Leu Arg Leu Pro Pro Arg Arg Leu Ala Val  
 20 25 30  
 Arg Leu Arg Arg Gly Asp Met Gly Ala Arg Cys Leu Arg Arg Gly Gly  
 35 40 45  
 Arg Ser Gly Arg Asp Asp Arg Ile Val Arg Leu Lys Pro Gly Asn Glu  
 50 55 60  
 Thr Asp Gln Cys Ala Gly Leu Met Gly Gly Ala Ser Leu Asp Ala Gln  
 65 70 75 80  
 Arg Leu Asp Ala Ser Val Met Met Ala Ser Ala Arg Ala Cys Arg Arg  
 85 90 95  
 Cys Arg Ser Ser Arg Tyr Ala Arg Pro Arg Arg Ala Ala Ile  
 100 105 110

<210> 687  
 <211> 412  
 <212> DNA  
 <213> Homo sapiens

<400> 687  
 nnacgcgtga ccgaccaact gcgagccacc ctgctcgcca tggctgctat ggggttgac  
 60  
 gacggcatcg atattccgtc tggggcgatt attgaaagct gccgcacctt atcagccgtt  
 120  
 ctcgatgaaa cccacgggtg tgcgacgac gagcttcggg taccacctgc gtgcgcggtt  
 180  
 caattggcgg ccattgagtc gggccccaac caccaccggg gcactccgcc caatgtggcc  
 240  
 gagaccgacc ctgtcacctt cctgcagttg gcaactggct tctcacactg gccagaaatg  
 300  
 cgctcagcag gacgggttca ggcgtctgga tcccacgtcg acgacgttgc tggcgtgttc  
 360  
 ccagtcgttg atatggccgg ggttttccgc gacatttttg ccgacgacta ga  
 412

<210> 688  
 <211> 136  
 <212> PRT  
 <213> Homo sapiens

<400> 688  
 Xaa Arg Val Thr Asp Gln Leu Arg Ala Thr Leu Leu Ala Met Ala Ala  
 1 5 10 15  
 Met Gly Leu His Asp Gly Ile Asp Ile Pro Ser Gly Ala Ile Ile Glu  
 20 25 30  
 Ser Cys Arg Thr Leu Ser Ala Val Leu Asp Glu Thr His Gly Gly Arg

```

      35              40              45
Thr Ile Glu Leu Arg Val Pro Pro Ala Cys Ala Val Gln Leu Ala Ala
      50              55              60
Ile Glu Ser Gly Pro Asn His His Arg Gly Thr Pro Pro Asn Val Ala
65              70              75              80
Glu Thr Asp Pro Val Thr Phe Leu Gln Leu Ala Thr Gly Phe Ser His
      85              90              95
Trp Pro Glu Met Arg Ser Ala Gly Arg Val Gln Ala Ser Gly Ser His
      100             105             110
Val Asp Asp Val Ala Gly Val Phe Pro Val Val Asp Met Ala Gly Val
      115             120             125
Phe Arg Asp Ile Phe Ala Asp Asp
      130             135

```

<210> 689  
 <211> 499  
 <212> DNA  
 <213> Homo sapiens

```

<400> 689
cgcgctgcg c tactcgacgt cgattttcat cacggtaacg gcacccagaa cattttttac
60
ccgcgcaatg acgtgatgtt catatcgctg cacggcgagc cggccgtgtc ctatccctac
120
tattcggggt tcagcgatga agtcggcgca ggtgttggcg aagggttcaa cctcaactac
180
ccgctgccga aaaacaccgc ctgggatacc taccgcgacg ccctgctgca tgcctgcagg
240
aaactccagc aattctcgcc gcaggtattg gtgatctcac tgggggtcga caccttcaag
300
gacgacccga tcagtcactt cctgctggaa ggcgaggatt tcacggggat cggcgagctg
360
atagcgagtg tgggttgccc caccctgttt gtgatggaag gcggctatat ggtcgatgaa
420
atcggaatca acgcggtgaa cgtactgcat ggcttcgaga gcaagcgcgc ttgagcatcc
480
gcccgaagac ggcgtgata
499

```

<210> 690  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

```

<400> 690
Arg Val Ala Val Leu Asp Val Asp Phe His His Gly Asn Gly Thr Gln
      1              5              10              15
Asn Ile Phe Tyr Pro Arg Asn Asp Val Met Phe Ile Ser Leu His Gly
      20              25              30
Glu Pro Ala Val Ser Tyr Pro Tyr Tyr Ser Gly Phe Ser Asp Glu Val
      35              40              45
Gly Ala Gly Val Gly Glu Gly Phe Asn Leu Asn Tyr Pro Leu Pro Lys
      50              55              60
Asn Thr Ala Trp Asp Thr Tyr Arg Asp Ala Leu Leu His Ala Cys Arg

```

```

65          70          75          80
Lys Leu Gln Gln Phe Ser Pro Gln Val Leu Val Ile Ser Leu Gly Val
          85          90          95
Asp Thr Phe Lys Asp Asp Pro Ile Ser His Phe Leu Leu Glu Gly Glu
          100         105         110
Asp Phe Ile Gly Ile Gly Glu Leu Ile Ala Ser Val Gly Cys Pro Thr
          115         120         125
Leu Phe Val Met Glu Gly Gly Tyr Met Val Asp Glu Ile Gly Ile Asn
          130         135         140
Ala Val Asn Val Leu His Gly Phe Glu Ser Lys Arg Ala
145          150          155

```

&lt;210&gt; 691

&lt;211&gt; 336

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 691

```

ntgctgctg aaaacgtgca ggcggcgca tcagcgactg gcgagcgctt tggctggagt
60
tcgcaaaggc aaggcccctg ggagttggcc tgcgacatcg cgctgccgtg cgccaccag
120
aacgaactgg acgccgacgc cgccgcacg ctgctgcgca acggtgcct ttgctggct
180
ggaggcgcca atatgccgcc cgcgcttgag gctgtggata tctttatcga ggcgggcatt
240
ctgttcgcgc ccggcaaggc atccaatgcc ggcggcgctgg cctggaatg
300
tcgcagaacg ccatgcccct gctgtggacc gccggc
336

```

&lt;210&gt; 692

&lt;211&gt; 112

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 692

```

Xaa Leu Arg Glu Asn Val Gln Arg Gly Ala Ser Ala Thr Gly Glu Arg
1      5      10      15
Phe Gly Trp Ser Ser Gln Arg Gln Gly Pro Trp Glu Leu Ala Cys Asp
20     25     30
Ile Ala Leu Pro Cys Ala Thr Gln Asn Glu Leu Asp Ala Asp Ala Ala
35     40     45
Arg Thr Leu Leu Arg Asn Gly Cys Leu Cys Val Ala Gly Gly Ala Asn
50     55     60
Met Pro Pro Ala Leu Glu Ala Val Asp Ile Phe Ile Glu Ala Gly Ile
65     70     75     80
Leu Phe Ala Pro Gly Lys Ala Ser Asn Ala Gly Gly Val Ala Val Ser
85     90     95
Gly Leu Glu Met Ser Gln Asn Ala Met Arg Leu Leu Trp Thr Ala Gly
100    105    110

```

&lt;210&gt; 693

&lt;211&gt; 580

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 693

```

ngggcaaccc ggaaggtccg gcgtcccagc cgcctacctc gctgggaccc tggctcttgc
60
gtcccccgct ggctcctgc ccaagcgact gcggccagga tgggccggaa ggtgaccgtg
120
gccacctgcg cactcaacca gtggggccctg gacttcgagg gcaatttgca aagaatttta
180
aagagtattg aaattgccaa aaacagagga gcaagatata ggcttggacc agagctggaa
240
atatgcccgt gcggatgttg ggatcattat tacgagtcgg acacctctt gcactcgttt
300
caagtcctag cggcccttgt ggagtctccc gtcactcagg acatcatctg cgacgtgggg
360
atacctgtaa tgcaccgaaa cgctccgtac aactgcagag tgatattcct caacaggaag
420
atcctgctca tcagacccaa gatggccttg gccaatgaag gcaactaccg cgagctgcgc
480
tggttcacc cgtggctcag gagtcggtga gtcgggtgcc tgaccactcc tgggatgtgc
540
gttaagcacc tccgctgtgt gtagccttgg gtctgatca
580

```

&lt;210&gt; 694

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 694

```

Met Gly Arg Lys Val Thr Val Ala Thr Cys Ala Leu Asn Gln Trp Ala
1      5      10      15
Leu Asp Phe Glu Gly Asn Leu Gln Arg Ile Leu Lys Ser Ile Glu Ile
20     25     30
Ala Lys Asn Arg Gly Ala Arg Tyr Arg Leu Gly Pro Glu Leu Glu Ile
35     40     45
Cys Gly Cys Gly Cys Trp Asp His Tyr Tyr Glu Ser Asp Thr Leu Leu
50     55     60
His Ser Phe Gln Val Leu Ala Ala Leu Val Glu Ser Pro Val Thr Gln
65     70     75     80
Asp Ile Ile Cys Asp Val Gly Ile Pro Val Met His Arg Asn Val Arg
85     90     95
Tyr Asn Cys Arg Val Ile Phe Leu Asn Arg Lys Ile Leu Leu Ile Arg
100    105    110
Pro Lys Met Ala Leu Ala Asn Glu Gly Asn Tyr Arg Glu Leu Arg Trp
115    120    125
Phe Thr Pro Trp Ser Arg Ser Arg
130    135

```

&lt;210&gt; 695

&lt;211&gt; 439

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 695  
 ntgggtgactc aggcgtccaa tggcacgatg gctgacgtcg tcaatatgcc gtcctcgacc  
 60  
 atcatggctc tgtcgagggc tgattacctg ctcgatatcg agacttcggt gcccggtatc  
 120  
 ggcgacaagt tcgtcccga cgtctggggc aaactcaaac tcggcaagga caacgagcac  
 180  
 accgctctgc cctggactt cggcccgctc gtcgtgacgt acaacaagga cattttcaag  
 240  
 gatgttgccc tcgatccga aatcccgccg aagacgatga ccgagtacct cgacttcgcc  
 300  
 aagaaaatca ccgctgccg caagcaggcg gtctatggca acacgtcgtg gtacatgctc  
 360  
 gcggaatggc gtgccctcg cgtcaaggc atgaatgacg acttcaccaa gtacactttt  
 420  
 gcctcggaat ccaacgcgt  
 439

<210> 696  
 <211> 146  
 <212> PRT  
 <213> Homo sapiens

<400> 696  
 Xaa Val Thr Gln Ala Ser Asn Gly Thr Met Ala Asp Val Val Asn Met  
 1 5 10 15  
 Pro Ser Ser Thr Ile Met Ala Leu Ser Arg Ala Asp Tyr Leu Leu Asp  
 20 25 30  
 Ile Glu Thr Ser Val Pro Gly Ile Gly Asp Lys Phe Val Pro Asp Val  
 35 40 45  
 Trp Gly Lys Leu Lys Leu Gly Lys Asp Asn Glu His Thr Ala Leu Pro  
 50 55 60  
 Trp Tyr Phe Gly Pro Phe Val Val Thr Tyr Asn Lys Asp Ile Phe Lys  
 65 70 75 80  
 Asp Val Gly Leu Asp Pro Glu Ile Pro Pro Lys Thr Met Thr Glu Tyr  
 85 90 95  
 Leu Asp Phe Ala Lys Lys Ile Thr Ala Ala Gly Lys Gln Ala Val Tyr  
 100 105 110  
 Gly Asn Thr Ser Trp Tyr Met Leu Ala Glu Trp Arg Ala Leu Gly Val  
 115 120 125  
 Lys Val Met Asn Asp Asp Phe Thr Lys Phe Thr Phe Ala Ser Glu Ser  
 130 135 140  
 Asn Ala  
 145

<210> 697  
 <211> 368  
 <212> DNA  
 <213> Homo sapiens

<400> 697  
 nggcaataac gccgtcgtcg aaatccgttc ccttgatctc gaacatgccg atgaagcggt  
 60

tgtcggatgat ggggtcggag atgtcgccct cccacaactt gaacttgatc ggaccaaccc  
 120  
 tttccaccct ggagagactc gcctgccttg aaagtcttct tgccttctt gggcaactga  
 180  
 tcgccctccc gaacgagata atccaagctc aagcgaccgc ccaccttgtc gcgcgcctcc  
 240  
 acaccgacgg aatgcgatgc cgggatcgca tcgatgctag cggcgggtgcg tgcaatgaca  
 300  
 atcttgtctt caccgagcga tacgggcccc cggttggaat cgaacacaaa caccttgaag  
 360  
 gcgttgtn  
 368

<210> 698  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 698  
 Met Pro Met Lys Arg Leu Ser Val Met Gly Ser Glu Met Ser Pro Ser  
 1 5 10 15  
 His Asn Leu Asn Leu Ile Gly Pro Thr Leu Ser Thr Leu Glu Arg Leu  
 20 25 30  
 Ala Cys Leu Glu Ser Leu Leu Ala Leu Leu Gly Gln Leu Ile Ala Leu  
 35 40 45  
 Pro Asn Glu Ile Ile Gln Ala Gln Ala Thr Ala His Leu Val Ala Arg  
 50 55 60  
 Leu His Thr Asp Gly Met Arg Cys Arg Asp Arg Ile Asp Ala Ser Gly  
 65 70 75 80  
 Gly Ala Cys Asn Asp Asn Leu Val Phe Thr Gln Arg Tyr Gly Pro Ala  
 85 90 95  
 Val Gly Ile Glu His Lys His Leu Glu Gly Val Val  
 100 105

<210> 699  
 <211> 363  
 <212> DNA  
 <213> Homo sapiens

<400> 699  
 nacgcgtaca caaatagtat cggaatcatt tcctatcatg ctgctatgac gagatttctc  
 60  
 cacacctcag attggcaact ggggatgact cggcactacc tgtcgaagcg cggcgacgac  
 120  
 gacccacagg cacggtttac tgccgatcga atcgagacgg tgcgcaggct gggcgacggt  
 180  
 gcccggaagg agggctgcga gtttgtcgtc gtcgccggag atgtcttcga aaccacaaat  
 240  
 gtctccactc agatcattgc ccgcgcgtgt gaggcgatag cctccattga tctccccgtg  
 300  
 tacctgctgc ccggaaatca cgacagctta gagccgggggt gtctctggga tgggccagaa  
 360  
 ttc  
 363

<210> 700  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 700  
 Xaa Ala Tyr Thr Asn Ser Ile Gly Ile Ile Ser Tyr His Ala Ala Met  
 1 5 10 15  
 Thr Arg Phe Leu His Thr Ser Asp Trp Gln Leu Gly Met Thr Arg His  
 20 25 30  
 Tyr Leu Ser Lys Arg Gly Asp Asp Asp Pro Gln Ala Arg Phe Thr Ala  
 35 40 45  
 Asp Arg Ile Glu Thr Val Arg Arg Leu Gly Asp Val Ala Arg Lys Glu  
 50 55 60  
 Gly Cys Glu Phe Val Val Val Ala Gly Asp Val Phe Glu Thr His Asn  
 65 70 75 80  
 Val Ser Thr Gln Ile Ile Ala Arg Ala Cys Glu Ala Ile Ala Ser Ile  
 85 90 95  
 Asp Leu Pro Val Tyr Leu Leu Pro Gly Asn His Asp Ser Leu Glu Pro  
 100 105 110  
 Gly Cys Leu Trp Asp Gly Pro Glu Phe  
 115 120

<210> 701  
 <211> 585  
 <212> DNA  
 <213> Homo sapiens

<400> 701  
 nacgcgtccg ggacacaccgt caccgaggcg acgttccacg gccacccac gctgatctat  
 60  
 ttcggctacg tccattgctg cgatgtctgc ccgctgacac tgggcaacat ggtctcggcc  
 120  
 ctcgatcgcc tgggctcccg ggcggacggc atcgttccga tcttcatctc cgtcgatccg  
 180  
 gcccgcgaca caccgcgct ggtcggacag tatgtcgcgc atttctcgcc gcggatcgtc  
 240  
 gggctgaccg gcaccgcagc gcagctggcg ccggtacttg cggagttcca catcaccgcg  
 300  
 cgcgccgaac ctgcggcaca cgacatggcc gccgacatgt atgccgtcga ccacagcgcc  
 360  
 ctctctatc tgatggacgg caacaaccgc ctgttgccgg tgatggcggt cagcgccgac  
 420  
 gctgcctcgc tgacgcacca gctggcgccc ggcctggccc gggcaagaat gagaccatga  
 480  
 aagcgatcgg accgacggac gccccgaac aggcagcgcc gggctggctg ttcggcatca  
 540  
 tcctgtgct cgcatcgcc ggcgtgctg atttcgtcga ccggt  
 585

<210> 702  
 <211> 159  
 <212> PRT



&lt;213&gt; Homo sapiens

&lt;400&gt; 702

```

Xaa Ala Ser Gly His Thr Val Thr Glu Ala Thr Phe His Gly His Pro
 1           5           10           15
Thr Leu Ile Tyr Phe Gly Tyr Val His Cys Ala Asp Val Cys Pro Leu
 20           25           30
Thr Leu Gly Asn Met Val Ser Ala Leu Asp Arg Leu Gly Ser Arg Ala
 35           40           45
Asp Gly Ile Val Pro Ile Phe Ile Ser Val Asp Pro Ala Arg Asp Thr
 50           55           60
Pro Ala Leu Val Gly Gln Tyr Val Ala His Phe Ser Pro Arg Ile Val
 65           70           75           80
Gly Leu Thr Gly Thr Ala Ala Gln Leu Ala Pro Val Leu Ala Glu Phe
 85           90           95
His Ile Thr Ala Arg Ala Glu Pro Ala Ala His Asp Met Ala Ala Asp
100          105          110
Met Tyr Ala Val Asp His Ser Ala Leu Leu Tyr Leu Met Asp Gly Asn
115          120          125
Asn Arg Leu Leu Arg Val Met Ala Val Ser Ala Asp Ala Ala Ser Leu
130          135          140
Thr His Gln Leu Ala Ala Gly Leu Ala Gly Ala Arg Met Arg Pro
145          150          155

```

&lt;210&gt; 703

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 703

```

ttctctgctc catacacacc tcagcagaat ggcctcgccg agcgcaagaa cataactctt
60
attgagatgg cccgaacgat gcttgatgag tacaagactc cgcggaagtt ctggcctgaa
120
gccattgata ctgcttgta caccatcaac cgcgtttatc ttcacaaggt tttggagaaa
180
acctcttatg agttcctaac tggtaagaaa cccaatgtaa gctatttcag agtatttggg
240
gctaggtgct ggatcaagga tcctcatcac acttcaaaat ttgcaccgaa agcacatgaa
300
ggttttatgc ttggttacgg aaaggattcg cactcctaca gagtcttcaa cctctttcac
360
tataaagtgg ttcaaactgt ggatgtgcgn
390

```

&lt;210&gt; 704

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 704

```

Phe Ser Ala Pro Tyr Thr Pro Gln Gln Asn Gly Ile Ala Glu Arg Lys
 1           5           10           15
Asn Ile Thr Leu Ile Glu Met Ala Arg Thr Met Leu Asp Glu Tyr Lys

```

```

      20      25      30
Thr Pro Arg Lys Phe Trp Pro Glu Ala Ile Asp Thr Ala Cys His Thr
      35      40      45
Ile Asn Arg Val Tyr Leu His Lys Val Leu Glu Lys Thr Ser Tyr Glu
      50      55      60
Phe Leu Thr Gly Lys Lys Pro Asn Val Ser Tyr Phe Arg Val Phe Gly
65      70      75      80
Ala Arg Cys Trp Ile Lys Asp Pro His His Thr Ser Lys Phe Ala Pro
      85      90      95
Lys Ala His Glu Gly Phe Met Leu Gly Tyr Gly Lys Asp Ser His Ser
      100      105      110
Tyr Arg Val Phe Asn Leu Phe His Tyr Lys Val Val Gln Thr Val Asp
      115      120      125
Val Arg
      130

```

<210> 705  
 <211> 513  
 <212> DNA  
 <213> Homo sapiens

```

<400> 705
acgcgtat ttt cgtccaaatg attcaaatca aaacgccgcc gttaaaaacg atgcaggcga
60
agacaatg cg aataaaaaag gtggtaaata agcatgagtt ttaaaatgac acaatctcaa
120
tacacaagtc tttatggacc aactgtagga gactccgtga gattaggaga tacgaacttg
180
tttgacaaag ttgagaaaaga ctatgcaaat tatggggatg aagctacttt cgggtggcga
240
aaatcaattc gtgatggtat ggctcaaaat cctaattgta caagagatga taaaaatgta
300
gccgatttag ttttaactaa cgcattaatt attgattatg acaagattgt taaagcagat
360
atcgggtatta aaaatgggta tatttttaag attggtaaag ctggaaaccc agatataatg
420
gataacgttg acatcatcat tgggtgcaaca actgatatta ttgctgctga aggtaaaatt
480
gttactgccg gcggtatcga tacacacgtg cac
513

```

<210> 706  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

```

<400> 706
Met Ser Phe Lys Met Thr Gln Ser Gln Tyr Thr Ser Leu Tyr Gly Pro
1      5      10      15
Thr Val Gly Asp Ser Val Arg Leu Gly Asp Thr Asn Leu Phe Ala Gln
      20      25      30
Val Glu Lys Asp Tyr Ala Asn Tyr Gly Asp Glu Ala Thr Phe Gly Gly
      35      40      45
Gly Lys Ser Ile Arg Asp Gly Met Ala Gln Asn Pro Asn Val Thr Arg

```

```

      50              55              60
Asp Asp Lys Asn Val Ala Asp Leu Val Leu Thr Asn Ala Leu Ile Ile
65              70              75              80
Asp Tyr Asp Lys Ile Val Lys Ala Asp Ile Gly Ile Lys Asn Gly Tyr
      85              90              95
Ile Phe Lys Ile Gly Lys Ala Gly Asn Pro Asp Ile Met Asp Asn Val
      100             105             110
Asp Ile Ile Ile Gly Ala Thr Thr Asp Ile Ile Ala Ala Glu Gly Lys
      115             120             125
Ile Val Thr Ala Gly Gly Ile Asp Thr His Val His
      130             135             140

```

&lt;210&gt; 707

&lt;211&gt; 409

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 707

```

acgcgtggca tcctcagacc accaaagaca atcctgtcct gggaggcagg gagaaagccg
60
gcacactaca cagtgcacag gtgaagccct caggggggtcc tggagcaggg ccacctccct
120
gggggatccc caggtgccat ttcatggca gtgtctatgg acggctcccc ttggcatggt
180
gctgggtggc aatcctggct gtagctgcc cccctgccc tttttgcttc cctccgaggg
240
cattgtgatc atcagtgtga gtctgttggg aaggagagcc aggtccccag gtttgggaaa
300
ggagtagggt ttcccagcct gtctggccat cccccccag ccagcccct cctgctgggt
360
gacgtgctca gttcggcccc tgctgtactg ggagggggct aggagcata
409

```

&lt;210&gt; 708

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 708

```

Met Leu Leu Ala Pro Ser Gln Tyr Ser Arg Gly Arg Thr Glu His Val
 1              5              10              15
Thr Gln Gln Glu Gly Leu Gly Trp Gly Val Met Ala Arg Gln Ala Gly
      20              25              30
Lys Pro Tyr Ser Phe Pro Lys Pro Gly Asp Leu Ala Leu Leu Pro Asn
      35              40              45
Arg Leu Thr Leu Met Ile Thr Met Pro Ser Glu Gly Ser Lys Lys Gly
      50              55              60
Arg Gly Trp Gln Leu Gln Pro Gly Leu Pro Pro Ser Thr Met Pro Arg
65              70              75              80
Gly Ala Val His Arg His Cys His Glu Asn Gly Thr Trp Gly Ser Pro
      85              90              95
Arg Glu Val Ala Leu Leu Gln Asp Pro Leu Arg Ala Ser Pro Val His
      100             105             110
Cys Val Val Cys Arg Leu Ser Pro Cys Leu Pro Gly Gln Asp Cys Leu

```

115 120 125  
 Trp Trp Ser Glu Asp Ala Thr Arg  
 130 135

<210> 709  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 709  
 acgcgtctga cggagagcct cctgagtcctc cccacgcaga ggactcagaa agggaatcgg  
 60  
 tgaccacacc tgggccagcg acgtgtggtg cgccagcctc cccagcggat cacctcctcc  
 120  
 tccccctcca ggaggagagt ttctccgaag tccccatgag tgaagcaagc tcagcgaaaag  
 180  
 acactccact ctttaggatg gagggagagg atgcccttgt gactcagtat cagagcaaaag  
 240  
 ccagtgaacca cgaaggttta ttgtctgacc ccttgagtga ccttcagttg gtctcagatt  
 300  
 ttaaatctcc aatcatggcc gatctgaact taagccttcc ttccattcct gaagtcgcat  
 360  
 cggatgatga aagaatagat cagggttgaa atgacggaga tcagggttgaa gatgatggag  
 420  
 agacagcaaa gtcgtcaact ctggacatag gagctttgtc cttgggcttg gtagtccct  
 480  
 gtcctgagag gggaaagggg cccagtggcg aggcagatag gttggtactg ggggagggcc  
 540  
 tgtgtgattt caggctgcaa gcaccccagg catctgtgac agctccttca gagcagacca  
 600  
 cagagttcgg aattcacaaa ccacatcttg gcaagagctc aagcttggat aaacagctgc  
 660  
 caggccccag tgggtgtgag gaagaaaaac cgatgggaaa tgggagtcca agcccgctc  
 720  
 ctggcacatc cctggacaat cctgtaccca gcccctcccc ttctgagatc t  
 771

<210> 710  
 <211> 205  
 <212> PRT  
 <213> Homo sapiens

<400> 710  
 Met Ser Glu Ala Ser Ser Ala Lys Asp Thr Pro Leu Phe Arg Met Glu  
 1 5 10 15  
 Gly Glu Asp Ala Leu Val Thr Gln Tyr Gln Ser Lys Ala Ser Asp His  
 20 25 30  
 Glu Gly Leu Leu Ser Asp Pro Leu Ser Asp Leu Gln Leu Val Ser Asp  
 35 40 45  
 Phe Lys Ser Pro Ile Met Ala Asp Leu Asn Leu Ser Leu Pro Ser Ile  
 50 55 60  
 Pro Glu Val Ala Ser Asp Asp Glu Arg Ile Asp Gln Val Glu Asp Asp  
 65 70 75 80  
 Gly Asp Gln Val Glu Asp Asp Gly Glu Thr Ala Lys Ser Ser Thr Leu

```

      85              90              95
Asp Ile Gly Ala Leu Ser Leu Gly Leu Val Val Pro Cys Pro Glu Arg
      100              105              110
Gly Lys Gly Pro Ser Gly Glu Ala Asp Arg Leu Val Leu Gly Glu Gly
      115              120              125
Leu Cys Asp Phe Arg Leu Gln Ala Pro Gln Ala Ser Val Thr Ala Pro
      130              135              140
Ser Glu Gln Thr Thr Glu Phe Gly Ile His Lys Pro His Leu Gly Lys
      145              150              155              160
Ser Ser Ser Leu Asp Lys Gln Leu Pro Gly Pro Ser Gly Gly Glu Glu
      165              170              175
Glu Lys Pro Met Gly Asn Gly Ser Pro Ser Pro Pro Pro Gly Thr Ser
      180              185              190
Leu Asp Asn Pro Val Pro Ser Pro Ser Pro Ser Glu Ile
      195              200              205

```

<210> 711  
 <211> 432  
 <212> DNA  
 <213> Homo sapiens

```

<400> 711
nnggatccga cggcgcaaag ccttaatgaa gggtaggcag ttacctcttt ttctgtagga
60
attctcctgt tttatatcta ctccccctta ggttcacatc actccctcat cttctgagct
120
aatgtgcccc ctttatttgc acttgcatgg aatatgatta tgaacacagt ttttatcatt
180
gatgaccacc ccgttatcag gttggcgatt cgtatgttgt tggaacacga gggttataag
240
gtcggttggtg aaacggacaa cggttgtgac gcgatccaaa tggttcgca atgcctgccc
300
gacctgatca tcctggatat cagcatcccc aaactcgacg gcctcgaagt gctctgccga
360
ttcaacgcca tgaacacatc catgaaaacc ctgattctta ccgccagag tccgacgttg
420
ttcgccacgc gt
432

```

<210> 712  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

```

<400> 712
Met Ile Met Asn Thr Val Phe Ile Ile Asp Asp His Pro Val Ile Arg
1      5      10      15
Leu Ala Ile Arg Met Leu Leu Glu His Glu Gly Tyr Lys Val Val Gly
20     25     30
Glu Thr Asp Asn Gly Cys Asp Ala Ile Gln Met Val Arg Glu Cys Leu
35     40     45
Pro Asp Leu Ile Ile Leu Asp Ile Ser Ile Pro Lys Leu Asp Gly Leu
50     55     60
Glu Val Leu Cys Arg Phe Asn Ala Met Asn Thr Ser Met Lys Thr Leu

```

```

65                               70                               75                               80
Ile Leu Thr Ala Gln Ser Pro Thr Leu Phe Ala Thr Arg
      85                               90

<210> 713
<211> 465
<212> DNA
<213> Homo sapiens

<400> 713
atcctgatcg ccaacggtgg tatgcagaac ccggtgggcg cggtgttcaa ccccgacacc
60
atgcgcatgg aaatgaccga cttcgccgcg gtgatettca acccggtggc gcaggccaag
120
ttcgtgcata cggtcagcgc gggctacgtg gccggcgcca tgttcgtcat gtcgatcagc
180
gcctggtac c tgctcaaggg ccgccacacc gacctggcca agcgcctcgat ggcggtcgcc
240
gccagcttcg gcctggcgtc ggcgctgtcg gtcgtcgtgc tgggtgacga aagcggttat
300
ctcaccaccg aacaccagaa gatgaagatc gcggccatgg aatccatgtg gcacaccgag
360
cggcgccccg cgtccttcaa cctgatcgcg ctgcccaacc aggccgaacg caagaacgac
420
ttgcccatcg agattcccta cgtcatgngc ctcatcggca cgcgt
465

```

```
<210> 714
<211> 155
<212> PRT
<213> Homo sapiens
```

<400> 714															
Ile	Leu	Ile	Ala	Asn	Gly	Gly	Met	Gln	Asn	Pro	Val	Gly	Ala	Val	Phe
1				5					10					15	
Asn	Pro	Asp	Thr	Met	Arg	Met	Glu	Met	Thr	Asp	Phe	Ala	Ala	Val	Ile
			20					25					30		
Phe	Asn	Pro	Val	Ala	Gln	Ala	Lys	Phe	Val	His	Thr	Val	Ser	Ala	Gly
			35				40						45		
Tyr	Val	Ala	Gly	Ala	Met	Phe	Val	Met	Ser	Ile	Ser	Ala	Trp	Tyr	Leu
			50			55						60			
Leu	Lys	Gly	Arg	His	Thr	Asp	Leu	Ala	Lys	Arg	Ser	Met	Ala	Val	Ala
65				70						75					80
Ala	Ser	Phe	Gly	Leu	Ala	Ser	Ala	Leu	Ser	Val	Val	Val	Leu	Gly	Asp
				85					90					95	
Glu	Ser	Gly	Tyr	Leu	Thr	Thr	Glu	His	Gln	Lys	Met	Lys	Ile	Ala	Ala
				100				105					110		
Met	Glu	Ser	Met	Trp	His	Thr	Glu	Pro	Ala	Pro	Ala	Ser	Phe	Asn	Leu
			115				120						125		
Ile	Ala	Leu	Pro	Asn	Gln	Ala	Glu	Arg	Lys	Asn	Asp	Phe	Ala	Ile	Glu
	130					135					140				
Ile	Pro	Tyr	Val	Met	Xaa	Leu	Ile	Gly	Thr	Arg					
145					150					155					

<210> 715  
 <211> 354  
 <212> DNA  
 <213> Homo sapiens

<400> 715  
 nnaccggtgg atgccaacga atatcgtggc gagctgaaag tcggcgccat caccaccgcc  
 60  
 cagaccggcc tgctgcctca ggcactggtg cgtttgcgcc aggcagcgcc gacggtggag  
 120  
 tgcaagttgg taccggggggt ttccctggag ttgctcagcc aggtggacgc aggcgagctg  
 180  
 gactcggcga tcatcattcg cccgcccttt gatttgccca aggagttgca cgtacaggta  
 240  
 ctgcgcaagg agccgtttgt gttgatcgtg ccccaggcgg tcgggggtga tgaccggtg  
 300  
 caactgctcg aagctcatcc ccacgtgcgc tacgaccgcg cttcgtttgg cggg  
 354

<210> 716  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 716  
 Xaa Pro Val Asp Ala Asn Glu Tyr Arg Gly Glu Leu Lys Val Gly Ala  
 1 5 10 15  
 Ile Thr Thr Ala Gln Thr Gly Leu Leu Pro Gln Ala Leu Val Arg Leu  
 20 25 30  
 Arg Gln Ala Ala Pro Thr Val Glu Cys Lys Leu Val Pro Gly Val Ser  
 35 40 45  
 Leu Glu Leu Leu Ser Gln Val Asp Ala Gly Glu Leu Asp Ser Ala Ile  
 50 55 60  
 Ile Ile Arg Pro Pro Phe Asp Leu Pro Lys Glu Leu His Val Gln Val  
 65 70 75 80  
 Leu Arg Lys Glu Pro Phe Val Leu Ile Val Pro Gln Ala Val Gly Gly  
 85 90 95  
 Asp Asp Pro Leu Gln Leu Leu Glu Ala His Pro His Val Arg Tyr Asp  
 100 105 110  
 Arg Ala Ser Phe Gly Gly  
 115

<210> 717  
 <211> 401  
 <212> DNA  
 <213> Homo sapiens

<400> 717  
 acgcgtatct tttcggtaaa cctactaatt tttcattcaa cgctcgacgc ccaggtaaag  
 60  
 ccgttaagtc atctaaatag gccattctgt ggctctccat cagtaagaac caaatccata  
 120  
 ggagaagttg agcggatagt aatgcatcaa attgatgctg agaaaccgaa aaatgggaca  
 180

atataatcaa gctgacaata ctgatcaaac cactcgcatg aaagctacta ccgcttgacc  
 240  
 accaagcaga aaaaaccaat gaaatgctta aaaataaaat cgtccaaagt aaaaagctag  
 300  
 accagggtggt agccagatta aaaataggcc gctctagaaa atgaaaagaa atccaatgag  
 360  
 attcaacggc gtagcaccag cacagcaaca tagccactag t  
 401

<210> 718  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 718  
 Met Leu Leu Cys Trp Cys Tyr Ala Val Glu Ser His Trp Ile Ser Phe  
 1 5 10 15  
 His Phe Leu Glu Arg Pro Ile Phe Asn Leu Ala Thr Thr Trp Ser Ser  
 20 25 30  
 Phe Leu Leu Trp Thr Ile Leu Phe Leu Ser Ile Ser Leu Val Phe Ser  
 35 40 45  
 Ala Trp Trp Ser Ser Gly Ser Ser Phe His Ala Ser Gly Leu Ile Ser  
 50 55 60  
 Ile Val Ser Leu Ile Ile Leu Ser His Phe Ser Val Ser Gln His Gln  
 65 70 75 80  
 Phe Asp Ala Leu Leu Ser Ala Gln Leu Leu Leu Trp Ile Trp Phe Leu  
 85 90 95  
 Leu Met Glu Ser His Arg Met Ala Tyr Leu Asp Asp Leu Thr Ala Leu  
 100 105 110  
 Pro Gly Arg Arg Ala Leu Asn Glu Lys Leu Val Gly Leu Pro Lys Arg  
 115 120 125  
 Tyr Ala  
 130

<210> 719  
 <211> 685  
 <212> DNA  
 <213> Homo sapiens

<400> 719  
 tatatagggc tatctacctt attcacagca cattccatct acacaacctt gtagcggtca  
 60  
 ctcttgaagg cggattttca taggcgctgc gcctctcata ttcaagcatc aaggcaatcc  
 120  
 aatctccctg cgttggtaac tgggcaaaag aaagacctct gcagtccagc aacctcatcg  
 180  
 tgcaaatgcc gtggcggtggt caactctgac ggcttggaag ctgcagacct tgtcaaagga  
 240  
 cctcgccga aattcaccct tgatctcttt gtcttggtcca actcttggtcc ctgagaatga  
 300  
 aactgtcttc tgagagtcca tcaatgcgac gctgactcgt gagaagtgtc gaatcacgtc  
 360  
 gccattttgg agacctgcca acgcagctct ggaacctgcc aggacgcctt ccacaacacc  
 420



agaacgcagc gactttgctg taaatccaag ctcaaacacc tcttgctcca caggcctgag  
 480  
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 540  
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 Gln Glu Asp Ser Gly Ile Asp Ile Gly Asp Ile Thr Ala Arg Lys Ala  
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 Val Tyr Pro Glu Met Arg Met Tyr Ser Asp Ile Ile Ala Tyr Gly Val  
 100 105 110  
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 115 120 125  
 Thr Glu Asn Val Pro Ile Met Tyr Ile Cys His Gly Met Thr Pro Gln  
 130 135 140  
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 145 150 155 160  
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<211> 128

<212> PRT

<213> Homo sapiens

<400> 724

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Ile	Asp	Thr	Arg	Ser	Gly	Thr	Pro	Thr	Leu	Met	Leu	Thr	Val	Gln	Ser
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Val	Thr	Asp	Lys	Pro	Val	Thr	Asp	Val	Thr	Arg	Gln	Cys	Pro	Lys	Trp
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Asp	Gly	Lys	Pro	Leu	Thr	Leu	Asp	Val	Thr	Asn	Thr	Phe	Pro	Glu	Gly
			85					90					95		
Ser	Val	Val	Arg	Asp	Phe	Tyr	Ser	Lys	Gln	Thr	Ala	Met	Val	Gln	Gln
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<211> 521

<212> DNA

<213> Homo sapiens

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 Ser Thr Pro Ser Pro Ser Ser Cys Ser Leu Pro Glu Arg Leu Cys Trp  
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 Glu Trp Cys Ile Gly Gly Leu Gln Ala Leu Leu Gly Ser Arg Cys Ser  
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 Ser Val Glu Leu Met Leu Asn Ala Ala Asn Leu Ala Leu Val Thr Phe  
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 Ala His Val His Gly Ser Leu Asp Gly Gln Val Gly Val Phe Phe Val  
 50 55 60  
 Met Ile Val Ala Ala Ala Glu Val Val Val Gly Leu Ala Ile Ile Val  
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 <213> Homo sapiens

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<211> 797

<212> PRT

<213> Homo sapiens

<400> 730

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Val	Thr	Arg	Leu	Pro	Ser	Pro	Thr	Ser	Pro	Phe	Ser	Ser	Leu	Ser	Gln
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Lys Leu Arg Glu Glu Trp Gln Arg Ala Lys Gln Glu Ala Glu Arg Glu
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          450          455          460
Glu Gln Gln Leu Gln Glu Glu Gln Glu Gln Lys Arg Leu Gln Ala Glu
465          470          475          480
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Ile Glu Arg Glu Thr Ser Val Arg Ile Tyr Gln Tyr Arg Arg Pro Val
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Ser Thr Asn Lys Asn Gly Asn Asn Lys Tyr Leu Asp Gln Ile Gly Asn
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Thr Thr Ser Ser Gln Arg Arg Ser Lys Lys Glu Gln Val Pro Ser Gly
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Phe	Ser	Arg	Pro	Pro	Pro	Gln	Leu	Val	Ser	Thr	Ser	Asn	Arg	Ala	Tyr
			660						665				670		
Met	Arg	Asn	Pro	Ser	Ser	Ser	Val	Pro	Pro	Pro	Ser	Ala	Gly	Ser	Val
		675					680					685			
Lys	Thr	Ser	Thr	Thr	Gly	Val	Ala	Thr	Thr	Gln	Ser	Pro	Thr	Pro	Arg
	690						695					700			
Ser	His	Ser	Pro	Ser	Ala	Ser	Gln	Ser	Gly	Ser	Gln	Leu	Arg	Asn	Arg
	705				710					715					720
Ser	Val	Ser	Gly	Lys	Arg	Ile	Cys	Ser	Tyr	Cys	Asn	Asn	Ile	Leu	Gly
			725						730					735	
Lys	Gly	Ala	Ala	Met	Ile	Ile	Glu	Ser	Leu	Gly	Leu	Cys	Tyr	His	Leu
			740						745				750		
His	Cys	Phe	Lys	Cys	Val	Ala	Cys	Glu	Cys	Asp	Leu	Gly	Gly	Ser	Ser
		755					760					765			
Ser	Gly	Ala	Glu	Val	Arg	Ile	Arg	Asn	His	Gln	Leu	Tyr	Cys	Asn	Asp
	770					775						780			
Cys	Tyr	Leu	Arg	Phe	Lys	Ser	Gly	Arg	Pro	Thr	Ala	Met			
	785				790					795					

&lt;210&gt; 731

&lt;211&gt; 513

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 731

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60  
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120  
tcttcaaagt actgactggg gaaacagatt gttggaaaaa cactttcggg ttgcctcgat  
180  
ggggtcaata ccttatcagg ccacaggaaa gacaaaggaa aatgcttcct gctggagcat  
240  
gtgcacatat gttgttcctt taactcaaaa tacgtatgca ggggtggtgg taggatcaga  
300  
aaatgtgtga tcagaaagt accagttccc caccattttg tgtgggtttt attttctttc  
360  
tgctccgtgt tgactctttt cccacaaca cggaagctgc ttaatccaaa gacttggacc  
420  
atttcattct gtttcagatc cattccaaca aaatgatcag ttgggtggctt atgtaaaaag  
480  
cagctccatg actacattta aatattgact agt  
513

&lt;210&gt; 732

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 732

```

Met Asp Leu Lys Gln Asn Glu Met Val Gln Val Phe Gly Leu Ser Ser
 1             5             10             15
Phe Arg Val Val Gly Lys Arg Val Asn Thr Glu Gln Lys Glu Asn Lys
      20             25             30
Thr His Thr Lys Trp Trp Gly Thr Gly His Phe Leu Ile Thr His Phe
      35             40             45
Leu Ile Leu Pro Pro Pro Leu His Thr Tyr Leu Glu Leu Lys Glu Gln
      50             55             60
His Met Cys Thr Cys Ser Ser Arg Lys His Phe Pro Leu Ser Phe Leu
65             70             75             80
Trp Pro Asp Lys Val Leu Thr Pro Ser Arg Gln Pro Glu Ser Val Phe
      85             90             95
Pro Thr Ile Cys Phe Pro Ser Gln Ser Phe Glu Glu Ser Arg Glu Ala
      100            105            110
Glu

```

&lt;210&gt; 733

&lt;211&gt; 4366

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 733

```

nttttaacaa aaaaaatata ttaataaaaa agttcaaaaa agggggggga ttgtcatctc
60
ctttgggggtg cgatggcttc aaatccaaac tgaggctctc cgggtggtaa ggatgtgcga
120
ggaggcctct tgaagaactc caggcctatc atgctgtctc tccgctaaag cctgaggccc
180
gaggtcagag gattcaggaa ggctctgcag tcggcccagg agggcggggg cccgtggtgg
240
aggcggggag agggaaggac cgcacggagc accaaccctt gctcggtccc gtaccaggaa
300
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360
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420
ggaagaaaca gcggagggtt cgtggaaaaa aaagcaatgg ctgagctaag ggatggggta
480
ccaggttagg gggaggaaac ggtagagaga aataggtggg gctcccgcgc atgctcaata
540
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600
ggcgcggaat ttggagacct acttcgggaa aggtaaaatg cgggcgcaat ttaggggtac
660
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720
acgcccgacc agagagtgtt tctccactcc cggactctgc cagtcaggat ggtggtgcct
780

```

tcgctgaagc ttcaggacct catcgaagag attcgcgggg ccaagactca ggcccaggag  
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900  
gtgcacaggc accggcagct ggccaaactg ctctacgtcc acatgttggg ctaccccgcc  
960  
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1140  
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1380  
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1740  
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1800  
cagcggcatc ggcccactgt ggtggaatgt ctacgggaaa ctgatgcctc cctcagccgg  
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1920  
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1980  
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2160  
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2280  
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2340  
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2400

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3300  
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3600  
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 4080  
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 4140  
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 4200  
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 4260  
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 4366

<210> 734

<211> 364

<212> PRT

<213> Homo sapiens

<400> 734

Met	Val	Val	Pro	Ser	Leu	Lys	Leu	Gln	Asp	Leu	Ile	Glu	Glu	Ile	Arg
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Gly	Ala	Lys	Thr	Gln	Ala	Gln	Glu	Arg	Glu	Val	Ile	Gln	Lys	Glu	Cys
			20					25					30		
Ala	His	Ile	Arg	Ala	Ser	Phe	Arg	Asp	Gly	Asp	Pro	Val	His	Arg	His
		35					40					45			
Arg	Gln	Leu	Ala	Lys	Leu	Leu	Tyr	Val	His	Met	Leu	Gly	Tyr	Pro	Ala
	50				55					60					
His	Phe	Gly	Gln	Met	Glu	Cys	Leu	Lys	Leu	Ile	Ala	Ser	Ser	Arg	Phe
65					70					75				80	
Thr	Asp	Lys	Arg	Val	Gly	Tyr	Leu	Gly	Ala	Met	Leu	Leu	Leu	Asp	Glu
			85						90					95	
Arg	His	Asp	Ala	His	Leu	Leu	Ile	Thr	Asn	Ser	Ile	Lys	Asn	Asp	Leu
			100					105					110		
Ser	Gln	Gly	Ile	Gln	Pro	Val	Gln	Gly	Leu	Ala	Leu	Cys	Thr	Leu	Ser
		115					120					125			
Thr	Met	Gly	Ser	Ala	Glu	Met	Cys	Arg	Asp	Leu	Ala	Pro	Glu	Val	Glu
	130					135				140					
Lys	Leu	Leu	Leu	Gln	Pro	Ser	Pro	Tyr	Val	Arg	Lys	Lys	Ala	Ile	Leu
145				150						155				160	
Thr	Ala	Val	His	Met	Ile	Arg	Lys	Val	Pro	Glu	Leu	Ser	Ser	Val	Phe
			165						170					175	
Leu	Pro	Pro	Cys	Ala	Gln	Leu	Leu	His	Glu	Arg	His	His	Gly	Ile	Leu
			180					185					190		
Leu	Gly	Thr	Ile	Thr	Leu	Ile	Thr	Glu	Leu	Cys	Glu	Arg	Ser	Pro	Ala
		195					200					205			
Ala	Leu	Arg	His	Phe	Arg	Lys	Val	Val	Pro	Gln	Leu	Val	His	Ile	Leu
	210					215					220				
Arg	Thr	Leu	Val	Thr	Met	Gly	Tyr	Ser	Thr	Glu	His	Ser	Ile	Ser	Gly
225				230						235				240	
Val	Ser	Asp	Pro	Phe	Leu	Gln	Val	Gln	Ile	Leu	Arg	Leu	Leu	Arg	Ile
				245					250				255		
Leu	Gly	Arg	Asn	His	Glu	Glu	Ser	Ser	Glu	Thr	Met	Asn	Asp	Leu	Leu
			260					265				270			
Ala	Gln	Val	Ala	Thr	Asn	Thr	Asp	Thr	Ser	Arg	Asn	Ala	Gly	Asn	Ala

```

      275              280              285
Val Leu Phe Glu Thr Val Leu Thr Ile Met Asp Ile Arg Ser Ala Ala
      290              295              300
Gly Leu Arg Val Leu Ala Val Asn Ile Leu Gly Arg Phe Leu Leu Asn
305              310              315              320
Ser Asp Arg Asn Ile Arg Tyr Val Ala Leu Thr Ser Leu Leu Arg Leu
      325              330              335
Val Gln Ser Asp His Ser Ala Val Gln Arg His Arg Pro Thr Val Val
      340              345              350
Glu Cys Leu Arg Glu Thr Asp Ala Ser Leu Ser Arg
      355              360

```

<210> 735  
 <211> 597  
 <212> DNA  
 <213> Homo sapiens

```

<400> 735
gtcgactagc caaaccgccc gggaaagtct tgtaccaccg atcctgggtt atgcggatct
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120
tgcttggtgt cctcgatccc gctctgaccg cccactggac cgctcaaccc aggacatcct
180
cagtgccatc cacgacgtgg ctgcaccgct ggcactaccc atcttcgtgg tgggtgccac
240
agcgcgcgac attctgctga cacacgtgtt cggtatcgag accggacgtg ccacgctcga
300
cgtggatttc gccgttgccg tagaacattg gccgcagttc gaaaacatca agcagcacct
360
gctagccaac gaccatttcg actctgccgc cagcatcacc catcgactgc tctatcgcac
420
gagcgacaac acgatcgccc ggccaatcga tctcatccca ttcgggcgga tcgaacagcc
480
gccagccacc atcaaatggc cgcccacat ggctgtcatg atgaatgttg ctggctacgc
540
agatgccttg cgggccgcag tcgaagtaga gtttgtgccc gggcgagca tacgcgt
597

```

<210> 736  
 <211> 175  
 <212> PRT  
 <213> Homo sapiens

```

<400> 736
Met Asp Ser Arg Asn Leu Glu Thr Ala Asn Leu Ile Pro Glu Lys Ile
1      5      10      15
Ile Ala Trp Cys Pro Arg Ser Arg Ser Asp Arg Pro Leu Asp Arg Ser
20      25      30
Thr Gln Asp Ile Leu Ser Ala Ile His Asp Val Ala Ala Pro Leu Ala
35      40      45
Leu Pro Ile Phe Val Val Gly Ala Thr Ala Arg Asp Ile Leu Leu Thr
50      55      60
His Val Phe Gly Ile Glu Thr Gly Arg Ala Thr Leu Asp Val Asp Phe

```

```

65          70          75          80
Ala Val Ala Val Glu His Trp Pro Gln Phe Glu Asn Ile Lys Gln His
          85          90          95
Leu Leu Ala Asn Asp His Phe Asp Ser Ala Ala Ser Ile Thr His Arg
          100          105          110
Leu Leu Tyr Arg Thr Ser Asp Asn Thr Ile Ala Arg Pro Ile Asp Leu
          115          120          125
Ile Pro Phe Gly Gly Ile Glu Gln Pro Pro Ala Thr Ile Lys Trp Pro
          130          135          140
Pro Asp Met Ala Val Met Met Asn Val Ala Gly Tyr Ala Asp Ala Trp
145          150          155          160
Arg Ala Ala Val Glu Val Glu Phe Val Pro Gly Arg Ser Ile Arg
          165          170          175

```

<210> 737  
 <211> 497  
 <212> DNA  
 <213> Homo sapiens

```

<400> 737
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60
cgcgccggca tcgttgggta cggatacga cccaaccctc acgccgaccg tgccgacctt
120
caccctgccc tgcctgggat cagccacgac accttcgtta aaactgtcag tgtgggggat
180
accatcggtt acggcagaac atggacagcc agcgaaacga caaaaatcgc caccgtccca
240
gtcgggttacg ccgacggact gtcccagaga ctgtcaaata aaggacacgt tctcattaga
300
gggtccgttc atcccatcgt cggtcggatac tgcattggac aattcatggt cgatcttggc
360
cccgattcga acgtcacggt gggagatgag gtggtgctca ttggaaccca ggaggacgaa
420
actctgaccg ctgatgacat ggccgaactc ctcggaacca ttagctacga gatcacttgc
480
gccatttcca aacgcgt
497

```

<210> 738  
 <211> 165  
 <212> PRT  
 <213> Homo sapiens

```

<400> 738
Xaa Arg Leu Ala Asn Ser Gly Ala Ile Leu Gly His Asp Leu Gly Lys
1          5          10          15
Thr Ser Met Val Arg Ala Gly Ile Val Gly Tyr Gly Tyr Asp Pro Asn
          20          25          30
Pro His Ala Asp Arg Ala Asp Leu His Pro Ala Leu Ser Trp Ile Ser
          35          40          45
His Val Thr Phe Val Lys Thr Val Ser Val Gly Asp Thr Ile Gly Tyr
          50          55          60
Gly Arg Thr Trp Thr Ala Ser Glu Thr Thr Lys Ile Ala Thr Val Pro

```



```

65          70          75          80
Val Gly Tyr Ala Asp Gly Leu Ser Arg Gly Leu Ser Asn Lys Gly His
          85          90          95
Val Leu Ile Arg Gly Ser Val His Pro Ile Val Gly Arg Ile Cys Met
          100          105          110
Asp Gln Phe Met Val Asp Leu Gly Pro Asp Ser Asn Val Thr Val Gly
          115          120          125
Asp Glu Val Val Leu Ile Gly Thr Gln Glu Asp Glu Thr Leu Thr Ala
          130          135          140
Asp Asp Met Ala Glu Leu Leu Gly Thr Ile Ser Tyr Glu Ile Thr Cys
145          150          155          160
Ala Ile Ser Lys Arg
          165

```

<210> 739  
 <211> 438  
 <212> DNA  
 <213> Homo sapiens

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<400> 739
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acggcctcat cagcagctgt gggctcaggc cccctcccc aggcggagca ggcgtagccg
120
cagagcagcg gggaggagga gctgcagctc cagctggccc tggccatgag caaggaggag
180
gccgaccagc cccgcctctg cggccccgag gacgacgcc agctccagct ggcccttagt
240
ttgagccgag aagagcatga taaggaggag cggatccgct gcggggatga cctgcggctg
300
cagatggcaa tcgaggagag caagagggag actgggggca aggaggagtc gtccctcatg
360
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420
ccagcaccca tggctgct
438

```

<210> 740  
 <211> 146  
 <212> PRT  
 <213> Homo sapiens

```

<400> 740
Arg Leu Arg Glu Glu Arg Ala His Ala Leu Lys Thr Lys Glu Lys Leu
1      5      10      15
Ala Gln Thr Ala Thr Ala Ser Ser Ala Ala Val Gly Ser Gly Pro Pro
20     25     30
Pro Glu Ala Glu Gln Ala Trp Pro Gln Ser Ser Gly Glu Glu Leu
35     40     45
Gln Leu Gln Leu Ala Leu Ala Met Ser Lys Glu Glu Ala Asp Gln Pro
50     55     60
Pro Ser Cys Gly Pro Glu Asp Asp Ala Gln Leu Gln Leu Ala Leu Ser
65     70     75     80
Leu Ser Arg Glu Glu His Asp Lys Glu Glu Arg Ile Arg Arg Gly Asp

```

```

      85          90          95
Asp Leu Arg Leu Gln Met Ala Ile Glu Glu Ser Lys Arg Glu Thr Gly
      100          105          110
Gly Lys Glu Glu Ser Ser Leu Met Asp Leu Ala Asp Val Phe Thr Pro
      115          120          125
Pro Ala Pro Ala Pro Thr Thr Asp Pro Trp Gly Gly Pro Ala Pro Met
      130          135          140
Ala Ala
145

```

```

<210> 741
<211> 726
<212> DNA
<213> Homo sapiens

```

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<400> 741
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60
aatttgccgg tcatctgcct cgtcggggccc actgctagcg gaaaatcagg gctagcgggtg
120
cgagtgtgcc gccgcttgta tgcgatgag caccgcgccg aaattattaa tactgactcg
180
atggtggtgt atcgcgggat ggacattggc actgccaccc ctacactgcg cgagcagcgc
240
acggtagtgc atcacctggt gtcgattctt gatgtgactg tgccctcctc gctagtactg
300
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420
actgatccgg aagtgagggc tcggtggcag gagaagctag atgccgaggg gccgcgagtt
480
ctgcatgacg agcttgcccg tcgcgatccc aaggcggctg agtcaatctt gcccggaac
540
ggcaggcgaa tcgtttcgtg ccctcgaagt ttattgacct tgacagggtc ctttactgcc
600
accgatcccc gacgggaccc tccactggcc aagacggtgc aaatgggctt agaactgtcg
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720
gtcgac
726

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```

<210> 742
<211> 242
<212> PRT
<213> Homo sapiens

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<400> 742
Ala Ser Leu Arg Pro Arg Cys Cys Lys Asp Val Ala Thr Val Arg Lys
1      5      10      15
Asn Glu Tyr Val Asn Leu Pro Val Ile Cys Leu Val Gly Pro Thr Ala
20     25     30
Ser Gly Lys Ser Gly Leu Ala Val Arg Val Cys Arg Arg Leu Tyr Val

```

```

      35      40      45
Asp Glu His Pro Ala Glu Ile Ile Asn Thr Asp Ser Met Val Val Tyr
 50      55      60
Arg Gly Met Asp Ile Gly Thr Ala Thr Pro Thr Leu Arg Glu Gln Arg
 65      70      75      80
Thr Val Val His His Leu Val Ser Ile Leu Asp Val Thr Val Pro Ser
      85      90      95
Ser Leu Val Leu Met Gln Thr Leu Ala Arg Asp Ala Val Glu Asp Cys
      100      105      110
Leu Ser Arg Gly Val Ile Pro Val Leu Val Gly Gly Ser Ala Leu Tyr
      115      120      125
Thr Lys Ala Ile Ile Asp Glu Met Ser Ile Pro Pro Thr Asp Pro Glu
      130      135      140
Val Arg Ala Arg Trp Gln Glu Lys Leu Asp Ala Glu Gly Pro Arg Val
 145      150      155      160
Leu His Asp Glu Leu Ala Arg Arg Asp Pro Lys Ala Ala Glu Ser Ile
      165      170      175
Leu Pro Gly Asn Gly Arg Arg Ile Val Ser Cys Pro Arg Ser Leu Leu
      180      185      190
Thr Leu Thr Gly Ser Phe Thr Ala Thr Asp Pro Arg Arg Asp Pro Pro
      195      200      205
Leu Ala Lys Thr Val Gln Met Gly Leu Glu Leu Ser Arg Lys Asp Ile
      210      215      220
Asp Gln Arg Ile Ala Asp Arg Val Asp Gln Met Trp Ala Tyr Gly Phe
 225      230      235      240
Val Asp

```

<210> 743  
 <211> 430  
 <212> DNA  
 <213> Homo sapiens

```

<400> 743
naaaaaagtg atggtttcgg atctgtggcc agtcgtcttg caagaaatca ttatgacgtg
60
gatgagggca acagcancat tcatgttaat caagacattg cgcgcagaac agggacggga
120
aagctattgg tacgagtgtg cccggcgcac gtgtactcag aggagcccga tggcactatt
180
tccgtggagt acgcagcgtg tctggagtgt ggcacttgtc tggcggttgc tgcgccaggg
240
tcgcttgaat ggcactatcc cgcaggtgca atgggtatatt cgttcagaga aggatgaagt
300
ccttggtggc gactgtaaag cgacatggcc gtcgctcggg aggaggaatt gtggtgtccg
360
caccaaatag tgctcaggat gaagttcgtc atggaaatcc ggctccaacc gtttcgggag
420
ctggtcgcga
430

```

<210> 744  
 <211> 98  
 <212> PRT

<213> Homo sapiens

<400> 744

```

Xaa Lys Ser Asp Gly Phe Gly Ser Val Ala Ser Arg Leu Ala Arg Asn
 1           5           10          15
His Tyr Asp Val Asp Glu Gly Asn Ser Xaa Ile His Val Asn Gln Asp
      20           25           30
Ile Ala Arg Arg Thr Gly Thr Gly Lys Leu Leu Val Arg Val Cys Pro
      35           40           45
Ala His Val Tyr Ser Glu Glu Pro Asp Gly Thr Ile Ser Val Glu Tyr
      50           55           60
Ala Ala Cys Leu Glu Cys Gly Thr Cys Leu Ala Val Ala Ala Pro Gly
65           70           75           80
Ser Leu Glu Trp His Tyr Pro Ala Gly Ala Met Gly Ile Ser Phe Arg
      85           90           95
Glu Gly

```

<210> 745

<211> 362

<212> DNA

<213> Homo sapiens

<400> 745

```

cggccgattg aagcgctcgt cgggtttgag tcggtgatgg atgcggtgga cggtgcttcg
60
gcgtcgtggt ggcgcatggc gcggtatttc atcgccgagc ttgaacgcag cagcgagttg
120
tatgagcagg cggcgtttac ccgcgatctg gaaagctcgc tgatcaaggg cctgaccttc
180
gccagccga acaactactc cgaagaactg cgcgacgtac tcggcgtgaa gctgccgcat
240
tacttgattc gcgcgcggca gtacatccac gacaacgccc gcgaagccgt gcatctggaa
300
gacctggaaa ccgctgccgg ggtatcgagg ttcaagttgt tcgatgcggt tcgcaaatac
360
tt
362

```

<210> 746

<211> 108

<212> PRT

<213> Homo sapiens

<400> 746

```

Met Asp Ala Val Asp Gly Ala Ser Ala Ser Trp Trp Arg Met Ala Arg
 1           5           10          15
Tyr Phe Ile Ala Glu Leu Glu Arg Ser Ser Glu Leu Tyr Glu Gln Ala
      20           25           30
Ala Phe Thr Arg Asp Leu Glu Ser Ser Leu Ile Lys Gly Leu Ile Leu
      35           40           45
Ala Gln Pro Asn Asn Tyr Ser Glu Glu Leu Arg Asp Val Leu Gly Val
      50           55           60
Lys Leu Pro His Tyr Leu Ile Arg Ala Arg Gln Tyr Ile His Asp Asn

```

```

65              70              75              80
Ala Arg Glu Ala Val His Leu Glu Asp Leu Glu Thr Ala Ala Gly Val
              85              90              95
Ser Arg Phe Lys Leu Phe Asp Ala Phe Arg Lys Tyr
              100              105

```

<210> 747  
 <211> 416  
 <212> DNA  
 <213> Homo sapiens

```

<400> 747
naccggttga tcgccgccga ccgtttcatc ccgcaatcac ccgacatggc ggcctatattt
60
ctgaatgccg atggcacgcc taaagccacc ggcacgctgc tcaagaaccc agcgctggcc
120
gccgtgttca aacgtatcgc caaggaagga ccggacgcgc tgtaccacgg gccgattgcc
180
gacgagatcg cgcgcaaggt tcagggcaac cgcaatgcgg gcagcctgtc gcaagcggac
240
ctcaaggctt acaccgcaa ggaacgcacg ccgctgtgca ccgactacaa gcaatatcag
300
gtgtgcggca tgccaccgcc gtcgtcaggc gggattgcgg tggcgcagat cctcggcacg
360
ctgcaggccg tggaagcccg cgaccacgc ctggccatcg ccccatgaa accggt
416

```

<210> 748  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens

```

<400> 748
Xaa Ala Leu Ile Ala Ala Asp Arg Phe Ile Pro Gln Ser Pro Asp Met
1      5      10      15
Ala Ala Tyr Phe Leu Asn Ala Asp Gly Thr Pro Lys Ala Thr Gly Thr
20     25     30
Leu Leu Lys Asn Pro Ala Leu Ala Ala Val Phe Lys Arg Ile Ala Lys
35     40     45
Glu Gly Pro Asp Ala Leu Tyr His Gly Pro Ile Ala Asp Glu Ile Ala
50     55     60
Arg Lys Val Gln Gly Asn Arg Asn Ala Gly Ser Leu Ser Gln Ala Asp
65     70     75     80
Leu Lys Ala Tyr Thr Ala Lys Glu Arg Thr Pro Leu Cys Thr Asp Tyr
85     90     95
Lys Gln Tyr Gln Val Cys Gly Met Pro Pro Pro Ser Ser Gly Gly Ile
100    105    110
Ala Val Ala Gln Ile Leu Gly Thr Leu Gln Ala Val Glu Ala Arg Asp
115    120    125
Pro Arg Leu Ala Ile Ala Pro Met Lys Pro
130    135

```

<210> 749  
 <211> 1211

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 749

nagtcctaga cgccagaccc gtcagaccc tcctgccagg tgacagccgc caagatgggg  
60  
tcctggggccc tgctgtggcc tccctgctg ttcaccgggc tgctcgtccg acccccgggg  
120  
accatggccc aggcccagta ctgctctgtg aacaaggaca tctttgaagt agaggagaac  
180  
acaaatgtca ccgagccgct ggtggacatc cacgtcccgg agggccagga ggtgaccctc  
240  
ggagccttgt ccacccctt tgcatttcgg atccagggaa accagctgtt tctcaactg  
300  
actcctgatt acgaggagaa gtcactgctt gaggtcagc tgctgtgtca gagcggaggc  
360  
acattggtga cccagctaag ggtgttcgtg tcagtgtgag acgtcaatga caatgcccc  
420  
gaattcccct ttaagaccaa ggagataagg gtggaggagg acacgaaagt gaactccacc  
480  
gtcatccccg agacgcaact gcaggctgag gaccgcgaca aggacgacat tctgttctac  
540  
accctccagg aaatgacagc aggtgccagt gactacttct ccctgggtgag tgtaaaccgt  
600  
cccgccctga ggctggaccg gccctggac ttctacgagc ggccgaacat gaccttctgg  
660  
ctgctggtgc gggacactcc gggggagaat gtggaacca gccacactgc caccgccaca  
720  
ctagtgtga acgtggtgcc cgccgacctg cggccccctg ggttcctgcc ctgcacctc  
780  
tcagatggct acgtctgcat tcaagctcag taccacgggg ctgtccccac ggggcacata  
840  
ctgccatctc ccctcgctct gcgtcccga ccatctacg ctgaggacgg agaccgcggc  
900  
atcaaccagc ccatcatcta cagcatcttt aggggaaacg tgaatgttac attcatcatc  
960  
caccagact cgggcaacct caccgtggcc aggagtgtcc ccagcccat gaccttcctt  
1020  
ctgctggtga agggccaaca ggccgacctt gccgctact cagtgaacca ggtcaccgtg  
1080  
gagggctgtg gctgcggccg ggagcccgc ccgcttcccc cagagcctgt atcgtggcac  
1140  
cgtggcgctg ggcgctggag cgggcgttgt ggtcaaggat gcagctgccc cttttcagcc  
1200  
tctgaggatc c  
1211

&lt;210&gt; 750

&lt;211&gt; 385

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 750

Met Gly Ser Trp Ala Leu Leu Trp Pro Pro Leu Leu Phe Thr Gly Leu

1	5	10	15
Leu Val Arg Pro Pro Gly Thr Met Ala Gln Ala Gln Tyr Cys Ser Val			
20	25	30	
Asn Lys Asp Ile Phe Glu Val Glu Glu Asn Thr Asn Val Thr Glu Pro			
35	40	45	
Leu Val Asp Ile His Val Pro Glu Gly Gln Glu Val Thr Leu Gly Ala			
50	55	60	
Leu Ser Thr Pro Phe Ala Phe Arg Ile Gln Gly Asn Gln Leu Phe Leu			
65	70	75	80
Asn Val Thr Pro Asp Tyr Glu Glu Lys Ser Leu Leu Glu Ala Gln Leu			
85	90	95	
Leu Cys Gln Ser Gly Gly Thr Leu Val Thr Gln Leu Arg Val Phe Val			
100	105	110	
Ser Val Leu Asp Val Asn Asp Asn Ala Pro Glu Phe Pro Phe Lys Thr			
115	120	125	
Lys Glu Ile Arg Val Glu Glu Asp Thr Lys Val Asn Ser Thr Val Ile			
130	135	140	
Pro Glu Thr Gln Leu Gln Ala Glu Asp Arg Asp Lys Asp Asp Ile Leu			
145	150	155	160
Phe Tyr Thr Leu Gln Glu Met Thr Ala Gly Ala Ser Asp Tyr Phe Ser			
165	170	175	
Leu Val Ser Val Asn Arg Pro Ala Leu Arg Leu Asp Arg Pro Leu Asp			
180	185	190	
Phe Tyr Glu Arg Pro Asn Met Thr Phe Trp Leu Leu Val Arg Asp Thr			
195	200	205	
Pro Gly Glu Asn Val Glu Pro Ser His Thr Ala Thr Ala Thr Leu Val			
210	215	220	
Leu Asn Val Val Pro Ala Asp Leu Arg Pro Pro Trp Phe Leu Pro Cys			
225	230	235	240
Thr Phe Ser Asp Gly Tyr Val Cys Ile Gln Ala Gln Tyr His Gly Ala			
245	250	255	
Val Pro Thr Gly His Ile Leu Pro Ser Pro Leu Val Leu Arg Pro Gly			
260	265	270	
Pro Ile Tyr Ala Glu Asp Gly Asp Arg Gly Ile Asn Gln Pro Ile Ile			
275	280	285	
Tyr Ser Ile Phe Arg Gly Asn Val Asn Gly Thr Phe Ile Ile His Pro			
290	295	300	
Asp Ser Gly Asn Leu Thr Val Ala Arg Ser Val Pro Ser Pro Met Thr			
305	310	315	320
Phe Leu Leu Leu Val Lys Gly Gln Gln Ala Asp Leu Ala Arg Tyr Ser			
325	330	335	
Val Thr Gln Val Thr Val Glu Gly Cys Gly Cys Gly Arg Glu Pro Ala			
340	345	350	
Pro Leu Pro Pro Glu Pro Val Ser Trp His Arg Gly Ala Trp Arg Trp			
355	360	365	
Ser Gly Arg Cys Gly Gln Gly Cys Ser Cys Pro Phe Ser Ala Ser Glu			
370	375	380	
Asp			
385			

&lt;210&gt; 751

&lt;211&gt; 345

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 751

cgcgtcgcgg tcacgtcaa cgacatgagc gaggtcaaca tcgacgcggc gctggtggcg  
 60  
 gcaggcggcg ggctgtcgcg caccgaggag aagctcgtcg agatgtcgaa cggctgcatc  
 120  
 tgctgcacgc tcgcgcacga cctgatgcag gaagtggcga gactggcggg cgaaggccgc  
 180  
 ttcgatgcgc tggatcatga gagcaccggc gtgtccgagc cgatgccggt cggccccacg  
 240  
 ttcgatttcc gtgaccagga cggcgtctcg ctccgccagc tcgcgcgggt ggataccatg  
 300  
 gtcaccgtcg tcgacgcgc gtccttcctg cgcgactacg gctcg  
 345

&lt;210&gt; 752

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 752

Arg Val Ala Val Ile Val Asn Asp Met Ser Glu Val Asn Ile Asp Ala  
 1 5 10 15  
 Ala Leu Val Ala Ala Gly Gly Gly Leu Ser Arg Thr Glu Glu Lys Leu  
 20 25 30  
 Val Glu Met Ser Asn Gly Cys Ile Cys Cys Thr Leu Arg Asp Asp Leu  
 35 40 45  
 Met Gln Glu Val Ala Arg Leu Ala Gly Glu Gly Arg Phe Asp Ala Leu  
 50 55 60  
 Val Ile Glu Ser Thr Gly Val Ser Glu Pro Met Pro Val Ala Ala Thr  
 65 70 75 80  
 Phe Asp Phe Arg Asp Gln Asp Gly Val Ser Leu Ala Asp Val Ala Arg  
 85 90 95  
 Leu Asp Thr Met Val Thr Val Val Asp Ala Ala Ser Phe Leu Arg Asp  
 100 105 110  
 Tyr Gly Ser  
 115

&lt;210&gt; 753

&lt;211&gt; 352

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 753

gcgcgccagt acgccaagac cgtccgcaag gaccgcaagg gcgaacggcg gcgtcggggc  
 60  
 gcgtcggact agtccacgat gcatccgaac cgcgccttcc gctttgccga tgatgtctcg  
 120  
 atgctcgatt tcgcggccaa gcgagccttt gcgcacatct tcgtgagcac gcccgagggg  
 180  
 cctatggtag cgcattgcccc gggtacgccc ttcgacggag ccttccgctt ccatgtcgcg  
 240  
 cgcggcaatc ggatcgcgcg gcacctggat ggcgcgacgc tgctgctcag catcagcgcg  
 300



accgacggct atatcagccc gagctggtac gccgacccgc agggaccaca gt  
352

<210> 754

<211> 91

<212> PRT

<213> Homo sapiens

<400> 754

Met	His	Pro	Asn	Arg	Ala	Phe	Arg	Phe	Ala	Asp	Asp	Val	Ser	Met	Leu
1			5						10					15	
Asp	Phe	Ala	Ala	Lys	Arg	Ala	Phe	Ala	His	Ile	Phe	Val	Ser	Thr	Pro
		20						25					30		
Glu	Gly	Pro	Met	Val	Ala	His	Ala	Pro	Val	Thr	Pro	Phe	Asp	Gly	Ala
		35					40					45			
Phe	Arg	Phe	His	Val	Ala	Arg	Gly	Asn	Arg	Ile	Ala	Arg	His	Leu	Asp
	50					55					60				
Gly	Ala	Thr	Leu	Leu	Leu	Ser	Ile	Ser	Ala	Thr	Asp	Gly	Tyr	Ile	Ser
65					70					75				80	
Pro	Ser	Trp	Tyr	Ala	Asp	Pro	Gln	Gly	Pro	Gln					
				85						90					

<210> 755

<211> 301

<212> DNA

<213> Homo sapiens

<400> 755

tgggatgcag ggtctttctt ctccaaggat ttcattcctg gagggagaaa agggccccag  
60  
ctgtctgcc acaaacccgg ttgccgggct ggagctcctc ccaggcccggt gtgaggaaga  
120  
gcaaaaggccg gcaggggctc gatgggacca gtcgctcgct caggcccagg aaaaccacac  
180  
agctgggggc tgtcaggatt ggaccagggt caggccggcc aggcgatggc gggaaaagca  
240  
ggcccactct gcagacctca atgtctcagg tgcactgcag ggcaaccccg cctaccccg  
300  
g  
301

<210> 756

<211> 99

<212> PRT

<213> Homo sapiens

<400> 756

Met	Gln	Gly	Leu	Ser	Ser	Pro	Arg	Ile	Ser	Phe	Leu	Glu	Gly	Glu	Lys
1				5					10					15	
Gly	Pro	Ser	Cys	Leu	Pro	Ser	Asn	Arg	Val	Ala	Gly	Leu	Glu	Leu	Leu
			20					25					30		
Pro	Gly	Pro	Cys	Glu	Glu	Glu	Gln	Arg	Pro	Ala	Gly	Ala	Arg	Trp	Asp
		35					40					45			
Gln	Ser	Leu	Ala	Gln	Ala	Gln	Glu	Asn	His	Thr	Ala	Gly	Gly	Cys	Gln

50                      55                      60  
 Asp Trp Thr Arg Val Arg Pro Ala Arg Arg Trp Arg Glu Lys Gln Ala  
 65                      70                      75                      80  
 His Ser Ala Asp Leu Asn Val Ser Gly Ala Leu Gln Gly Asn Pro Ala  
                     85                      90                      95  
 Tyr Pro Gly

<210> 757  
 <211> 311  
 <212> DNA  
 <213> Homo sapiens

<400> 757  
 actgaggcga tcgccagagg ggtgggcgtg cgagggtgc tcaacatcca gttcgccctg  
 60  
 gtctccgatg ttctctacgt catcgaggcc aaccccaggg catcgcgcac agtccccttc  
 120  
 gtctcaaagg catccggcgt gcagctcgcc aaagcggcgg ccctcatcat gacaggggag  
 180  
 acgatcgctt cgctcaggcg ctccggccac ctgcccaggg ccgaagccgc cgtcaccgat  
 240  
 cccgatgacc cgatcgccgt caaggaggcg gtcctaccct tcaaacgatt ccgcaccacc  
 300  
 gagggacgcg t  
 311

<210> 758  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 758  
 Thr Glu Ala Ile Ala Arg Gly Val Gly Val Arg Gly Leu Leu Asn Ile  
 1                      5                      10                      15  
 Gln Phe Ala Leu Val Ser Asp Val Leu Tyr Val Ile Glu Ala Asn Pro  
                     20                      25                      30  
 Arg Ala Ser Arg Thr Val Pro Phe Val Ser Lys Ala Ser Gly Val Gln  
                     35                      40                      45  
 Leu Ala Lys Ala Ala Ala Leu Ile Met Thr Gly Glu Thr Ile Ala Ser  
                     50                      55                      60  
 Leu Arg Arg Ser Gly His Leu Pro Glu Ala Asp Ala Ala Val Thr Asp  
 65                      70                      75                      80  
 Pro Asp Asp Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Lys Arg  
                     85                      90                      95  
 Phe Arg Thr Thr Glu Gly Arg  
                     100

<210> 759  
 <211> 391  
 <212> DNA  
 <213> Homo sapiens

<400> 759

gtgcacaccg gcaagctggt gtggaactgg gacagcggca acccggaaga cactacgccg  
 60  
 attgccgagg gcaagaccta caccgcaac tcgccgaaca tgtggtccat gttcgccgtc  
 120  
 gacgaaaaac tcggcatgct ctacctgccg atgggcaacc agaccccgga ccagttcggg  
 180  
 ggctaccgca cgctcgctc ggaactgcac gctgccggcc tgacagcgct ggatatcgac  
 240  
 actggtaaag tgcgctggca ctaccagttc acccaccatg acctgtggga catggacgtg  
 300  
 ggctggccagc cgagcctgat cgacatcaag accgccgccg gcgtgaaaca agccgtgatg  
 360  
 gcctcgacca agcaaggcag catctacgct t  
 391

<210> 760  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 760  
 Val His Thr Gly Lys Leu Val Trp Asn Trp Asp Ser Gly Asn Pro Asp  
 1 5 10 15  
 Asp Thr Thr Pro Ile Ala Glu Gly Lys Thr Tyr Thr Arg Asn Ser Pro  
 20 25 30  
 Asn Met Trp Ser Met Phe Ala Val Asp Glu Lys Leu Gly Met Leu Tyr  
 35 40 45  
 Leu Pro Met Gly Asn Gln Thr Pro Asp Gln Phe Gly Gly Tyr Arg Thr  
 50 55 60  
 Pro Ala Ser Glu Leu His Ala Ala Gly Leu Thr Ala Leu Asp Ile Asp  
 65 70 75 80  
 Thr Gly Lys Val Arg Trp His Tyr Gln Phe Thr His His Asp Leu Trp  
 85 90 95  
 Asp Met Asp Val Gly Gly Gln Pro Ser Leu Ile Asp Ile Lys Thr Ala  
 100 105 110  
 Ala Gly Val Lys Gln Ala Val Met Ala Ser Thr Lys Gln Gly Ser Ile  
 115 120 125  
 Tyr Ala  
 130

<210> 761  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

<400> 761  
 cctaggtagg cccaaagggg cctaactttc ttgctgccct ggtggagcaa gaaatatctt  
 60  
 ctaggagagg ccaatccttc cctgccccac agctccttct ctgcaaagct cagggggcaa  
 120  
 tcaggtagct cctgccccag agggccccat ggttcctcgc ctaaggaagg cagggcgggg  
 180  
 cattggggagc cgttgacagc tgggctcagc tggggggagg ggtcagtttg ggagcaggtg  
 240

cagatttcag ggaggggggg gcctaaaggg aagtagggat cttggtaggc tgcaaaattt  
 300  
 tcctcccat ccccatcca caga  
 324

<210> 762

<211> 105

<212> PRT

<213> Homo sapiens

<400> 762

Met Gly Asp Gly Glu Asn Phe Ala Ala Tyr Gln Asp Pro Tyr Phe  
 1 5 10 15  
 Pro Leu Gly Pro Leu Pro Glu Ile Cys Thr Cys Ser Gln Thr Asp  
 20 25 30  
 Pro Ser Pro Gln Leu Ser Pro Ala Val Asn Gly Ser Gln Cys Pro Ala  
 35 40 45  
 Leu Pro Ser Leu Gly Glu Glu Pro Trp Gly Pro Leu Gly Gln Glu Val  
 50 55 60  
 Pro Asp Cys Pro Leu Ser Phe Ala Glu Lys Glu Leu Trp Gly Arg Glu  
 65 70 75 80  
 Gly Leu Ala Ser Pro Arg Arg Tyr Phe Leu Leu His Gln Gly Ser Lys  
 85 90 95  
 Lys Val Arg Pro Leu Trp Ala Tyr Leu  
 100 105

<210> 763

<211> 301

<212> DNA

<213> Homo sapiens

<400> 763

acgcgttatg ggcgccccgg atgggcgatg cgctatccca cacctcgatg atggcggaca  
 60  
 tcctcggcgg tgtgctggaa gtggcgccca atatcgcat tactgcgggc ggcaccgctg  
 120  
 ccgcggtggc cgccaccggc ttaccgagg ccaccggcgg cctcggctgc ttctgctgg  
 180  
 gcgctgcctt gggcaccatt gccggcctgg ccatgagcaa cattggcgcg gacacagggc  
 240  
 tgaccaagat atgcaatgcc tttacaacg ccttatttgc gccaccgtg catgcgaaca  
 300  
 t  
 301

<210> 764

<211> 100

<212> PRT

<213> Homo sapiens

<400> 764

Met Phe Ala Cys Thr Val Gly Ala Asn Lys Ala Leu Leu Lys Ala Leu  
 1 5 10 15  
 His Ile Leu Val Ser Pro Val Ser Ala Pro Met Leu Leu Met Ala Arg

```

      20      25      30
Pro Ala Met Val Pro Lys Ala Ala Pro Ser Arg Lys Gln Pro Arg Pro
      35      40      45
Pro Val Ala Ser Val Lys Pro Val Ala Ala Thr Ala Ala Val Ala
      50      55      60
Pro Ala Val Ile Ala Ile Leu Ala Ala Thr Ser Ser Thr Pro Pro Arg
      65      70      75      80
Met Ser Ala Ile Ile Glu Val Trp Asp Ser Ala Ser Pro Ile Arg Ala
      85      90      95
Ala His Asn Ala
      100

```

<210> 765  
 <211> 831  
 <212> DNA  
 <213> Homo sapiens

```

<400> 765
ngcacactcc agcctctgtt ctttctctcc ttgtgccttt gcccttacca cggttcctca
60
taacattgtt gttcctgtat ttaaggcctt ataaacaggg agatgcgcca cctcatcagt
120
agcctccaga atcacaatca ccagctgaaa ggggaggtcc tgagatataa gcggaaattg
180
agagaagccc agtctgacct gaacaagaca cgcttgcgta gtggtagtgc cctcctgcag
240
tcccagtcta gtactgagga cccgaaggat gagcctgcgg agctaaaacc agattctggg
300
gacttattcct ccagctcctc agcttcaaag gcattctcagg aggatgccaa tgaaatcaag
360
tctaaacggg atgaagaaga acgagaacga gaaaggaggg agaaggagag ggaacgagaa
420
agagaacggg agaaggagaa ggagagagaa cgagagaagc agaagctaaa agagtcagaa
480
aaagagagag attctgctaa ggataaagag aaaggcaaac atgatgatgg acggaaaaag
540
gaagcagaaa ttatcaaaca attgaagatt gaactcaaga aggcacagga gagccaaaag
600
gagatgaaac tattgctgga tatgtaccgt tctgccccaa aggaacagag agacaaagtt
660
cagctgatgg cagctgagaa gaagtctaag gcagagttgg aagatctaag gcaaagactc
720
aaggatctgg aagataaaga gaagaaagag aacaagaaaa tggctgatga ggatgccttg
780
aggaagatcc gggcagtggg ggagcagata gaatacctac agaagaagct a
831

```

<210> 766  
 <211> 243  
 <212> PRT  
 <213> Homo sapiens

```

<400> 766
Met Arg His Leu Ile Ser Ser Leu Gln Asn His Asn His Gln Leu Lys

```

1	5	10	15
Gly Glu Val	Leu Arg Tyr	Lys Arg Lys Leu Arg	Glu Ala Gln Ser Asp
	20	25	30
Leu Asn Lys	Thr Arg Leu Arg	Ser Gly Ser Ala Leu	Leu Gln Ser Gln
	35	40	45
Ser Ser Thr	Glu Asp Pro	Lys Asp Glu Pro	Ala Glu Leu Lys Pro Asp
	50	55	60
Ser Gly Asp	Leu Ser Ser	Gln Ser Ser Ala	Ser Lys Ala Ser Gln Glu
65		70	75
Asp Ala Asn	Glu Ile Lys	Ser Lys Arg Asp	Glu Glu Glu Arg Glu Arg
	85	90	95
Glu Arg Arg	Glu Lys Glu Arg	Glu Arg Glu Arg	Glu Lys Glu
	100	105	110
Lys Glu Arg	Glu Arg Glu Lys	Gln Lys Leu Lys	Glu Ser Glu Lys Glu
	115	120	125
Arg Asp Ser	Ala Lys Asp	Lys Glu Lys Gly	Lys His Asp Asp Gly Arg
	130	135	140
Lys Lys Glu	Ala Glu Ile	Lys Gln Leu Lys	Ile Glu Leu Lys Lys
145		150	155
Ala Gln Glu	Ser Gln Lys	Glu Met Lys	Leu Leu Leu Asp Met Tyr Arg
	165	170	175
Ser Ala Pro	Lys Glu Gln Arg	Asp Lys Val	Gln Leu Met Ala Ala Glu
	180	185	190
Lys Lys Ser	Lys Ala Glu Leu	Glu Asp Leu Arg	Gln Arg Leu Lys Asp
	195	200	205
Leu Glu Asp	Lys Glu Lys	Lys Glu Asn Lys	Lys Met Ala Asp Glu Asp
	210	215	220
Ala Leu Arg	Lys Ile Arg	Ala Val Glu Glu	Gln Ile Glu Tyr Leu Gln
225		230	235
Lys Lys Leu			240

&lt;210&gt; 767

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 767

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120

gaggccggca gctggcgctg gggatccctg ctcttcgctc tcttcttggc tgcgtcccta  
180

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240

cagaacgtca ccctcacctg caggctcttg ggcctgttg acaaagggca cgatgtgacc  
300

ttctacaaga cgtggtaccg cagctcgagg ggcgaggtgc agacctgctc agagcgccg  
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420

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431

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 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 768  
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 Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln  
 35 40 45  
 Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His  
 50 55 60  
 Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val  
 65 70 75 80  
 Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp  
 85 90 95  
 Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser  
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<210> 769  
 <211> 422  
 <212> DNA  
 <213> Homo sapiens

<400> 769  
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 180  
 aaaaatcccg ggtcggccca caaataaatc aattgcgccg ctctccgag ttcttccatg  
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 an  
 422

<210> 770  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 770  
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 1 5 10 15  
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          20          25          30
Ser Ser Glu Phe Phe His Val Asn Asp Leu Pro Trp Leu Leu Lys Pro
      35          40          45
Arg Pro Ser Arg Pro Trp Asp Ser Lys Val Asp Val Asp Pro Thr Asp
      50          55          60
Phe Gly Pro Val Gly Val Gly Ile Gly Gly Arg Val Val Thr Ala His
65          70          75          80
Val Asp Asp Leu His Arg His Arg Gln Arg Val Phe Val Val Val Met
      85          90          95
Pro Asp Xaa

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&lt;210&gt; 771

&lt;211&gt; 369

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 771

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120
ctggtgccac acgtgcagac gttaactgc aaagtggcgg cctcgcgcct gcgtgattgc
180
gccagggcca tgggtgtcga tgtcagtcaa atgacagcag aacagggcgc acaggcgtgt
240
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300
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360
ttgattaat
369

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&lt;210&gt; 772

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 772

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Ala Tyr Ala Gln Phe Leu Ala Gly Met Ala Phe Asn Asn Ala Ser Leu
 1          5          10          15
Gly Tyr Val His Ala Met Ala His Gln Leu Gly Gly Phe Tyr Asp Leu
      20          25          30
Pro His Gly Val Cys Asn Ala Ile Leu Leu Pro His Val Gln Thr Phe
      35          40          45
Asn Cys Lys Val Ala Ala Ser Arg Leu Arg Asp Cys Ala Gln Ala Met
      50          55          60
Gly Val Asp Val Ser Gln Met Thr Ala Glu Gln Gly Ala Gln Ala Cys
65          70          75          80
Ile Ala Glu Ile Arg Ser Leu Ala Arg Gln Val Asn Ile Pro Val Gly
      85          90          95
Leu Arg Asp Leu Asn Val Lys Glu Ala Asp Phe Pro Ile Leu Ala Thr
      100          105          110
Asn Ala Leu Lys Asp Pro Val Gly Leu Ile Asn

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115

120

<210> 773  
 <211> 309  
 <212> DNA  
 <213> Homo sapiens

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 309

<210> 774  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 774  
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 Ala Ala Asp Ile Gly Tyr Leu Ile Arg Val Glu Pro Gly Val Gln Thr  
 20 25 30  
 Pro Glu Phe Thr Leu Glu Asn Ala Ser Gly Ser Cys Arg Asp Ser Ala  
 35 40 45  
 Trp Leu Leu Val Gln Leu Leu Arg Asn Leu Gly Leu Ala Ala Arg Phe  
 50 55 60  
 Val Ser Gly Tyr Leu Ile Gln Leu Thr Ala Asp Val Lys Ala Leu Asp  
 65 70 75 80  
 Gly Pro Ser Gly Thr Glu Val Asp Phe Thr Asp Leu His Ala Trp Cys  
 85 90 95  
 Glu Val Tyr Leu Pro Gly Ala  
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<210> 775  
 <211> 4125  
 <212> DNA  
 <213> Homo sapiens

<400> 775  
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240  
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360  
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420  
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<210> 776

<211> 483

<212> PRT

<213> Homo sapiens

<400> 776

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Ser	Ser	Thr	Asp	His	Thr	Pro	Thr	Lys	Ala	Gln	Lys	Asn	Val	Ala	Thr
			20					25					30		
Ser	Glu	Asp	Ser	Asp	Leu	Ser	Met	Arg	Thr	Leu	Ser	Thr	Pro	Ser	Pro
		35				40						45			
Ala	Leu	Ile	Cys	Pro	Pro	Asn	Leu	Pro	Gly	Phe	Gln	Asn	Gly	Arg	Gly
	50					55				60					
Ser	Ser	Thr	Ser	Ser	Ser	Ser	Ile	Thr	Gly	Glu	Thr	Val	Ala	Met	Val
65					70				75					80	
His	Ser	Pro	Pro	Pro	Thr	Arg	Leu	Thr	His	Pro	Leu	Ile	Arg	Leu	Ala
			85					90					95		
Ser	Arg	Pro	Gln	Lys	Asp	Gln	Ala	Ser	Ile	Asp	Arg	Leu	Pro	Asp	His
		100						105					110		
Ser	Met	Val	Gln	Ile	Phe	Ser	Phe	Leu	Pro	Thr	Asn	Gln	Leu	Cys	Arg
	115					120					125				
Cys	Ala	Arg	Val	Cys	Arg	Arg	Trp	Tyr	Asn	Leu	Ala	Trp	Asp	Pro	Arg
	130				135					140					
Leu	Trp	Arg	Thr	Ile	Arg	Leu	Thr	Gly	Glu	Thr	Ile	Asn	Val	Asp	Arg
145				150					155					160	
Ala	Leu	Lys	Val	Leu	Thr	Arg	Arg	Leu	Cys	Gln	Asp	Thr	Pro	Asn	Val
			165					170					175		
Cys	Leu	Met	Leu	Glu	Thr	Val	Thr	Val	Ser	Gly	Cys	Arg	Arg	Leu	Thr

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Leu Glu Val Ser Gly Cys Tyr Asn Ile Ser Asn Glu Ala Val Phe Asp
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Val Val Ser Leu Cys Pro Asn Leu Glu His Leu Asp Val Ser Gly Cys
      225      230      235      240
Ser Lys Val Thr Cys Ile Ser Leu Thr Arg Glu Ala Ser Ile Lys Leu
      245      250      255
Ser Pro Leu His Gly Lys Gln Ile Ser Ile Arg Tyr Leu Asp Met Thr
      260      265      270
Asp Cys Phe Val Leu Glu Asp Glu Gly Leu His Thr Ile Ala Ala His
      275      280      285
Cys Thr Gln Leu Thr His Leu Tyr Leu Arg Arg Cys Val Arg Leu Thr
      290      295      300
Asp Glu Gly Leu Arg Tyr Leu Val Ile Tyr Cys Ala Ser Ile Lys Glu
      305      310      315      320
Leu Ser Val Ser Asp Cys Arg Phe Val Ser Asp Phe Gly Leu Arg Glu
      325      330      335
Ile Ala Lys Leu Glu Ser Arg Leu Arg Tyr Leu Ser Ile Ala His Cys
      340      345      350
Gly Arg Val Thr Asp Val Gly Ile Arg Tyr Val Ala Lys Tyr Cys Ser
      355      360      365
Lys Leu Arg Tyr Leu Asn Ala Arg Gly Cys Glu Gly Ile Thr Asp His
      370      375      380
Gly Val Glu Tyr Leu Ala Lys Asn Cys Thr Lys Leu Lys Ser Leu Asp
      385      390      395      400
Ile Gly Lys Cys Pro Leu Val Ser Asp Thr Gly Leu Glu Cys Leu Ala
      405      410      415
Leu Asn Cys Phe Asn Leu Lys Arg Leu Ser Leu Lys Ser Cys Glu Ser
      420      425      430
Ile Thr Gly Gln Gly Leu Gln Ile Val Ala Ala Asn Cys Phe Asp Leu
      435      440      445
Gln Thr Leu Asn Val Gln Asp Cys Glu Val Ser Val Glu Ala Leu Arg
      450      455      460
Phe Val Lys Arg His Cys Lys Arg Cys Val Ile Glu His Thr Asn Pro
      465      470      475      480
Ala Phe Phe

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&lt;210&gt; 777

&lt;211&gt; 705

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 777

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120
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240

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 420  
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 705

&lt;210&gt; 778

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 778

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Gly	Gly	Ala	Glu	Lys	Ala	Asp	Phe	Asn	Ala	Lys	Arg	Lys	Lys	Lys	Val
		20						25					30		
Leu	Glu	Ile	His	Gln	Ala	Leu	Asn	Ser	Asp	Pro	Thr	Asp	Val	Ala	Ala
	35						40					45			
Leu	Arg	Arg	Met	Ala	Ile	Ser	Glu	Gly	Gly	Leu	Leu	Thr	Asp	Glu	Ile
	50					55					60				
Arg	Arg	Lys	Val	Trp	Pro	Lys	Leu	Leu	Asn	Val	Asn	Ala	Asn	Asp	Pro
65					70				75					80	
Pro	Pro	Ile	Ser	Gly	Lys	Asn	Leu	Arg	Gln	Met	Ser	Lys	Asp	Tyr	Gln
			85					90					95		
Gln	Val	Leu	Leu	Asp	Val	Arg	Arg	Ser	Leu	Arg	Arg	Phe	Pro	Pro	Gly
		100					105					110			
Glu	Lys	Leu	Ser	Arg	Ser	Cys	His	Ile	Trp	Glu	Glu	Arg	Ile	Cys	Phe
	115						120					125			
Arg	Ser	Tyr	His	Val	Thr										
	130														

&lt;210&gt; 779

&lt;211&gt; 322

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 779

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<210> 780  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 780  
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 35 40 45  
 Ala Arg Pro Ser Lys Tyr Glu Ser Pro Asn Ala Ser Asn Phe Ile Val  
 50 55 60  
 Arg His Val Ala Thr Gly Lys Glu Gly Thr Asp Asp Glu Tyr Ala Asn  
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 Thr Glu Glu Met Ile Gly Leu Ala Thr  
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<210> 781  
 <211> 297  
 <212> DNA  
 <213> Homo sapiens

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 gaatgtgtgt ctgtgtatgg aatatgtgtg agtatngaa tgtgtgtgtg tgtttggaat  
 180  
 gtatcgaatg tgtgtctgtg tgtaaggaat gtgtgtgtat ggaatgtgtt tacgtgcatg  
 240  
 tgtctggaat gtgtgtgtat ggaatgtgtg tgtatgtgta tgngaattgt tgtgtgt  
 297

<210> 782  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 782  
 Xaa Arg Val Pro Gly Met Cys Val Cys Val Cys Val Cys Met Tyr Val  
 1 5 10 15  
 Cys Met Glu Cys Val Cys Met Xaa Ile Cys Val Cys Met Xaa Met Cys

```

      20      25      30
Val Cys Val Trp Asn Val Cys Met Glu Cys Val Ser Val Tyr Gly Ile
      35      40      45
Cys Val Ser Met Xaa Met Cys Val Cys Val Trp Asn Val Ser Asn Val
      50      55      60
Cys Leu Cys Val Arg Asn Val Cys Val Trp Asn Val Phe Thr Cys Met
      65      70      75      80
Cys Leu Glu Cys Val Cys Met Glu Cys Val Cys Met Cys Met Xaa Met
      85      90      95
Cys Val Cys

```

<210> 783  
 <211> 612  
 <212> DNA  
 <213> Homo sapiens

```

<400> 783
accggtgacg taactgctcc cgctggcagc ttcgagggcg atgtcgattt gcggtgcccg
60
caccgggtcg agtgagctgc ccagcagcaa gcccaccaca tcggtgacca gaccgatcac
120
tttgttgagc acgtcgatga cgggcaactt caaggaaatc caggtgcgga cttgcgcggt
180
ccgcacaaaa atcggctggg tgcgatcaa ctgctgggtg ccaatcgag aatttgcgcg
240
gttcgatgac acgtgtcttc accgtgatat tcagcagccc cagtacgtcc accggcaact
300
cgacggccac cgcgctggtt ttgttgga gctgcacaaa gccctgaatc aggttgaaca
360
gttgacaggtt gacgtccagg gcgctcttgt ccgtgccgtt ttgtatattg atcaggtcgc
420
ccaggtgcag gatctgcgtg cctggggcaa tcagcttgat tgcttcgagg ttattgatca
480
ccacctggac cgcattaccg cccagcttga gcacatcgat ggcggcctgg atcaactggc
540
cgacggctgc gtcggtcttg agcaactggt cgtagtgtgc ggcgctgacg ttgaggcgga
600
tggccgacgc gt
612

```

<210> 784  
 <211> 190  
 <212> PRT  
 <213> Homo sapiens

```

<400> 784
Met Ser Ile Cys Val Pro Gly Thr Gly Ser Ser Glu Leu Pro Ser Ser
1      5      10      15
Lys Pro Thr Thr Ser Val Thr Arg Pro Ile Thr Leu Leu Ser Thr Ser
20      25      30
Met Thr Gly Asn Phe Lys Glu Ile Gln Val Arg Thr Cys Ala Val Arg
35      40      45
Thr Lys Ile Gly Trp Val Ser Ile Asn Cys Gly Leu Pro Ile Ala Glu

```



```

      50              55              60
Phe Ala Arg Phe Asp Asp Thr Cys Leu His Arg Asp Ile Gln Gln Pro
65              70              75              80
Gln Tyr Val His Arg Gln Leu Asp Gly His Arg Ala Gly Phe Val Gly
      85              90              95
Gln Leu His Lys Ala Leu Asn Gln Val Glu Gln Leu Gln Val Asp Val
      100              105              110
Gln Gly Ala Leu Val Arg Ala Val Leu Tyr Ile Asp Gln Val Ala Gln
      115              120              125
Val Gln Asp Leu Arg Ala Trp Gly Asn Gln Leu Asp Cys Phe Glu Val
      130              135              140
Ile Asp His His Leu Asp Arg Ile Thr Ala Gln Leu Glu His Ile Asp
145              150              155              160
Gly Gly Leu Asp Gln Leu Ala Asp Gly Arg Val Gly Leu Glu Gln Leu
      165              170              175
Val Val Val Ala Gly Ala Asp Val Glu Ala Asp Gly Arg Arg
      180              185              190

```

<210> 785  
 <211> 408  
 <212> DNA  
 <213> Homo sapiens

```

<400> 785
accttggaact acttcactat cgaccctcgg ctaggcgacg acgatgactt cgatcacctg
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cttcaggccg cccacgctcg tggctgtgca gtactgctcg acgggggtggt caaccacgtc
120
tcgcgctgca accgcatcgt gcaggatgcg cagagtgtcg ggccagattc agacgccggc
180
cgtatgggttc gctgggtgtga ggggcgcctc gacgttttcg agggtcatag tgacctggtc
240
gcactcaacc acgacaaccc cgcagtgcgg gaacatgtca cccggatcat gaactattgg
300
tgcggtcgcg gtgttgacgg ctggcggctg gacgccgcta ttccgtcaat cctgagttct
360
gggctgcggt gctgcctccg gtgcgagaga agcgccctga cgtgagga
408

```

<210> 786  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

```

<400> 786
Thr Leu Asp Tyr Phe Thr Ile Asp Pro Arg Leu Gly Asp Asp Asp Asp
1      5      10      15
Phe Asp His Leu Leu Gln Ala Ala His Ala Arg Gly Leu Ser Val Leu
      20      25      30
Leu Asp Gly Val Val Asn His Val Ser Arg Arg Asn Arg Ile Val Gln
      35      40      45
Asp Ala Gln Ser Ala Gly Pro Asp Ser Asp Ala Gly Arg Met Val Arg
      50      55      60
Trp Cys Glu Gly Arg Leu Asp Val Phe Glu Gly His Ser Asp Leu Val

```

```

65          70          75          80
Ala Leu Asn His Asp Asn Pro Ala Val Arg Glu His Val Thr Arg Ile
      85          90          95
Met Asn Tyr Trp Cys Gly Arg Gly Val Asp Gly Trp Arg Leu Asp Ala
      100        105        110
Ala Ile Pro Ser Ile Leu Ser Ser Gly Leu Arg Cys Cys Leu Arg Cys
      115        120        125
Glu Arg Ser Ala Leu Thr
      130

```

&lt;210&gt; 787

&lt;211&gt; 310

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 787

```

acgcgtgaag gggaatgaaa gggtttttcc tggatcaaaa tgatgcttgt ggcagacaca
60
gttggaacca cagacgatgc cacgcttggtg tcagcagtgc gacactggcc cacgtggcgt
120
ccttgggtctc tectcattgc tgccgtcact gtgtgctggg catgccctgc agttacccca
180
aagctttatg tcacaacatt gaggctggcg gagaaagacc ggcccccttca cccacacctta
240
gacttcctgg aagggccgcc cgggtccaca acctggcccc ttaactccct gggcagctgc
300
tggggggagaa
310

```

&lt;210&gt; 788

&lt;211&gt; 90

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 788

```

Met Met Leu Val Ala Asp Thr Val Gly Thr Thr Asp Asp Ala Thr Leu
1          5          10          15
Val Ser Ala Val Arg His Trp Pro Thr Trp Arg Pro Trp Ser Leu Leu
      20          25          30
Ile Ala Ala Val Thr Val Cys Trp Ala Cys Pro Ala Val Thr Pro Lys
      35          40          45
Leu Tyr Val Thr Thr Leu Arg Leu Ala Glu Lys Asp Arg Pro Leu His
      50          55          60
Pro Thr Leu Asp Phe Leu Glu Gly Pro Pro Gly Ser Thr Thr Trp Pro
65          70          75          80
Val Asn Ser Leu Gly Ser Cys Trp Gly Arg
      85          90

```

&lt;210&gt; 789

&lt;211&gt; 369

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 789

acgcgtgaag ttgcagcagc aagcaatctg cctcgcttct ggtgccacc gaaaccaagg  
 60  
 tctgccagac agcagcgtg ggacctctcc cctccccagc aggatgggcc ggctctggaa  
 120  
 gcacgaggtg ttccaaagt caaacaagct gctgttaaata aattattccc aaacgccaaa  
 180  
 gcccttgctg gtttgcttgc ttgctttttt ctttttttgc ctgcacaga tatcgctagg  
 240  
 gcagagtatt gacatttcgt tttctttttg ttatgggtga taaagcacgg tgtttcttgt  
 300  
 gagtgtatgc ctgtatttcc ctgcagagct gattgccagt ccattttctt ctatcccatc  
 360  
 cccattttc  
 369

<210> 790  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

<400> 790  
 Met Asp Trp Gln Ser Ala Leu Gln Gly Asn Thr Gly Ile His Ser Gln  
 1 5 10 15  
 Glu Thr Pro Cys Phe Ile Thr His Asn Lys Lys Lys Thr Lys Cys Gln  
 20 25 30  
 Tyr Ser Ala Leu Ala Ile Ser Val Arg Gly Lys Lys Arg Lys Lys Gln  
 35 40 45  
 Ala Ser Lys Pro Ala Arg Ala Leu Ala Phe Gly Asn Asn Tyr Leu Thr  
 50 55 60  
 Ala Ala Cys Leu His Phe Gly Thr Pro Arg Ala Ser Arg Ala Gly Pro  
 65 70 75 80  
 Ser Cys Trp Gly Gly Glu Arg Ser Gln Arg Cys Cys Leu Ala Asp Leu  
 85 90 95  
 Gly Phe Gly Gly His Gln Lys Arg Gly Arg Leu Leu Ala Ala Ala Thr  
 100 105 110  
 Ser Arg

<210> 791  
 <211> 420  
 <212> DNA  
 <213> Homo sapiens

<400> 791  
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 60  
 ggtcttccag ttcttggtgt gaaatggtat cgaaataaat ctttactaga gccagatgaa  
 120  
 agaatcaaaa tggaaagagt gggtaatgtg tgttcactgg aaatttctaa cattcaaaaa  
 180  
 ggagaagggg gagagtacat gtgtcatgct gtaaacatca taggggaagc aaagagcttt  
 240  
 gcaaatgtag acataatgcc ccaggaagaa agagtgggtg cactaccacc tccagtaaca  
 300

catcagcatg tcatggagtt tgatttggaa cacaccacat catcaagaac accttctcct  
360

caagaaattg tcctggaagt tgaattaagt gaaaaagacg ttaaagaatt tgagaagcag  
420

<210> 792

<211> 138

<212> PRT

<213> Homo sapiens

<400> 792

Thr	Lys	Arg	Lys	Val	Tyr	Glu	Asn	Thr	Thr	Leu	Gly	Phe	Ile	Val	Glu
1				5					10					15	
Val	Glu	Gly	Leu	Pro	Val	Pro	Gly	Val	Lys	Trp	Tyr	Arg	Asn	Lys	Ser
			20					25					30		
Leu	Leu	Glu	Pro	Asp	Glu	Arg	Ile	Lys	Met	Glu	Arg	Val	Gly	Asn	Val
			35				40					45			
Cys	Ser	Leu	Glu	Ile	Ser	Asn	Ile	Gln	Lys	Gly	Glu	Gly	Gly	Glu	Tyr
	50					55					60				
Met	Cys	His	Ala	Val	Asn	Ile	Ile	Gly	Glu	Ala	Lys	Ser	Phe	Ala	Asn
	65				70					75					80
Val	Asp	Ile	Met	Pro	Gln	Glu	Glu	Arg	Val	Val	Ala	Leu	Pro	Pro	Pro
				85					90					95	
Val	Thr	His	Gln	His	Val	Met	Glu	Phe	Asp	Leu	Glu	His	Thr	Thr	Ser
			100					105					110		
Ser	Arg	Thr	Pro	Ser	Pro	Gln	Glu	Ile	Val	Leu	Glu	Val	Glu	Leu	Ser
		115					120					125			
Glu	Lys	Asp	Val	Lys	Glu	Phe	Glu	Lys	Gln						
	130						135								

<210> 793

<211> 479

<212> DNA

<213> Homo sapiens

<400> 793

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60  
ccgcgaacag tactgcggga acccaaacga tcatttttaa cccagacgt ccctgaacca  
120  
aagccaaagt ctacaggtca ctggggcaga ggccgccga aaccagcttc ccctcccggc  
180  
ctaggcgcgc caggtccccg ccagccggg gegatccttt ggtcggacag tgaggttggg  
240  
agccccaccgc acccaagtcc gccgcattcca ccggcgagc gcgacccccg acgggcagcc  
300  
gctcaccttc tcctggcccc ggcttcagga aaactgcctg gaggtggccg gggttcctta  
360  
gcggaggctg ggcggggggc ttcgcgcctg cctcagcttc cccatccgtg gcccggggga  
420  
tgagagccgc tgcgcgcaga ggtgcggca ggtcccagcc aggtgccctg gaacgtgga  
479

<210> 794

<211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 794  
 Xaa Ala Cys Arg Phe Ser Glu Ile His Tyr Gly Asn Val Arg Val Val  
 1 5 10 15  
 Glu Met Leu Arg Pro Arg Thr Val Leu Arg Glu Pro Lys Arg Ser Phe  
 20 25 30  
 Leu Thr Pro Asp Val Pro Glu Pro Lys Pro Lys Ser Thr Gly His Trp  
 35 40 45  
 Gly Arg Gly Arg Pro Lys Pro Ala Ser Pro Pro Gly Leu Gly Ala Pro  
 50 55 60  
 Gly Pro Arg Pro Ala Gly Ala Ile Leu Trp Ser Asp Ser Glu Val Gly  
 65 70 75 80  
 Ser Pro Pro His Pro Ser Pro Pro His Pro Pro Gly Ala Gly Asp Pro  
 85 90 95  
 Arg Arg Ala Ala Ala His Leu Leu Leu Ala Pro Ala Ser Gly Lys Leu  
 100 105 110  
 Pro Gly Gly Gly Arg Gly Ser Leu Ala Glu Ala Gly Arg Arg Ala Ser  
 115 120 125  
 Arg Leu Pro Gln Ser Pro His Pro Trp Pro Gly Gly Trp Ser Pro Leu  
 130 135 140  
 Arg Ala Glu Ala Ala Ala Gly Pro Ser Gln Val Pro Trp Asn Val  
 145 150 155

<210> 795  
 <211> 1418  
 <212> DNA  
 <213> Homo sapiens

<400> 795  
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 60  
 ccggactacg aggcgctgcc ggctggagcc actgtcacca cgcacatggt ggcaggcgcc  
 120  
 gtggcaggga tcctggagca ctgcgtgatg taccctatcg actgctcaa gaccgggatg  
 180  
 cagagtctac agcctgaccc agctgcccgc tatcgcaatg tggtggaggc cctctggagg  
 240  
 attataagaa cggagggcct atggaggccc atgagggggc tgaacgtcac agcaacaggc  
 300  
 gcagggcctg cccacgcctt ttattttgcc tgctacgaaa agttaaaaaa gacattgagt  
 360  
 gatgtaatcc accctggggg caatagccat attgccaatg gtgcggccgg gtgtgtggca  
 420  
 acattacttc atgatgcagc catgaaccct gcggaaggct gatctgctga cttggggctc  
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 gactgtgtac gggcagtgtg gcaaaatgaa ggggcccggg ccttttaccg cagctacacc  
 660

acccagctga ccatgaacgt tcctttccaa gccattcact tcatgaccta tgaattcctg  
 720  
 caggagcact ttaaccccc gagacggtag aacccaagct cccacgtcct ctctggagct  
 780  
 tgcgcaggag ctgtagctgc cgcagccaca accccactgg acgtttgcaa aacactgctc  
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 aacacccagg agtccttggc tttgaactca cacattacag gacatatcac aggcattggct  
 900  
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 960  
 gccagagtaa ttaccagat cccctccaca gccatcgcat ggtctgtgta tgagttcttc  
 1020  
 aaatacctaa tcactaaaag gcaagaagag tggagggtg gcaagtgaag tagcactgaa  
 1080  
 cgaagccagg ggttcagatg aactgctgc atcctgggtca cattctctgt ctctggaat  
 1140  
 gctccacact caagtggagt tagaaggaa gtagaggggc tctccccag gattttggtg  
 1200  
 ttttgactaa caccagtcc tgccaacctc tgttgccacc acctttcctt ccaggcccta  
 1260  
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 1380  
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 1418

<210> 796

<211> 176

<212> PRT

<213> Homo sapiens

<400> 796

Met	Ala	Leu	Leu	Val	Lys	Gln	Arg	Met	Gln	Met	Tyr	Asn	Ser	Pro
1			5					10				15		
Tyr	His	Arg	Val	Thr	Asp	Cys	Val	Arg	Ala	Val	Trp	Gln	Asn	Glu
		20					25					30		Gly
Ala	Gly	Ala	Phe	Tyr	Arg	Ser	Tyr	Thr	Thr	Gln	Leu	Thr	Met	Asn
		35					40				45			Val
Pro	Phe	Gln	Ala	Ile	His	Phe	Met	Thr	Tyr	Glu	Phe	Leu	Gln	Glu
	50				55					60				His
Phe	Asn	Pro	Gln	Arg	Arg	Tyr	Asn	Pro	Ser	Ser	His	Val	Leu	Ser
65				70					75					80
Ala	Cys	Ala	Gly	Ala	Val	Ala	Ala	Ala	Thr	Thr	Pro	Leu	Asp	Val
			85					90					95	
Cys	Lys	Thr	Leu	Leu	Asn	Thr	Gln	Glu	Ser	Leu	Ala	Leu	Asn	Ser
		100					105						110	His
Ile	Thr	Gly	His	Ile	Thr	Gly	Met	Ala	Ser	Ala	Phe	Arg	Thr	Val
		115				120						125		Tyr
Gln	Val	Gly	Gly	Val	Thr	Ala	Tyr	Phe	Arg	Gly	Val	Gln	Ala	Arg
	130					135				140				Val
Ile	Tyr	Gln	Ile	Pro	Ser	Thr	Ala	Ile	Ala	Trp	Ser	Val	Tyr	Glu
145				150					155					160
Phe	Lys	Tyr	Leu	Ile	Thr	Lys	Arg	Gln	Glu	Glu	Trp	Arg	Ala	Gly
													Lys	

165

170

175

&lt;210&gt; 797

&lt;211&gt; 585

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 797

aaatttaccg gcggcaaaac ccacgtcacc gactacacca acgcctcgcg caccatgctc  
60

ttcaacatcc acacgctgga gtgggatgcg aagatgctgg agattctcga cgtgccgcgc  
120

gagatgctgc cggaagttaa gtcgtcttca gaaatctacg gccgcaccaa aagcgggtatc  
180

gctatcggcg gcatcgcggg cgaccaacag gctgctctgt tcggccagat gtgctggaa  
240

gccgggcagg ccaagaacac ttatggcacc ggctgcttcc tgctgatgaa caccggcgac  
300

aaagccgtca aatccaaaca cggcatgctc accaccatcg cctgcgggtcc acgcggcgaa  
360

gtggcttatg cgctggaagg cgcggtgttc aacggtggtt ccccgtgca gtggctgcgt  
420

gatgagctga agatcatcgc ggacgccacc gacaccgaat acttcgccgg caaggtcaag  
480

gacagcaacg gcgtctacct ggtgccggcc ttaccggcc tgggcgctcc gtactgggac  
540

ccgtatgccc gtggcgcttt gtttgacctg actcgtggcg tacgc  
585

&lt;210&gt; 798

&lt;211&gt; 195

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 798

Lys Phe Thr Gly Gly Lys Thr His Val Thr Asp Tyr Thr Asn Ala Ser  
1 5 10 15

Arg Thr Met Leu Phe Asn Ile His Thr Leu Glu Trp Asp Ala Lys Met  
20 25 30

Leu Glu Ile Leu Asp Val Pro Arg Glu Met Leu Pro Glu Val Lys Ser  
35 40 45

Ser Ser Glu Ile Tyr Gly Arg Thr Lys Ser Gly Ile Ala Ile Gly Gly  
50 55 60

Ile Ala Gly Asp Gln Gln Ala Ala Leu Phe Gly Gln Met Cys Val Glu  
65 70 75 80

Ala Gly Gln Ala Lys Asn Thr Tyr Gly Thr Gly Cys Phe Leu Leu Met  
85 90 95

Asn Thr Gly Asp Lys Ala Val Lys Ser Lys His Gly Met Leu Thr Thr  
100 105 110

Ile Ala Cys Gly Pro Arg Gly Glu Val Ala Tyr Ala Leu Glu Gly Ala  
115 120 125

Val Phe Asn Gly Gly Ser Pro Val Gln Trp Leu Arg Asp Glu Leu Lys  
130 135 140

Ile Ile Ala Asp Ala Thr Asp Thr Glu Tyr Phe Ala Gly Lys Val Lys

```

145          150          155          160
Asp Ser Asn Gly Val Tyr Leu Val Pro Ala Phe Thr Gly Leu Gly Ala
          165          170          175
Pro Tyr Trp Asp Pro Tyr Ala Arg Gly Ala Leu Phe Gly Leu Thr Arg
          180          185          190
Gly Val Arg
          195

<210> 799
<211> 2152
<212> DNA
<213> Homo sapiens

<400> 799
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60
caagtgtccc agcagcatga ctgaacatca ctcaattccc ctacttgatc tacaaggcca
120
acgcccagag cccagaccag gattccaaac aactgcacg agaatattgt ggatccgctg
180
tcaggtaagt gtccgtcact gacccagacg ctgttacgtg gcacatgact gtacagtgcc
240
acgtaacagc actgtacttt tctcccataa acagttacct gccatgtatc tacatgattc
300
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360
ctttgatgtt gtaacgacaa catagcatca ctttacgaca gaatcatctg gaaaaacaga
420
acaacgaata catacatctt aaaaaatgct ggggtgggccc aggcacagct cagcctgtga
480
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660
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720
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780
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840
cctccgcaaa accggccaaa caaacgcgga caggcggccc tggcgtcagc gcacgacagt
900
cacgtgggga ggggcagtgg ccaggtcggc cttggacggg tacaccacct tcaggctccc
960
ttccagatcc accaccgga cctgctccac caccagaagg gagggcccgt cctttccagc
1020
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1080
gagtgatcct tcctctttat tttctaaagt gtactttttc atttctgcca ttttcagaat
1140
gagggcatcc atgacatcct tgcaaatctg cagactgggtg gcacttgta cttccaaaaa
1200

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caaatcagaa gtcgttttct taacctttgt cttctcactg ttggttattg gtgggaagga  
 1260  
 aatcacatca cegtctgcat ccacaagaca cgggtaattt tcatttccat ccagcaagtg  
 1320  
 aaggatatctg tgcaggcccc acacactctg ccgtttcttc tgettctctt gtcctctggc  
 1380  
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 aatcttgagg tcctgtgggg gccgggcgca gtacagcagg ggccctttga cggcacggag  
 1500  
 ctctggtggg gcaaggggtg cagccgtcct cttctcacag agatcttcgt ggagcttggg  
 1560  
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 1620  
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 1680  
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 1920  
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<212> PRT

<213> Homo sapiens

<400> 800

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		20						25					30		
Ala	Gln	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	Glu	Ala	Glu	Ala	Gly
	35						40				45				
Gly	Ser	Arg	Asn	Pro	Ser	Thr	Leu	Arg	Gly	Arg	Gly	Gly	Gln	Ile	Met
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Arg	Ser	Arg	Asp	Gln	Asp	His	Pro	Gly	Gln	Asn	Gly	Glu	Thr	Pro	Ser
65				70				75						80	
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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 801

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atgn
424

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&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 802

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Leu Lys Asn Ile Ser Val Thr Phe Pro Thr Asn Lys Ile Thr Ala Ile
      20             25             30
Ile Gly Pro Asn Gly Cys Gly Lys Ser Thr Leu Leu Ser His Leu Tyr
      35             40             45
Arg Leu His Ser Thr Lys Asn Lys Ile Thr Leu Asn Gly Lys Pro Leu
      50             55             60
Glu Ser Tyr Lys Gly Arg Glu Phe Ala Gln Leu Val Ala Val Leu Thr
      65             70             75             80
Gln Ser Arg Asp Ala Met Ile Asp Asp Phe Leu Val Lys Asp Ile Val
      85             90             95
Leu Met Gly Arg Asp Pro Tyr Lys Gln His Phe Gly Thr Tyr Ser Ser
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Glu Asp Val Lys Ile Ala Glu His Tyr Met
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&lt;210&gt; 803

&lt;211&gt; 6863

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 803

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 Ala Pro Pro Leu Asp Lys Leu Cys Ser Ile Cys Lys Ala Met Glu Thr  
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 260 265 270  
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 275 280 285  
 Asn Ser Ser Pro Leu Phe Leu His Tyr Val Leu Ile Pro Met Leu Pro

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Gly Asp Val Met Val Thr Cys Tyr His Lys Gly Gly Arg Gly Thr Asp		350
	355	360
Arg Thr Leu Val Phe Arg Val Gln Phe His Thr Cys Thr Ile His Gly		365
	370	375
Pro Gln Leu Thr Phe Pro Lys Asp Gln Leu Asp Glu Ala Trp Thr Asp		380
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Pro Glu Lys Ile Lys Gly Ser Thr Pro Arg Asn Asp Pro Ser Val Ser		415
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Val Asp Tyr Asn Thr Thr Glu Pro Ala Val Arg Trp Asp Ser Tyr Glu		430
	435	440
Asn Phe Asn Gln His His Glu Asp Ser Val Asp Gly Ser Leu Thr His		445
	450	455
Thr Arg Gly Pro Leu Asp Gly Ser Pro Tyr Ala Gln Val Gln Arg Pro		460
465	470	475
Pro Arg Gln Thr Pro Pro Ala Pro Ser Pro Glu Pro Pro Pro Pro Pro		480
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Met Leu Ser Val Ser Ser Asp Ser Gly His Ser Ser Thr Leu Thr Thr		495
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Arg Gln Glu Leu Asp Arg Leu Leu Gly Gly Cys Gly Val Ala Ser Gly		525
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Gly Arg Gly Ala Gly Arg Glu Thr Ala Ile Leu Asp Asp Glu Glu Gln		540
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Pro Thr Val Gly Gly Gly Pro His Leu Gly Val Tyr Pro Gly His Arg		560
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Pro Gly Leu Ser Arg His Cys Ser Cys Arg Gln Gly Tyr Arg Glu Pro		575
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Cys Gly Val Pro Asn Gly Gly Tyr Tyr Arg Pro Glu Gly Thr Leu Glu		590
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Phe Gly Tyr Arg Ala Pro Gly Tyr Arg Glu Val Val Ile Leu Glu Asp		655
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Pro Gly Leu Pro Ala Leu Tyr Pro Cys Pro Ala Cys Glu Glu Lys Leu		670
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Ala Leu Pro Thr Ala Ala Leu Tyr Gly Leu Arg Leu Glu Arg Glu Ala		685
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Arg Pro Gly His Pro Leu Pro Leu Leu Leu Pro Ala Cys Gly His His		720



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Ser Leu Glu Pro Val Ser Trp Arg Glu Gly Pro Ser Gly His Ser Thr
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Phe Leu Ile Arg Asp Ser His Ser Phe Gln Gly Ala Tyr Gly Leu Ala

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 1285                      1290                      1295  
 Ser Pro Arg Pro Thr Pro Ala Val Val His Phe Lys Val Ser Ala Gln  
 1300                      1305                      1310  
 Gly Ile Thr Leu Thr Asp Asn Gln Arg Lys Leu Phe Phe Arg Arg His  
 1315                      1320                      1325  
 Tyr Pro Val Asn Ser Ile Thr Phe Ser Ser Thr Asp Pro Gln Asp Arg  
 1330                      1335                      1340  
 Arg Trp Thr Asn Pro Asp Gly Thr Thr Ser Lys Ile Phe Gly Phe Val  
 1345                      1350                      1355                      1360  
 Ala Lys Lys Pro Gly Ser Pro Trp Glu Asn Val Cys His Leu Phe Ala  
 1365                      1370                      1375  
 Glu Leu Asp Pro Asp Gln Pro Ala Gly Ala Ile Val Thr Phe Ile Thr  
 1380                      1385                      1390  
 Lys Val Leu Leu Gly Gln Arg Lys  
 1395                      1400

<210> 805  
 <211> 550  
 <212> DNA  
 <213> Homo sapiens

<400> 805  
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 120  
 agtcatccat ttacttatca agctgttact gtgtgtgcaa gaagcgccag agagatgata  
 180  
 tcaaggagct cttaccatgg ctggcataga gcggctgatg agtaagttcc gtctgcacaa  
 240  
 agagtcccta agcattcatt cttggctgac attcttggct caggggggtct ccatggcctt  
 300  
 gttccctccc tcgggtcacc agttcaggtc gagggggcct atgcttgga gggccacacc  
 360  
 aatggacctt gccaggacac tcagtcacag gtttcacacc caaagagaag acagcccaac  
 420  
 ccagaccctc aaaagagagc acctggggga agggagcgtg gaaaccagga ctcagaaaga  
 480

cacaagagaa aaagaagctg tacactgggg aggcttccgg ggtacctgtg cctgccatgt  
 540  
 ctctgaaggc  
 550

<210> 806  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 806  
 Met Ala Gly Ile Glu Arg Leu Met Ser Lys Phe Arg Leu His Lys Glu  
 1 5 10 15  
 Ser Leu Ser Ile His Ser Trp Leu Thr Phe Leu Ala Gln Gly Val Ser  
 20 25 30  
 Met Ala Leu Phe Pro Ser Ser Gly His Gln Phe Arg Ser Arg Gly Pro  
 35 40 45  
 Met Leu Gly Arg Ala Thr Pro Met Asp Leu Ala Arg Thr Leu Ser His  
 50 55 60  
 Arg Phe His Thr Gln Arg Glu Asp Ser Pro Thr Gln Thr Leu Lys Arg  
 65 70 75 80  
 Glu His Leu Gly Glu Gly Ser Val Glu Thr Arg Thr Gln Lys Asp Thr  
 85 90 95  
 Arg Glu Lys Glu Ala Val His Trp Gly Gly Phe Arg Gly Thr Cys Ala  
 100 105 110  
 Cys His Val Ser Glu Gly  
 115

<210> 807  
 <211> 287  
 <212> DNA  
 <213> Homo sapiens

<400> 807  
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 cccgaggtgg gagagcgcg gcgcggatggcga ccgtaaactg atcggtgtcc gatgcgatga  
 120  
 ccgagtggtg cgaagctcag accgggacag gccgctatac cagcgcgagc gattatatct  
 180  
 gcgcctctgat tcgccaggac caggagcgaa gcgacggcct caggcagctt caaacgttga  
 240  
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 287

<210> 808  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 808  
 Met Ala Val Ala Leu Pro His Trp Gln Asp Ala Lys Phe Leu Ala Met  
 1 5 10 15  
 Ile Ser Arg Gly Gly Arg Ala Arg Gly Met Ala Thr Val Asn Val Ser

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      20      25      30
Leu Ser Asp Ala Met Thr Glu Trp Val Glu Ala Gln Thr Gly Thr Gly
      35      40      45
Arg Tyr Thr Ser Ala Ser Asp Tyr Ile Cys Ala Leu Ile Arg Gln Asp
      50      55      60
Gln Glu Arg Ser Asp Gly Leu Arg Gln Leu Gln Thr Leu Ile Thr Glu
      65      70      75      80
Gly Phe Asp Ser Gly Ile Ser Ala Ser Ser Leu Asp Asp
      85      90

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&lt;210&gt; 809

&lt;211&gt; 405

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 809

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60
gggccccccc cccccccccc cctttttttt ccccgggggg tttattccca gggccaacag
120
gacgcgtggt cgcgtcaaat ggagagacga tcggtgccgc ccttgcccca cgatcctgat
180
ggccccgaga ttcttgacga tgtcaccacc ctgcaccaac aggtaatggg tctgccacgt
240
cacctgggta tccactcagc tggaatggtg ctgacgcgag aaccagtagg acgcatctgc
300
cccattgagc cggctcgaat gtttggtcgc acggggctgc agtgggacaa anaaaactgt
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gcctggatgg ggttggggaa gtttgatctg cttgggttgg ggatg
405

```

&lt;210&gt; 810

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 810

```

Xaa Gly Gly Gly Gly Gly Val Phe Phe Pro Pro Lys Lys Lys Lys
 1      5      10      15
Gly Gly Gly Gly Gly Pro Pro Pro Pro Pro Pro Leu Phe Phe Pro Arg
      20      25      30
Gly Val Tyr Ser Gln Gly Gln Asp Ala Trp Ser Arg Gln Met Glu
      35      40      45
Arg Arg Ser Val Pro Pro Leu Pro His Asp Pro Asp Gly Pro Glu Ile
      50      55      60
Pro Asp Asp Val Thr Thr Leu Ala Gln Gln Val Met Gly Leu Pro Arg
      65      70      75      80
His Leu Gly Ile His Ser Ala Gly Met Val Leu Thr Arg Glu Pro Val
      85      90      95
Gly Arg Ile Cys Pro Ile Glu Pro Ala Arg Met Phe Gly Arg Thr Gly
      100      105      110
Leu Gln Trp Asp Lys Xaa Asn Cys Ala Trp Met Gly Leu Gly Lys Phe
      115      120      125
Asp Leu Leu Gly Leu Gly Met

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130 135

<210> 811  
 <211> 642  
 <212> DNA  
 <213> Homo sapiens

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 120  
 tgggtgacaca ttaacaacac cggggaagca gtactgccaac cacctagata tgagaaaaag  
 180  
 aaaacaggca cttaaagcga ggctaaccac ctttcaggaa tgataaaggg cagaggaccc  
 240  
 tgtcacctct acccctgcta ctaaaggcgt ggcccacaga gcagcagcac cagcagcaca  
 300  
 taaaatgggg ttaaatatga caggaaaaac aagggtgacag ggaaatgggg tgaagatcaa  
 360  
 gtctgtggta ngctcttctt tcctagaggc tttgggcctg agctcttgga gaaagctctc  
 420  
 caacacctca ggggtgtgctt gttcccttgc cctgtgggga tgctctttgt acgggtggct  
 480  
 gactggctcc cactttcttc cgtattgttg tcttgtctct tccctcaca ccatcaaggc  
 540  
 tctttccctt aattctataa gacagtacct ctggcttaga aattatatgc cctcctttaa  
 600  
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 642

<210> 812  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 812  
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 Pro Val Ser His Pro Tyr Lys Glu His Pro His Arg Ala Gly Glu Gln  
 20 25 30  
 Ala His Pro Glu Val Leu Glu Ser Phe Leu Gln Glu Leu Arg Pro Lys  
 35 40 45  
 Ala Ser Arg Lys Glu Arg Xaa Thr Thr Asn Leu Ile Phe Thr Pro Phe  
 50 55 60  
 Pro Cys His Leu Val Phe Pro Val Ile Phe Asn Pro Ile Leu Cys Ala  
 65 70 75 80  
 Ala Gly Ala Ala Ala Leu Trp Ala Thr Pro Leu Val Ala Gly Val Glu  
 85 90 95  
 Val Thr Gly Ser Ser Ala Leu Tyr His Ser  
 100 105

<210> 813  
 <211> 558

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 813

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cgcccgactc cgatcagccg ttcggaaagg cgacgccgaa gatcatgaca ttctcggccg
120
gttcgctgac cagcaccggg ccgcccggct gggccgggaa accgtggaac aaggaagcg
180
ggggcgggcg ggggggtgac gccttcggcc ccctcgctt cggtcagcgt gcggcgcaat
240
tcggggtcga ggatgatccg cggcccttcg atcttgacca cgatctccag ttgcccgcca
300
ttgtcttcgc cgccgacatc cagcgtgccg ccgcgcacca gcgcctcgct ggcgatcagg
360
gcgaggttca gcatcacctt cagcgcggac ttgggcagcg tctccgtttc caccaccag
420
ttgaattgcg tgcgcttatt gtcggcaacc agccctcgt tcgcggtttt cgcttcgcgc
480
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540
ttgttgccgg atacgcgt
558

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&lt;210&gt; 814

&lt;211&gt; 151

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 814

```

Met Thr Phe Ser Ala Gly Ser Leu Thr Ser Thr Gly Pro Pro Gly Trp
1           5           10          15
Ala Gly Lys Pro Trp Asn Lys Gly Ser Gly Gly Gly Ala Arg Gly Asp
20          25          30
Ala Phe Gly Pro Leu Ala Phe Gly Gln Arg Ala Ala Gln Phe Gly Val
35          40          45
Glu Asp Asp Pro Arg Pro Phe Asp Leu Asp His Asp Leu Gln Leu Pro
50          55          60
Ala Ile Val Phe Ala Ala Asp Ile Gln Arg Ala Ala Ala His Gln Arg
65          70          75          80
Leu Ala Gly Asp Gln Gly Glu Val Gln His Leu Gln Arg Gly Leu
85          90          95
Gly Gln Arg Leu Arg Phe His Pro Pro Val Glu Leu Arg Ala Leu Ile
100         105         110
Val Gly Asn Gln Pro Leu Val Arg Gly Phe Arg Phe Ala Arg Val Asp
115         120         125
Leu Phe Ala Glu Pro Ala Gly Gly Ala Glu Gly Glu Ala Glu Glu Phe
130         135         140
Glu Leu Val Gly Gly Tyr Ala
145         150

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&lt;210&gt; 815

&lt;211&gt; 315

<212> DNA  
 <213> Homo sapiens

<400> 815  
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 agctagcgca ggagaaagcc gagacctcac gtccgaagcg gattcagcaa gtgcacaacc  
 180  
 ttctaccac gctgaggttt ccagtgaagt tactgctacg tccagtatag atgagcaggt  
 240  
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 300  
 tgaggccgat acatc  
 315

<210> 816  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 816  
 Met Pro Ser Asp Leu Pro Lys Val Asp Asp Glu Lys Ala His Asp Ala  
 1 5 10 15  
 Pro His Thr Asp Gly Ser Glu Pro Gly Gln Ala Ser Ala Gly Glu Ser  
 20 25 30  
 Arg Asp Leu Thr Ser Glu Ala Asp Ser Ala Ser Ala Gln Pro Ser Thr  
 35 40 45  
 His Ala Glu Val Ser Ser Glu Val Thr Ala Thr Ser Ser Ile Asp Glu  
 50 55 60  
 Gln Val Asp Leu Ile Ala Ala Pro Leu Ser Glu Glu Ser Asn Val Ser  
 65 70 75 80  
 Lys Leu Gly Pro Ser Pro Glu Ala Asp Thr  
 85 90

<210> 817  
 <211> 321  
 <212> DNA  
 <213> Homo sapiens

<400> 817  
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 ctgaaaggaa tcacacaata ttatgctttt gttgaagagg ggcagaaggt tcattgcctg  
 120  
 aatacacttt tctcaaagct tcaaattaat caatccatta tattctgcaa ctctgttaat  
 180  
 agtgttgagc tgctggctaa aaaaataact gaactcgggt attcatgctt ctacattcat  
 240  
 gctaagatgt tgcaagacca cagaaatcga gtattccatg attgtcgtaa tgggtgcttg  
 300  
 agaaaccttg tgtgcacaga t  
 321

<210> 818  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 818  
 Glu Phe Lys Glu Lys Tyr Leu Pro Arg Pro Tyr Val Ile Asn Leu Met  
 1 5 10 15  
 Asp Glu Leu Thr Leu Lys Gly Ile Thr Gln Tyr Tyr Ala Phe Val Glu  
 20 25 30  
 Glu Gly Gln Lys Val His Cys Leu Asn Thr Leu Phe Ser Lys Leu Gln  
 35 40 45  
 Ile Asn Gln Ser Ile Ile Phe Cys Asn Ser Val Asn Ser Val Glu Leu  
 50 55 60  
 Leu Ala Lys Lys Ile Thr Glu Leu Gly Tyr Ser Cys Phe Tyr Ile His  
 65 70 75 80  
 Ala Lys Met Leu Gln Asp His Arg Asn Arg Val Phe His Asp Cys Arg  
 85 90 95  
 Asn Gly Ala Cys Arg Asn Leu Val Cys Thr Asp  
 100 105

<210> 819  
 <211> 3422  
 <212> DNA  
 <213> Homo sapiens

<400> 819  
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 180  
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 240  
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 360  
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 420  
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 780



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 3420  
 ca  
 3422

<210> 820

<211> 494

<212> PRT

<213> Homo sapiens

<400> 820

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Phe	Thr	Ser	Pro	Glu	Ala	Leu	Gln	Pro	Gly	Gly	Thr	Ala	Leu	Ala	Pro
			20					25					30		
Lys	Lys	Arg	Ser	Arg	Lys	Gly	Arg	Ala	Gly	Ala	His	Gly	Leu	Ser	Lys
		35				40					45				
Gly	Pro	Leu	Glu	Lys	Arg	Pro	Tyr	Leu	Gly	Pro	Ala	Leu	Pro	Leu	Thr
	50				55					60					
Pro	Arg	Asp	Arg	Ala	Ser	Gly	Thr	Gln	Gly	Ala	Ser	Glu	Asp	Asn	Ser
65				70					75					80	
Gly	Gly	Gly	Gly	Lys	Lys	Pro	Lys	Met	Glu	Glu	Leu	Gly	Leu	Ala	Ser

					85					90					95	
His	Pro	Pro	Glu	Gly	Arg	Pro	Cys	Gln	Pro	Gln	Thr	Arg	Ala	Gln	Lys	
			100					105					110			
Gln	Pro	Gly	His	Thr	Asn	Tyr	Ser	Tyr	Ser	Lys	Arg	Lys	Arg	Leu		
			115				120					125				
Thr	Arg	Gly	Arg	Ala	Lys	Asn	Thr	Thr	Ser	Ser	Pro	Cys	Lys	Gly	Arg	
			130				135				140					
Ala	Lys	Arg	Arg	Arg	Gln	Gln	Gln	Val	Leu	Pro	Leu	Asp	Pro	Ala	Glu	
145					150				155						160	
Pro	Glu	Ile	Arg	Leu	Lys	Tyr	Ile	Ser	Ser	Cys	Lys	Arg	Leu	Arg	Ser	
				165					170						175	
Asp	Ser	Arg	Thr	Pro	Ala	Phe	Ser	Pro	Phe	Val	Arg	Val	Glu	Lys	Arg	
				180					185				190			
Asp	Ala	Phe	Thr	Thr	Ile	Cys	Thr	Val	Val	Asn	Ser	Pro	Gly	Asp	Ala	
				195			200					205				
Pro	Lys	Pro	His	Arg	Lys	Pro	Ser	Ser	Ser	Ala	Ser	Ser	Ser	Ser	Ser	
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Ser	Ser	Ser	Phe	Ser	Leu	Asp	Ala	Ala	Gly	Ala	Ser	Leu	Ala	Thr	Leu	
225					230				235						240	
Pro	Gly	Gly	Ser	Ile	Leu	Gln	Pro	Arg	Pro	Ser	Leu	Pro	Leu	Ser	Ser	
				245					250						255	
Thr	Met	His	Leu	Gly	Pro	Val	Val	Ser	Lys	Ala	Leu	Ser	Thr	Ser	Cys	
				260					265					270		
Leu	Val	Cys	Cys	Leu	Cys	Gln	Asn	Pro	Ala	Asn	Phe	Lys	Asp	Leu	Gly	
				275			280					285				
Asp	Leu	Cys	Gly	Pro	Tyr	Tyr	Pro	Glu	His	Cys	Leu	Pro	Lys	Lys	Lys	
						295					300					
Pro	Lys	Leu	Lys	Glu	Lys	Val	Arg	Pro	Glu	Gly	Thr	Cys	Glu	Glu	Ala	
305					310					315					320	
Ser	Leu	Pro	Leu	Glu	Arg	Thr	Leu	Lys	Gly	Pro	Glu	Cys	Ala	Ala	Ala	
				325					330						335	
Ala	Thr	Ala	Gly	Lys	Pro	Pro	Arg	Pro	Asp	Gly	Pro	Ala	Asp	Pro	Ala	
				340					345				350			
Lys	Gln	Gly	Pro	Leu	Arg	Thr	Ser	Ala	Arg	Gly	Leu	Ser	Arg	Arg	Leu	
				355			360					365				
Gln	Ser	Cys	Tyr	Cys	Cys	Asp	Gly	Arg	Glu	Asp	Gly	Gly	Glu	Glu	Ala	
						375					380					
Ala	Pro	Ala	Asp	Lys	Gly	Arg	Lys	His	Glu	Cys	Ser	Lys	Glu	Ala	Pro	
385					390					395					400	
Ala	Glu	Pro	Gly	Gly	Glu	Ala	Gln	Glu	His	Trp	Val	His	Glu	Ala	Cys	
				405					410						415	
Ala	Val	Trp	Thr	Gly	Gly	Val	Tyr	Leu	Val	Ala	Gly	Lys	Leu	Phe	Gly	
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<210> 821

<211> 420

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 821

acgcgtcccg tcacctgccc tatggaccaa gtgagttgtg tgctcgacaa tgggttcgcc  
60  
gccatcatgg atgtgcccggg tttcaactat cgcgcccata gttacaccga agcctatcgg  
120  
cgtttgccgc aaaatgtggt gctaggttcg gaaacgacct cgacggtgag cagccgtggt  
180  
gtctacaagt ttcctgttgt gctgaagtcc gatgccatct atccccacca tcagtcgtca  
240  
ggctacgaca cagagtattg ttcgtggtcg aacacccccg atgtcgattt cgccctcgcc  
300  
gaagactatc cctggacgat ggggcagttt gtctggacgg gcttcgacta cctcggtgaa  
360  
ccttcgcctt acgacaccga tgcctggccc tctcagcctt ccctcttcgg cattgtcgac  
420

&lt;210&gt; 822

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 822

Met Asp Gln Val Ser Cys Val Leu Asp Asn Gly Phe Ala Ala Ile Met  
1 5 10 15  
Asp Val Pro Gly Phe Asn Tyr Arg Ala His Arg Tyr Thr Glu Ala Tyr  
20 25 30  
Arg Arg Leu Pro Gln Asn Val Val Leu Gly Ser Glu Thr Thr Ser Thr  
35 40 45  
Val Ser Ser Arg Gly Val Tyr Lys Phe Pro Val Val Leu Lys Ser Asp  
50 55 60  
Ala Ile Tyr Pro Asp His Gln Ser Ser Gly Tyr Asp Thr Glu Tyr Cys  
65 70 75 80  
Ser Trp Ser Asn Thr Pro Asp Val Asp Phe Ala Leu Ala Glu Asp Tyr  
85 90 95  
Pro Trp Thr Met Gly Gln Phe Val Trp Thr Gly Phe Asp Tyr Leu Gly  
100 105 110  
Glu Pro Ser Pro Tyr Asp Thr Asp Ala Trp Pro Ser His Ala Ser Leu  
115 120 125  
Phe Gly Ile Val Asp  
130

&lt;210&gt; 823

&lt;211&gt; 550

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 823

tctagattct tgggcagccg agccccctctt gaattcctca gcctaccata atgatcaaca  
60  
cctcccatgt tccgtccatg aatgaccgca ctgacagcac tggagagatt taatgggtca  
120

ccaattgagg cagtgaaggc actcatggca ctcagagctg gaatggggct gatctgagtt  
 180  
 gtactgttga ctgcagtggg gatgacaacc tgcattcctt tgctggctgc atcgacaact  
 240  
 gctttgtaaa tggcatctac ggaagcatca cctggggccac ccacaacgag gccatccttc  
 300  
 acctgttgac caagagatgg gtcaatcctc ggttgcaact cacaaggtgt atcttgaaaa  
 360  
 ggtggaagtg tagtgtttgg attctcagga agtgctgtga gcccaggctg agtgcttatt  
 420  
 cttttgttta ggagagctgc atcttcctgc attctcacct gaaagttctg aaacagacaa  
 480  
 gccatggggg tattgttagc tgggcaagga attgtggact gtccttgga cgcctggaga  
 540  
 ttctggtacc  
 550

<210> 824  
 <211> 161  
 <212> PRT  
 <213> Homo sapiens

<400> 824  
 Met Ala Cys Leu Phe Gln Asn Phe Gln Val Arg Met Gln Glu Asp Ala  
 1 5 10 15  
 Ala Leu Leu Asn Lys Arg Ile Ser Thr Gln Pro Gly Leu Thr Ala Leu  
 20 25 30  
 Pro Glu Asn Pro Asn Thr Thr Leu Pro Pro Phe Gln Asp Thr Pro Cys  
 35 40 45  
 Glu Leu Gln Pro Arg Ile Asp Pro Ser Leu Gly Gln Gln Val Lys Asp  
 50 55 60  
 Gly Leu Val Val Gly Gly Pro Gly Asp Ala Ser Val Asp Ala Ile Tyr  
 65 70 75 80  
 Lys Ala Val Val Asp Ala Ala Ser Lys Gly Met Gln Val Val Ile Thr  
 85 90 95  
 Thr Ala Val Asn Ser Thr Thr Gln Ile Ser Pro Ile Pro Ala Leu Ser  
 100 105 110  
 Ala Met Ser Ala Phe Thr Ala Ser Ile Gly Asp Pro Leu Asn Leu Ser  
 115 120 125  
 Ser Ala Val Ser Ala Val Ile His Gly Arg Asn Met Gly Gly Val Asp  
 130 135 140  
 His Asp Gly Arg Leu Arg Asn Ser Arg Gly Ala Arg Leu Pro Lys Asn  
 145 150 155 160  
 Leu

<210> 825  
 <211> 327  
 <212> DNA  
 <213> Homo sapiens

<400> 825  
 gcgtttgcga ccggccgtaa cccgcagaat gcggcgggtg gttgcactga ggggtattttg  
 60

cagttgctgg atgagcgcgga gatgcgcggc gtgctcggcc acgagctgat gcacgtgtac  
 120  
 aaccgcgata tccctcacctc ttcgggtggcg gcgggtatcg cctccatcat cggtagcatt  
 180  
 gcgcagattc tttcgtttgg cgcgatgttc ggtggatcca accgcgatgg tgaacgttcc  
 240  
 aaccccctcg ccatgttcgt ggttgctatg ctggctccca ttgctactca ggtcatccag  
 300  
 atggctatta gccgcacccg tgaattc  
 327

<210> 826

<211> 109

<212> PRT

<213> Homo sapiens

<400> 826

Ala	Phe	Ala	Thr	Gly	Arg	Asn	Pro	Gln	Asn	Ala	Ala	Val	Cys	Cys	Thr
1			5					10				15			
Glu	Gly	Ile	Leu	Gln	Leu	Leu	Asp	Glu	Arg	Glu	Met	Arg	Gly	Val	Leu
			20				25					30			
Gly	His	Glu	Leu	Met	His	Val	Tyr	Asn	Arg	Asp	Ile	Leu	Thr	Ser	Ser
			35				40					45			
Val	Ala	Ala	Gly	Ile	Ala	Ser	Ile	Ile	Gly	Thr	Ile	Ala	Gln	Ile	Leu
			50				55				60				
Ser	Phe	Gly	Ala	Met	Phe	Gly	Gly	Ser	Asn	Arg	Asp	Gly	Glu	Arg	Ser
65					70				75					80	
Asn	Pro	Leu	Ala	Met	Phe	Val	Val	Ala	Met	Leu	Ala	Pro	Ile	Ala	Thr
			85						90					95	
Gln	Val	Ile	Gln	Met	Ala	Ile	Ser	Arg	Thr	Arg	Glu	Phe			
			100					105							

<210> 827

<211> 534

<212> DNA

<213> Homo sapiens

<400> 827

nacgcgtacg tcaatatgca tcgtccagtc gttatcgcaa cgccgaaatc gatgctgcgc  
 60  
 aacaagatgg cgacctcgga tcccgaagag ttcaccaccg gtaggtggcg tctgtttcta  
 120  
 cccgacccat cgatcaccga cccgacggcc gttacgagga ttatcttgtg ctctggcaag  
 180  
 gcgcgggtggg agctgggtcaa gcaacgtaag gccgccagtc ttgacggaca gctcgccatc  
 240  
 atccccgatgg agcgtctcta cccgctacca gtcgacgagt tggctgaggt ttttgcgcct  
 300  
 tacaccaacg tcacggatgt ccgctgggtc caagaagagc cagagaacca gggcgccctgg  
 360  
 tactacatgc tgacccacct gccccaggcc atgtcggaga agctgccagg attctttgat  
 420  
 gggttagtcg gcatcaccgg cccaccgtcc tcagctccgt cggtgggaca gcacagcgtc  
 480

cacatccgtg aagagcagga gttactcgag aaggctatag cctgagcgac ctga  
534

<210> 828  
<211> 174  
<212> PRT  
<213> Homo sapiens

<400> 828  
Xaa Ala Tyr Val Asn Met His Arg Pro Val Val Ile Ala Thr Pro Lys  
1 5 10 15  
Ser Met Leu Arg Asn Lys Met Ala Thr Ser Asp Pro Glu Glu Phe Thr  
20 25 30  
Thr Gly Arg Trp Arg Pro Val Leu Pro Asp Pro Ser Ile Thr Asp Pro  
35 40 45  
Thr Ala Val Thr Arg Ile Ile Leu Cys Ser Gly Lys Ala Arg Trp Glu  
50 55 60  
Leu Val Lys Gln Arg Lys Ala Ala Ser Leu Asp Gly Gln Leu Ala Ile  
65 70 75 80  
Ile Pro Met Glu Arg Leu Tyr Pro Leu Pro Val Asp Glu Leu Ala Glu  
85 90 95  
Val Phe Ala Pro Tyr Thr Asn Val Thr Asp Val Arg Trp Val Gln Glu  
100 105 110  
Glu Pro Glu Asn Gln Gly Ala Trp Tyr Tyr Met Leu Thr His Leu Pro  
115 120 125  
Gln Ala Met Ser Glu Lys Leu Pro Gly Phe Phe Asp Gly Leu Val Gly  
130 135 140  
Ile Thr Arg Pro Pro Ser Ser Ala Pro Ser Val Gly Gln His Ser Val  
145 150 155 160  
His Ile Arg Glu Glu Gln Glu Leu Leu Glu Lys Ala Ile Ala  
165 170

<210> 829  
<211> 492  
<212> DNA  
<213> Homo sapiens

<400> 829  
nagtggccgg gtggccggcg ggtgccagcc gccatggagg ccgtgccccg catgccccatg  
60  
atctggctgg acctgaagga ggccggtgac tttcacttcc agccagctgt gaagaagttt  
120  
gtcctgaaga attatggaga gaaccagaa gcctacaatg aagaactgaa gaagctggag  
180  
ttgctcagac agaatgctgt ccgtgtccca cgagactttg agggctgtag tgcctccgc  
240  
aagtacctcg gccagcttca ttacctgcag agtcgggtcc ccatgggctc gggccaggag  
300  
gccgctgtcc ctgtcacatg gacagagatc ttctcaggca agtctgtggc ccatgaggac  
360  
atcaagtacg agcaggcctg tattttctcc aacnttgag cgctgcactc catgctgggg  
420  
gccatggaca agcgggtgtc tgaggagggc atgaaggtct cctgtaccca ttccagtg  
480

gcagccggcg cc  
492

<210> 830  
<211> 164  
<212> PRT  
<213> Homo sapiens

<400> 830  
Xaa Trp Pro Gly Gly Arg Arg Val Pro Ala Ala Met Glu Ala Val Pro  
1 5 10 15  
Arg Met Pro Met Ile Trp Leu Asp Leu Lys Glu Ala Gly Asp Phe His  
20 25 30  
Phe Gln Pro Ala Val Lys Lys Phe Val Leu Lys Asn Tyr Gly Glu Asn  
35 40 45  
Pro Glu Ala Tyr Asn Glu Glu Leu Lys Lys Leu Glu Leu Leu Arg Gln  
50 55 60  
Asn Ala Val Arg Val Pro Arg Asp Phe Glu Gly Cys Ser Val Leu Arg  
65 70 75 80  
Lys Tyr Leu Gly Gln Leu His Tyr Leu Gln Ser Arg Val Pro Met Gly  
85 90 95  
Ser Gly Gln Glu Ala Ala Val Pro Val Thr Trp Thr Glu Ile Phe Ser  
100 105 110  
Gly Lys Ser Val Ala His Glu Asp Ile Lys Tyr Glu Gln Ala Cys Ile  
115 120 125  
Phe Ser Asn Xaa Gly Ala Leu His Ser Met Leu Gly Ala Met Asp Lys  
130 135 140  
Arg Val Ser Glu Glu Gly Met Lys Val Ser Cys Thr His Phe Gln Cys  
145 150 155 160  
Ala Ala Gly Ala

<210> 831  
<211> 303  
<212> DNA  
<213> Homo sapiens

<400> 831  
gcgttgctgc ggcgtggcga gaccatgacg gcggagaatc agcgtgccaa tgtgcgcac  
60  
gccgcaaacc acatcaagga ggttgcggtc gatcacgagg tcgttgtagc ccatggta  
120  
ggccccagg taggtctgtt ggctctgcaa tcgacagcct acgaggaagt cggtatctat  
180  
ccgctggatg tcctgggcgc agagtcacag gccatgatcg gctacatgat cgagcaggaa  
240  
ctcggcaatg tgatgcctca ggatcagcag atcgtcacca tgatcacgat gacagtcgtc  
300  
gac  
303

<210> 832  
<211> 101  
<212> PRT



<213> Homo sapiens

<400> 832

```

Ala Leu Leu Arg Arg Gly Glu Thr Met Thr Ala Glu Asn Gln Arg Ala
 1           5           10           15
Asn Val Arg Ile Ala Ala Asn His Ile Lys Glu Val Ala Val Asp His
 20           25           30
Glu Val Val Val Ala His Gly Asn Gly Pro Gln Val Gly Leu Leu Ala
 35           40           45
Leu Gln Ser Thr Ala Tyr Glu Glu Val Gly Ile Tyr Pro Leu Asp Val
 50           55           60
Leu Gly Ala Glu Ser Gln Ala Met Ile Gly Tyr Met Ile Glu Gln Glu
 65           70           75           80
Leu Gly Asn Val Met Pro Gln Asp Gln Gln Ile Val Thr Met Ile Thr
 85           90           95
Met Thr Val Val Asp
          100

```

<210> 833

<211> 466

<212> DNA

<213> Homo sapiens

<400> 833

```

nngatccgcg cgatcgacga ggcgggtgcg tgatgttgac agcgaaaatg cgcagccggc
60
catttgacga gggctgaaaa cgtcttctac cggctctgctg tgccgcctgg tgcagcaaaa
120
cgacgccatg atcgtccagt gggatcgaat ttgttctgctg gcgctggggg attcagttgc
180
ggattccacc aggccgggtg gcatgttgctg gcggcggttg agcacgacgt gtcggcgctct
240
ctgacctatg tcatgaatct cgctcggccc ggcgtcaaga ttcacatcga ccccgagcac
300
ccggagctgg gcccaagacc accgcgaacc aagaagaaga gcggcgggcg agtgccgttc
360
gatgcgcatg tcggaactgg gtggatcgcc agcgagcccg ccgacgatcc cggctgcgaa
420
cacttctacg tgtacgacgt caagaacctc agcgcgagcg ggatcc
466

```

<210> 834

<211> 142

<212> PRT

<213> Homo sapiens

<400> 834

```

Gln Arg Lys Cys Ala Gly His Leu Thr Arg Ala Glu Asn Val Phe
 1           5           10           15
Tyr Arg Ser Ala Val Pro Pro Gly Val Ser Lys Arg Arg His Asp Arg
 20           25           30
Pro Val Gly Ile Asp Leu Phe Cys Gly Ala Gly Gly Phe Ser Cys Gly
 35           40           45
Phe His Gln Ala Gly Trp His Val Ala Ala Ala Val Glu His Asp Val

```

```

      50              55              60
Ser Ala Ser Leu Thr Tyr Val Met Asn Leu Ala Arg Pro Gly Val Lys
65              70              75              80
Ile His Ile Asp Pro Glu His Pro Glu Leu Gly Pro Arg Pro Pro Arg
      85              90              95
Thr Lys Lys Lys Ser Gly Gly Ala Val Pro Phe Asp Ala His Val Gly
      100              105              110
Thr Gly Trp Ile Ala Ser Glu Pro Ala Asp Asp Pro Gly Cys Glu His
      115              120              125
Phe Tyr Val Tyr Asp Val Lys Asn Leu Ser Gly Glu Arg Ile
      130              135              140

```

<210> 835  
 <211> 482  
 <212> DNA  
 <213> Homo sapiens

```

<400> 835
acgcgtgaag ggattttgat caccagaac aaccacctgt ctttttagat caagaagcag
60
aagctcagag caaagaacat cacaccacgt ccctcagtga ttgaagcagt gattgagtca
120
cagaataaat ctggaactca ggtcttctga tctttgctcc agatgtaga gacaaaacta
180
aaagtaaaat accaagtga atcaaagcat cacgattgag ccagaacat gaaaaagaac
240
ttcctggccc acttgagaaa ctgttaaacc ggacatacct ttggggactt cttcccttct
300
ctggaataag attgatgttt ccattgctgtg aaagacgatg atgttccttc tcccagattc
360
ctgctgtctt caaaaggcct agcaaaaacc actgctgctg ggtgcagttg agaaagggaa
420
tgaagaacaa tcccatggcc atgcaggcac tcctccctc cactctctg cccttcacgc
480
gt
482

```

<210> 836  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

```

<400> 836
Met Ala Met Gly Leu Phe Phe Ile Pro Phe Leu Asn Cys Thr Gln Gln
1              5              10              15
Gln Trp Phe Leu Leu Gly Leu Leu Lys Thr Ala Gly Ile Trp Glu Lys
      20              25              30
Glu His His Arg Leu Ser Gln His Gly Asn Ile Asn Leu Ile Pro Glu
      35              40              45
Lys Gly Arg Ser Pro Gln Arg Tyr Val Arg Phe Asn Ser Phe Ser Ser
      50              55              60
Gly Pro Gly Ser Ser Phe Ser Cys Ser Gly Leu Asn Arg Asp Ala Leu
65              70              75              80
Ile Ser Leu Gly Ile Leu Leu Leu Val Leu Ser Leu Thr Ser Gly Ala

```

```

      85      90      95
Lys Ile Arg Arg Pro Glu Phe Gln Ile Tyr Ser Val Thr Gln Ser Leu
      100      105      110
Leu Gln Ser Leu Arg Asp Val Val
      115      120

```

<210> 837  
 <211> 509  
 <212> DNA  
 <213> Homo sapiens

```

<400> 837
acgcgtggac ccccggtctg cccgcctttg cagtcacgc cctccctgaa gtcaccgctg
60
cagaaatacg caggcactga cctgggggta cagccaggca agggagagac gaggggctca
120
ctctgcacca gcccaaggcct gtgtcctggc atggctcccc caggaagcga ggatggcggt
180
gcctggcggt cgagcccttc ttatcctggg gaatgctggg gggcgcttct gacgagacct
240
gcctgctgcc cctgctggct ggcaactgcc ctccccggg gaaagggttg gtggtcccc
300
caggggaact caaagcaggg gagccctgg aggcccaag tccctggaat atcttggcgc
360
tcagatggcc cccctcgaac accctcacac gggggggccg cgcgggtgga ggtgacctag
420
cagccactct tacttggcga agacttttct cccaatgcga gcgcggtggt tatcagcctg
480
agccttcagg ttggtgaggg tgggggtacc
509

```

<210> 838  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

```

<400> 838
Met Ala Pro Pro Gly Ser Glu Asp Gly Gly Ala Trp Arg Ser Ser Pro
1      5      10      15
Ser Tyr Pro Gly Glu Cys Trp Gly Ala Phe Leu Ser Arg Pro Ala Cys
      20      25      30
Cys Pro Cys Trp Leu Ala Leu Pro Leu Pro Arg Gly Lys Val Gly Trp
      35      40      45
Ser Pro Gln Gly Asn Ser Lys Gln Gly Ser Pro Trp Arg Pro Gln Val
      50      55      60
Pro Gly Ile Ser Trp Arg Ser Asp Gly Pro Pro Arg Thr Pro Ser His
      65      70      75      80
Gly Gly Ala Ala Arg Trp Glu Val Thr Gln Gln Pro Leu Leu Leu Gly
      85      90      95
Glu Asp Phe Ser Pro Asn Ala Ser Ala Gly Gly Ile Ser Leu Ser Leu
      100      105      110
Gln Val Gly Glu Ala Gly Val
      115

```

<210> 839  
 <211> 347  
 <212> DNA  
 <213> Homo sapiens

<400> 839  
 acgcgtctcg tgttcgtgcg gcacggcagg acggcggttca atgtggaggg tcgggtccag  
 60  
 ggccgtctcg acatgccgtt ggatgaggtg gggcgccgtc aggcactcac agtgggtcaa  
 120  
 gtcacgccc agatggaacc tgacgcgac atggcctctc cgctacaacg tgcgcgcgac  
 180  
 acagctcagg caatcgggtg ttgtgctgga ttgggcgtac agctggatga tcgactcatc  
 240  
 gagatcgatg tcggacgttg gtcgggacaa cgggctgcgg acctgcgtcg caacgacctc  
 300  
 gagtacgcag caagtgtggt cagccctatc gattaccggg tcggagn  
 347

<210> 840  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 840  
 Thr Arg Leu Val Phe Val Arg His Gly Arg Thr Ala Phe Asn Val Glu  
 1 5 10 15  
 Gly Arg Leu Gln Gly Arg Leu Asp Met Pro Leu Asp Glu Val Gly Arg  
 20 25 30  
 Arg Gln Ala Leu Thr Val Ala Gln Val Ile Ala Glu Met Glu Pro Asp  
 35 40 45  
 Ala Ile Met Ala Ser Pro Leu Gln Arg Ala Arg Asp Thr Ala Gln Ala  
 50 55 60  
 Ile Gly Ala Cys Ala Gly Leu Gly Val Gln Leu Asp Asp Arg Leu Ile  
 65 70 75 80  
 Glu Ile Asp Val Gly Arg Trp Ser Gly Gln Arg Ala Ala Asp Leu Arg  
 85 90 95  
 Arg Asn Asp Pro Glu Tyr Ala Ala Ser Val Val Ser Pro Ile Asp Tyr  
 100 105 110  
 Arg Val Gly  
 115

<210> 841  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 841  
 tccggaactc accccgacgc cgctcattatg gacgtcatga tgccgcgtct agatggcttg  
 60  
 gaagccaccc ggatgctgcg cagcaatggc aacgacgtcc cgatcctcgt cctcaccgcc  
 120  
 cgcgatgctg tcgacgatcg cggtgacggc ctcgacgctg gcgccgatga ctacatggtc  
 180

aagcccttcg ccctcgacga actcctcgt cgcctacgag ccctcactcg tcgttcccg  
 240  
 cccgagccag agcaaaacga ggcccctgaa caactctcct tcgctgacct cacccttgat  
 300  
 ccaggcaccc gcgagatcac ccgcgggaac cgtcgcatca gtttgacgag t  
 351

<210> 842  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 842  
 Ser Gly Thr His Pro Asp Ala Val Ile Met Asp Val Met Met Pro Arg  
 1 5 10 15  
 Leu Asp Gly Leu Glu Ala Thr Arg Met Leu Arg Ser Asn Gly Asn Asp  
 20 25 30  
 Val Pro Ile Leu Val Leu Thr Ala Arg Asp Ala Val Asp Asp Arg Val  
 35 40 45  
 Asp Gly Leu Asp Ala Gly Ala Asp Asp Tyr Met Val Lys Pro Phe Ala  
 50 55 60  
 Leu Asp Glu Leu Leu Ala Arg Leu Arg Ala Leu Thr Arg Arg Ser Arg  
 65 70 75 80  
 Pro Glu Pro Glu Gln Asn Glu Ala Pro Glu Gln Leu Ser Phe Ala Asp  
 85 90 95  
 Leu Thr Leu Asp Pro Gly Thr Arg Glu Ile Thr Arg Gly Asn Arg Arg  
 100 105 110  
 Ile Ser Leu Thr Arg  
 115

<210> 843  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<400> 843  
 ctagcccagg ctctcgtcca cgaggggctg cgcgctgtgg cctctggggc aaacccggtc  
 60  
 ggcctcaagc gcggtatcga gaaggctgtc gacgccgttg tggaggagct ccgctctatc  
 120  
 tcgcgcgcca tcgacaccac ctcgacatg gccagcgttg ccaccatctc cagccgtgac  
 180  
 gagaccatcg gcgcctcat cgctgaggcc ttcgacaagg ttggttaagga cggggttatc  
 240  
 accgtcgacg agtcgcagac cttcggcact gagcttgact tcaccgaggg catgcagttc  
 300  
 gacaaggggtt acctgtcgcc ctacatgggtc accgaccagg ttcgcatgga ggctgtgatc  
 360  
 gaggatecctt acatcctcat tcaactccgc aag  
 393

<210> 844  
 <211> 131  
 <212> PRT

<213> Homo sapiens

<400> 844

```

Leu Ala Gln Ala Leu Val His Glu Gly Leu Arg Ala Val Ala Ser Gly
 1           5           10           15
Ala Asn Pro Val Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Asp Ala
      20           25           30
Val Val Glu Glu Leu Arg Ser Ile Ser Arg Ala Ile Asp Thr Thr Ser
      35           40           45
Asp Met Ala Ser Val Ala Thr Ile Ser Ser Arg Asp Glu Thr Ile Gly
      50           55           60
Ala Leu Ile Ala Glu Ala Phe Asp Lys Val Gly Lys Asp Gly Val Ile
65           70           75           80
Thr Val Asp Glu Ser Gln Thr Phe Gly Thr Glu Leu Asp Phe Thr Glu
      85           90           95
Gly Met Gln Phe Asp Lys Gly Tyr Leu Ser Pro Tyr Met Val Thr Asp
      100          105          110
Gln Val Arg Met Glu Ala Val Ile Glu Asp Pro Tyr Ile Leu Ile His
      115          120          125
Ser Arg Lys
      130

```

<210> 845

<211> 505

<212> DNA

<213> Homo sapiens

<400> 845

```

gccacctgcc caaggctgga tgacgggcct agggcacatc taaggaacaa ggacaggaca
60
gaagcaaagc cacagctgct ggggcagggt gggggccggt atgtctggcc agcagcatca
120
cccctgcccc cggcggggct ccaggaccgg gagactcatc agccggaagc tcttgaggga
180
ggcggctgcc gtgaagacag gcacccttgc tcttgagagg ggcacccaga gaaccaagac
240
tcagcagagg gaacacaggg ctacgcccag gccccaggcc tgatatccag agtctaaatc
300
ccacctcagc ccagggggga gccttgagag gagctatgtc cctcatggac ccagtttcc
360
tctgcatacg ggctccgagc cctgcactgc ctccagggta gttcccaagg tcttttccca
420
ttacctccta cgtgagcact cagtaaacca atacacatac acaagggtga cattaattcc
480
agccacagaa tcccaggcca cgcgt
505

```

<210> 846

<211> 130

<212> PRT

<213> Homo sapiens

<400> 846

```

Met Gly Lys Asp Leu Gly Asn Tyr Pro Gly Gly Ser Ala Gly Leu Gly

```

```

      1           5           10           15
Ala Arg Met Gln Arg Lys Leu Gly Ser Met Arg Asp Ile Ala Pro Leu
      20           25           30
Lys Ala Pro Trp Trp Ala Glu Val Gly Phe Arg Leu Trp Ile Ser Gly
      35           40           45
Leu Gly Pro Gly Arg Ser Pro Val Phe Pro Leu Leu Ser Leu Gly Ser
      50           55           60
Leu Gly Ala Pro Leu Arg Ser Lys Gly Ala Cys Leu His Gly Ser Arg
      65           70           75           80
Leu Leu Gln Glu Leu Pro Ala Asp Glu Ser Pro Gly Pro Gly Ala Pro
      85           90           95
Pro Gly Ala Gly Val Met Leu Leu Ala Arg His Thr Gly Pro His Pro
      100          105          110
Ala Pro Ala Ala Val Ala Leu Leu Ser Cys Pro Cys Ser Leu Asp
      115          120          125
Val Pro
      130

```

<210> 847  
 <211> 448  
 <212> DNA  
 <213> Homo sapiens

```

<400> 847
aagctttttaa aggagcaaga aaacatgaaa gagctagtag tcaaccttct ccgcatgact
60
caaatcaaaa ttgatgaaaa ggaacaaaag tccaaggatt tcctgaaagc tcagcaaaaa
120
tacaccaaca ttgttaaaga aatgaaagca aaggatcttg aaatcaggat acacaagaag
180
aaaaaatgtg aaatttatcg gagactgaga gagcttgcta aactgtatga caccattcga
240
aatgaaagaa acaaatattgt taacttactc cacaaagctc atcagaaagt aaatgaaata
300
aaagaaaggc ataaaatgtc attaaatgaa cttgaaattc tgagaaatag tgccgttagt
360
caagaaagaa agctacaaaa ttccatgctg aaacacgcc acaatgttac catcagagag
420
agcatgcaaa acgatgtgcg caaaattt
448

```

<210> 848  
 <211> 149  
 <212> PRT  
 <213> Homo sapiens

```

<400> 848
Lys Leu Leu Lys Glu Gln Glu Asn Met Lys Glu Leu Val Val Asn Leu
      1           5           10           15
Leu Arg Met Thr Gln Ile Lys Ile Asp Glu Lys Glu Gln Lys Ser Lys
      20           25           30
Asp Phe Leu Lys Ala Gln Gln Lys Tyr Thr Asn Ile Val Lys Glu Met
      35           40           45
Lys Ala Lys Asp Leu Glu Ile Arg Ile His Lys Lys Lys Lys Cys Glu

```

```

      50      55      60
Ile Tyr Arg Arg Leu Arg Glu Leu Ala Lys Leu Tyr Asp Thr Ile Arg
65      70      75      80
Asn Glu Arg Asn Lys Phe Val Asn Leu Leu His Lys Ala His Gln Lys
      85      90      95
Val Asn Glu Ile Lys Glu Arg His Lys Met Ser Leu Asn Glu Leu Glu
      100      105      110
Ile Leu Arg Asn Ser Ala Val Ser Gln Glu Arg Lys Leu Gln Asn Ser
      115      120      125
Met Leu Lys His Ala Asn Asn Val Thr Ile Arg Glu Ser Met Gln Asn
      130      135      140
Asp Val Arg Lys Ile
145

```

<210> 849  
 <211> 463  
 <212> DNA  
 <213> Homo sapiens

```

<400> 849
nnacgcgtga ttgttggggc caaggaatgc catgtggaga gtgcaggtga agtgataagt
60
cttttggaga tggggaatgc agccagacat acaggtacca ctcaaataaa tgagcactcc
120
agcagatcac atgcaatttt tacaatcagc atttgtcaag ttcataaaaa tatggaggca
180
gctgaagatg gatcatggta ttcccctcgg catattgtct caaagtcca ctttgtggat
240
ttggcaggat cagaaagagt aacaaaaacg gggaatactg gtgaacggtt caaagaatcc
300
attcaaatca atagtggatt gctggcttta ggaaatgtaa taagcgctct tggggaccca
360
cgcaggaaga gttcacatat tccatatagg gatgctaaaa ttaccggct tctgaaagat
420
tctctgggag gcagtgctaa gactgtcatg atcacatgtg tca
463

```

<210> 850  
 <211> 154  
 <212> PRT  
 <213> Homo sapiens

```

<400> 850
Xaa Arg Val Ile Val Gly Ala Lys Glu Cys His Val Glu Ser Ala Gly
1      5      10      15
Glu Val Ile Ser Leu Leu Glu Met Gly Asn Ala Ala Arg His Thr Gly
      20      25      30
Thr Thr Gln Met Asn Glu His Ser Ser Arg Ser His Ala Ile Phe Thr
      35      40      45
Ile Ser Ile Cys Gln Val His Lys Asn Met Glu Ala Ala Glu Asp Gly
      50      55      60
Ser Trp Tyr Ser Pro Arg His Ile Val Ser Lys Phe His Phe Val Asp
65      70      75      80
Leu Ala Gly Ser Glu Arg Val Thr Lys Thr Gly Asn Thr Gly Glu Arg

```



```

      85              90              95
Phe Lys Glu Ser Ile Gln Ile Asn Ser Gly Leu Leu Ala Leu Gly Asn
      100              105              110
Val Ile Ser Ala Leu Gly Asp Pro Arg Arg Lys Ser Ser His Ile Pro
      115              120              125
Tyr Arg Asp Ala Lys Ile Thr Arg Leu Leu Lys Asp Ser Leu Gly Gly
      130              135              140
Ser Ala Lys Thr Val Met Ile Thr Cys Val
145              150

```

<210> 851  
 <211> 372  
 <212> DNA  
 <213> Homo sapiens

```

<400> 851
aaatttcctg tttctgatcg acgaaataaa gtttagcgtg atgagtgagc tgcttatgca
60
gttcctccat tcgcttataa acagttttat ttctcatttc gaaaactctc gatgcagaat
120
aaaggctaga gtctggggac caagtcccca gctccgttta cgcgacttcc ttgaccttgt
180
ttgttatgct gataagggtta ttcagcttga cgatttggtc gtggtctttc aaccgttttg
240
cagctgggtcg acgatattcc tggtaggaac tacgatagaa gaccagcatc ggaagaactt
300
tgtagatgct gaacaaacac ccaccgatca cttcagcctc gaagtaaggg ttatactgtc
360
taaccacgc gt
372

```

<210> 852  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

```

<400> 852
Met Ser Glu Leu Leu Met Gln Phe Leu His Ser Leu Ile Asn Ser Phe
  1              5              10              15
Ile Ser His Phe Glu Asn Ser Arg Cys Arg Ile Lys Ala Arg Val Trp
      20              25              30
Gly Pro Ser Pro Gln Leu Arg Leu Arg Asp Phe Leu Asp Leu Val Cys
      35              40              45
Tyr Ala Asp Lys Val Ile Gln Leu Asp Asp Leu Phe Val Val Phe Gln
      50              55              60
Pro Phe Cys Ser Trp Ser Thr Ile Phe Leu Val Gly Thr Thr Ile Glu
65              70              75              80
Asp Gln His Arg Lys Asn Phe Val Asp Ala Glu Gln Thr Pro Thr Asp
      85              90              95
His Phe Ser Leu Glu Val Arg Val Ile Leu Ser Asn Pro Arg
      100              105              110

```

<210> 853  
 <211> 423

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 853

acgcgttcag aaacttatgg tgaaatggcc gaactagaaa acctagtcga cgaatattac  
 60  
 caagctatgg gcatggatgt gcgtcgagaa acctggctgc gcgagcagat actcaagaaa  
 120  
 gtccaagaaa cgcatttggt agaagagctt gcaggcatag aatcaggtga tgatggcgca  
 180  
 gtggtggaag agagcgtatt agaaggcctc gatacctatt tatgtgagat aaaagaagca  
 240  
 cagattcgtc atggattgca tcgtcttgga gaattaccag aagacgataa attggccgat  
 300  
 accttggctg ccttattgcy ttaccctcgt ggcagtgaca ttaccagcaa gggaattttg  
 360  
 catgccttaa tggcagattt agagttagaa caagacgatt ttgaccaat gcaaagcagc  
 420  
 cgt  
 423

&lt;210&gt; 854

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 854

Thr	Arg	Ser	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Glu	Leu	Glu	Asn	Leu	Val
1				5					10					15	
Asp	Glu	Tyr	Tyr	Gln	Ala	Met	Gly	Met	Asp	Val	Arg	Arg	Glu	Thr	Trp
			20					25					30		
Leu	Arg	Glu	Gln	Ile	Leu	Lys	Lys	Val	Gln	Glu	Thr	His	Leu	Leu	Glu
			35				40					45			
Glu	Leu	Ala	Gly	Ile	Glu	Ser	Gly	Asp	Asp	Gly	Ala	Val	Val	Glu	Glu
			50			55				60					
Ser	Val	Leu	Glu	Gly	Leu	Asp	Thr	Tyr	Leu	Cys	Glu	Ile	Lys	Glu	Ala
					70					75				80	
Gln	Ile	Arg	His	Gly	Leu	His	Arg	Leu	Gly	Glu	Leu	Pro	Glu	Asp	Asp
			85					90					95		
Lys	Leu	Ala	Asp	Thr	Leu	Val	Ala	Leu	Leu	Arg	Leu	Pro	Arg	Gly	Ser
			100				105					110			
Asp	Ile	Thr	Ser	Lys	Gly	Ile	Leu	His	Ala	Leu	Met	Ala	Asp	Leu	Glu
			115				120					125			
Leu	Glu	Gln	Asp	Asp	Phe	Asp	Pro	Met	Gln	Ser	Thr	Arg			
			130			135					140				

&lt;210&gt; 855

&lt;211&gt; 338

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 855

acgcgtgaag ggggagctca aagtagatgg acctctgact agatggagct ctgagtaaga  
 60

tgaatgtctg tgcggatggt gctcacagca agatagtgtc tggagcgatt ggcacttcga  
 120  
 acaagatgga gcatggagca gatggagctc tgagcaagat ggagcgtgga gtagatagag  
 180  
 cttggagcaa gaaggagctc caagcaagat ggagcttgca gcagggtgctt ctcagtgtaa  
 240  
 gatggagctc agagaagatg atgctcagag taagattgag ctcgggtgatt ggcactccaa  
 300  
 acattgctct gagcccattg gagnctctga gcagaaag  
 338

<210> 856

<211> 93

<212> PRT

<213> Homo sapiens

<400> 856

Met	Asn	Val	Cys	Ala	Asp	Val	Ala	His	Ser	Lys	Ile	Val	Leu	Gly	Ala
1				5					10				15		
Ile	Gly	Thr	Ser	Asn	Lys	Met	Glu	His	Gly	Ala	Asp	Gly	Ala	Leu	Ser
		20						25				30			
Lys	Met	Glu	Arg	Gly	Val	Asp	Arg	Ala	Trp	Ser	Lys	Lys	Glu	Leu	Gln
		35				40					45				
Ala	Arg	Trp	Ser	Leu	Gln	Gln	Val	Leu	Leu	Ser	Val	Arg	Trp	Ser	Ser
	50				55					60					
Glu	Lys	Met	Met	Leu	Arg	Val	Arg	Leu	Ser	Ser	Val	Ile	Gly	Thr	Pro
65				70				75				80			
Asn	Ile	Ala	Leu	Ser	Pro	Leu	Glu	Xaa	Leu	Ser	Arg	Lys			
			85					90							

<210> 857

<211> 435

<212> DNA

<213> Homo sapiens

<400> 857

ccggacagtg ggccaccagt gtttgccccc agcaatcatg tcagtgaagc ccaacctcgg  
 60  
 gagacacccc ggccctcat gcctcctacc aagccttcc tagcacctga gaccaccagc  
 120  
 cctgggtgaca ggggtggagac ccctgtgggg gagagagccc caacctctgt ctcagcaagc  
 180  
 tctgaggtct cccctgagag ccaagaggac tcagagaccc cagcagagga ggacagtggc  
 240  
 tctgagcagc ctcccaacag cgtcctgcct gacaaactga aggtgagctg ggagaacccc  
 300  
 agccccagg agggccctgc tcagagagt gcagaaccgt cccaggcacc ctgttctgag  
 360  
 acttctgagg ctgccccag ggaggggtggg aagcccccta cccccacc caagatctta  
 420  
 tcagagaaac tgaaa  
 435

<210> 858

<211> 145  
 <212> PRT  
 <213> Homo sapiens

<400> 858  
 Pro Asp Ser Gly Pro Pro Val Phe Ala Pro Ser Asn His Val Ser Glu  
 1 5 10 15  
 Ala Gln Pro Arg Glu Thr Pro Arg Pro Leu Met Pro Pro Thr Lys Pro  
 20 25 30  
 Phe Leu Ala Pro Glu Thr Thr Ser Pro Gly Asp Arg Val Glu Thr Pro  
 35 40 45  
 Val Gly Glu Arg Ala Pro Thr Pro Val Ser Ala Ser Ser Glu Val Ser  
 50 55 60  
 Pro Glu Ser Gln Glu Asp Ser Glu Thr Pro Ala Glu Glu Asp Ser Gly  
 65 70 75 80  
 Ser Glu Gln Pro Pro Asn Ser Val Leu Pro Asp Lys Leu Lys Val Ser  
 85 90 95  
 Trp Glu Asn Pro Ser Pro Gln Glu Ala Pro Ala Ala Glu Ser Ala Glu  
 100 105 110  
 Pro Ser Gln Ala Pro Cys Ser Glu Thr Ser Glu Ala Ala Pro Arg Glu  
 115 120 125  
 Gly Gly Lys Pro Pro Thr Pro Pro Lys Ile Leu Ser Glu Lys Leu  
 130 135 140  
 Lys  
 145

<210> 859  
 <211> 561  
 <212> DNA  
 <213> Homo sapiens

<400> 859  
 nacgcgtggt gtggtaatcc gggtttctggt ggcgacggct gccacccctc gtggcaagac  
 60  
 atgccgttgc gtgccgatat gccatacgaa gcttggccta gtgcgaaaag ctgctggaa  
 120  
 ccctcgaaga ggcagggctcg gcaggttacc gtggtcgggtg tacgcatcgt ttcgacgatg  
 180  
 aaccccatc tgggagcaga tatgacgacg taccagtacc tcattgtcgg tggcgggatg  
 240  
 gccgctgatt ctgccgcccg cggtatccgc gacatcgaca agaaagggc gatcgccatc  
 300  
 ctacgcgtg acgtcgacgc cccgtatcct cggccagcgc tgagcaagaa gctgtggact  
 360  
 gacctgagt tcacctggga ccaggtcgac cttgctactg tcgctgacac cggcgcggaa  
 420  
 ttgcggctcg gcaactgaggt gctcagcatt gaccgtgacg gcaagaccgt cctgaccgt  
 480  
 tccggccagg tattcggcta ccagaagttg ctgctcgta ccggccttac cccgtcgcgc  
 540  
 attgacgacg acggcgtatgc c  
 561

<210> 860

<211> 187  
 <212> PRT  
 <213> Homo sapiens

<400> 860  
 Xaa Ala Trp Cys Gly Asn Pro Val Ser Gly Gly Asp Gly Cys His Pro  
 1 5 10 15  
 Ser Trp Gln Asp Met Pro Leu Arg Ala Asp Met Pro Tyr Glu Ala Trp  
 20 25 30  
 Pro Ser Ala Lys Ser Ser Leu Glu Pro Ser Lys Arg Gln Gly Arg Gln  
 35 40 45  
 Val Thr Val Val Gly Val Arg Ile Val Ser Thr Met Asn Pro Ile Leu  
 50 55 60  
 Gly Ala Asp Met Thr Thr Tyr Gln Tyr Leu Ile Val Gly Gly Gly Met  
 65 70 75 80  
 Ala Ala Asp Ser Ala Ala Arg Gly Ile Arg Asp Ile Asp Lys Lys Gly  
 85 90 95  
 Ser Ile Ala Ile Leu Ser Ala Asp Val Asp Ala Pro Tyr Pro Arg Pro  
 100 105 110  
 Ala Leu Ser Lys Lys Leu Trp Thr Asp Pro Glu Phe Thr Trp Asp Gln  
 115 120 125  
 Val Asp Leu Ala Thr Val Ala Asp Thr Gly Ala Glu Leu Arg Leu Gly  
 130 135 140  
 Thr Glu Val Leu Ser Ile Asp Arg Asp Gly Lys Thr Val Leu Thr Ala  
 145 150 155 160  
 Ser Gly Gln Val Phe Gly Tyr Gln Lys Leu Leu Leu Val Thr Gly Leu  
 165 170 175  
 Thr Pro Ser Arg Ile Asp Asp Asp Gly Asp Ala  
 180 185

<210> 861  
 <211> 352  
 <212> DNA  
 <213> Homo sapiens

<400> 861  
 ccattgggttt ctatgctctg aggtttcatc tgtggggaac agtattgact tacttacaaa  
 60  
 gagataatgg tcatacccta tggtcactca ccatagtctg gcggtacatg gacttctcag  
 120  
 cccagtaag atctgtatcc acaggacact taaagtcacc ttacagaggg ctatcccagt  
 180  
 gcctgaggcc tattagaggc gtctcttttc agccatcagt gttagaggcc atctgcatgg  
 240  
 gatcccagag cctgcctcgg gaatggcaga agctggctgg tgcttggcgt gggctttgcc  
 300  
 tgtttactg ctttcagga ggcctgccac aggggagaaa ctgggggggg ga  
 352

<210> 862  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 862

```

Met Gly Phe Tyr Ala Leu Arg Phe His Leu Trp Gly Thr Val Leu Thr
 1           5           10           15
Tyr Leu Gln Arg Asp Asn Gly His Thr Leu Trp Ser Leu Thr Ile Val
          20           25           30
Trp Arg Tyr Met Asp Phe Ser Ala Pro Val Arg Ser Val Ser Thr Gly
      35           40           45
His Leu Lys Ser Pro Tyr Arg Gly Leu Ser Gln Cys Leu Arg Pro Ile
      50           55           60
Arg Gly Val Ser Phe Gln Pro Ser Val Leu Glu Ala Ile Cys Met Gly
65           70           75           80
Ser Gln Ser Leu Pro Arg Glu Trp Gln Lys Leu Ala Gly Ala Trp Arg
          85           90           95
Gly Leu Cys Leu Phe His Cys Phe Gln Gly Gly Leu Pro Gln Gly Arg
          100          105          110
Asn Trp Gly Gly
          115

```

&lt;210&gt; 863

&lt;211&gt; 327

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 863

```

tccggatcga cccggacgaa ttccacggtc cagccattga cttccaaatg ctctttgaca
60
tacgccgtga catgttcaat gtccaactta cgcattgtcca cccgctcacc ggtctcattg
120
agttttgagct gcgagtagac gttgcggttag ttctcgttga ccgactgctc atacgagatg
180
tgcagaagca tcggttttgcg gccatcctcg gacggcattg gcttggttgta catggccgct
240
tggcggaaca tggttcagggt aaagcccgcac ttgaagtgtg gcgacagggc agaaacacac
300
agcattttctg accggcgtatg acccatn
327

```

&lt;210&gt; 864

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 864

```

Met Gly His Arg Arg Ser Glu Met Leu Cys Val Ser Ala Leu Ser His
 1           5           10           15
Asn Phe Lys Ser Gly Phe Thr Leu Asn Met Phe Arg Gln Ala Ala Met
          20           25           30
Tyr Asn Lys Pro Met Pro Ser Glu Asp Gly Arg Lys Pro Met Leu Leu
      35           40           45
His Ile Ser Tyr Glu Gln Ser Val Asn Glu Asn Tyr Arg Asn Val Tyr
      50           55           60
Ser Gln Leu Lys Leu Asn Glu Thr Gly Glu Arg Val Asp Met Arg Lys
65           70           75           80
Leu Asp Ile Glu His Val Thr Ala Tyr Val Lys Glu His Leu Glu Val

```

85 90 95  
 Asn Gly Trp Thr Val Glu Phe Val Arg Val Asp Pro  
 100 105

<210> 865  
 <211> 729  
 <212> DNA  
 <213> Homo sapiens

<400> 865  
 acgcgtcatc ctcattcaag aggccaggga ggagcaccac cctccgcata ttgcgcgtgc  
 60  
 agctctcggt ctgggtctctg agcatgccca cggcgctctg cacacagctt ctcagcagcc  
 120  
 tgggtggtgc caggatcgac acatcactgc ctccgagttc agaggtttcc tttccacact  
 180  
 tctcagaact ttctgtttcc atggcctcct ctgccacctc tgccacctcc cctgatgtgc  
 240  
 tggcctccgt ctccatcgcc tcctcatggc cgtcttccgc ccggtgttcc aagcccagct  
 300  
 caggcaagtc tccgggcgcg aacagctggc tgatggtgac atgctgcagc ctggtcacat  
 360  
 cagaaaccat gaggggtgat ctccggaggt catcgatgtg gacagactgc cacagccctc  
 420  
 cgtggaagcc cacataggtt gtctctcttc ccacccggga cagttttgtg atgaaataga  
 480  
 cgaagatacg gtcctcattt tctcgtattt tgttgatttc atttataaca gaatacttag  
 540  
 ctgaggcaat gagctgggag ctacggattc catcttcaaa atctgtctga aaaatgagga  
 600  
 ttttacattt ggctgtattc gttaaacagt ttcggacttc tttgaggaat gactactcgg  
 660  
 tgtcaaaactg ctgcagccac aggagtgtgg gtttcggagc cctgcctgtg acctctgatt  
 720  
 ctaaaattt  
 729

<210> 866  
 <211> 83  
 <212> PRT  
 <213> Homo sapiens

<400> 866  
 Ala Cys Pro Arg Arg Ser Ala His Ser Phe Ser Ala Ala Trp Trp Cys  
 1 5 10 15  
 Pro Gly Ser Thr His His Cys Leu Arg Val Gln Arg Phe Pro Phe Pro  
 20 25 30  
 Pro Ser Gln Asn Phe Leu Phe Pro Trp Pro Pro Leu Pro Pro Leu Pro  
 35 40 45  
 Pro Pro Leu Met Cys Trp Pro Pro Ser Pro Ser Pro Pro His Gly Arg  
 50 55 60  
 Leu Pro Pro Gly Val Pro Ser Pro Ala Gln Ala Ser Leu Arg Ala Arg  
 65 70 75 80  
 Thr Ala Gly

&lt;210&gt; 867

&lt;211&gt; 640

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 867

```

nntccggaac atcaagatcc aggcgcagaa gaccgtcaga agctgcactg gccacctcct
60
tcaggtggac tctcgttggg ggccggcgtc gctggccccc tcgcacccgg tcccgtgtca
120
catgctccag ggcgcagctc ttgtccacct ttacctcacc gaaagccttg tttttgctc
180
ggttaatccc ttcattgagg gctttgatcc aggattcctt ctctccccc gtgggtgcct
240
ggaatttgat gtcgctgacc ttgttccctg gggatcgag caggataaag cgggtgtttc
300
gcttgaggag ggcacgaagg tcctggcact tctcatagct gccagctcc acagtctcca
360
cacacttctg atcatcctca ttctcataga ccagcagctg ggcttggcag aggagcagat
420
atcggctctt ccagaaaccc aggaggcccc cactgctctt cttgatccag ccagccttgt
480
ccaccatctg tgctccccga ggcttctcac cggttctctt cacaccctcc tcctccatgg
540
cgagtcggcc gaggtccgc cgctccgcca ctgcttcca gcgcgcgcgc ggctctgcca
600
ccgcgtctac gcccggccag gcggcgactc tccgcgttct
640

```

&lt;210&gt; 868

&lt;211&gt; 52

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 868

```

Gly Gly His Glu Gly Pro Gly Thr Ser His Ser Cys Pro Ala Pro Gln
 1             5             10            15
Ser Pro His Thr Ser Asp His Pro His Ser His Arg Pro Ala Ala Gly
      20             25             30
Pro Gly Arg Gly Ala Asp Ile Gly Leu Ser Arg Asn Pro Gly Gly Pro
      35             40             45
His Cys Ser Ser
      50

```

&lt;210&gt; 869

&lt;211&gt; 321

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 869

```

nggggtgatgc tgctcgcggc attgagcacc tttgtgtcga gcgcgctgtt taccgacaac
60

```



ttcctgtcgc cgctgaatat gcgcgggctg ggcctggcga tttcgacggt gggcatcgct  
 120  
 gcgtgcacca tgctgttctg cctggcgctg gggcatttcg acttgctcgtt gggctcgggtg  
 180  
 atcgccctgtg ccggtgtggt cgcggggatt gtgattcgtg acaccgatag cgtggcactc  
 240  
 ggcgtgtccg ctgcgttggc catgggcctg gtagtggggc tgatcaacgg catcgtgatc  
 300  
 gccaaagctgc gcatcaacgc g  
 321

<210> 870  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 870  
 Xaa Val Met Leu Leu Ala Ala Leu Ser Ile Phe Val Leu Ser Ala Leu  
 1 5 10 15  
 Phe Ile Asp Asn Phe Leu Ser Pro Leu Asn Met Arg Gly Leu Gly Leu  
 20 25 30  
 Ala Ile Ser Thr Val Gly Ile Ala Ala Cys Thr Met Leu Phe Cys Leu  
 35 40 45  
 Ala Ser Gly His Phe Asp Leu Ser Val Gly Ser Val Ile Ala Cys Ala  
 50 55 60  
 Gly Val Val Ala Gly Ile Val Ile Arg Asp Thr Asp Ser Val Ala Leu  
 65 70 75 80  
 Gly Val Ser Ala Ala Leu Ala Met Gly Leu Val Val Gly Leu Ile Asn  
 85 90 95  
 Gly Ile Val Ile Ala Lys Leu Arg Ile Asn Ala  
 100 105

<210> 871  
 <211> 320  
 <212> DNA  
 <213> Homo sapiens

<400> 871  
 agatcttcag agtcctcgtc ttttaaatgg gggtaacagc agcaagtcct cagaggtgtc  
 60  
 ctgagcctca aaacacatcc tggtttgtaa cgtccgcagc ctccagcagg gctaggcaca  
 120  
 gaacaagcat tcaggacctg gaaggtagc ggcacacctg gtcctccctt cccaggcaca  
 180  
 aggcagcccc tctccattca agctctgccc cagcccagca aagagagggg tcctcagcca  
 240  
 ctgccccac cactaccaca atcatactca cctctcctgg tccatacgtg acaaaggacc  
 300  
 tgccacggcc agggagacaa  
 320

<210> 872  
 <211> 98  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 872

```

Met Gly Val Thr Ala Ala Ser Pro Gln Arg Cys Pro Glu Pro Gln Asn
 1           5           10          15
Thr Ser Trp Phe Val Thr Ser Ala Ala Ser Ala Gly Ala Arg His Arg
 20          25          30
Thr Ser Ile Gln Asp Leu Glu Gly Thr Ser Asp Thr Trp Ser Ser Leu
 35          40          45
Pro Arg His Lys Ala Ala Pro Leu His Ser Ser Ser Ala Pro Ala Gln
 50          55          60
Gln Arg Glu Gly Ser Ser Ala Thr Ala Pro Thr Thr Thr Thr Ile Ile
 65          70          75          80
Leu Thr Ser Pro Gly Pro Tyr Val Thr Lys Asp Leu Pro Arg Pro Gly
 85          90          95
Arg Gln

```

&lt;210&gt; 873

&lt;211&gt; 363

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 873

```

nttggttagc atcggttttt acgggtgtat cagcgcggttt agcagcggttt ttagcgggatg
60
catcagcatg ttttgcgtca cggttttaca ctgtgctacc gtgttttagca tcatttttga
120
cggaggtatc aatacgttta gcatcggttt taacagatgt atcaacacgg ggttcacccg
180
ctttagcaga atccccagct ctagtagcca ctttagatac ttcagatttt atatgagtcg
240
cagttgtttc agcgtgagcc atgctgaatg tagaaccaag ggccaatgta attgctaaag
300
acaaagataa tttatttagt ttcatgttcg gagagaagtg tgcgaattcg gcgatacagt
360
cag
363

```

&lt;210&gt; 874

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 874

```

Met Lys Leu Asn Lys Leu Ser Leu Ser Leu Ala Ile Thr Leu Ala Leu
 1           5           10          15
Gly Ser Thr Phe Ser Met Ala His Ala Glu Thr Thr Ala Thr His Ile
 20          25          30
Lys Ser Glu Val Ser Lys Val Ala Thr Arg Ala Gly Asp Ser Ala Lys
 35          40          45
Ala Asp Glu Pro Arg Val Asp Thr Ser Val Lys Asn Asp Ala Lys Arg
 50          55          60
Ile Asp Thr Ser Val Lys Asn Asp Ala Lys His Gly Ser Thr Val Val

```

```

65              70              75              80
Lys Arg Asp Ala Lys His Ala Asp Ala Ser Ala Lys Asn Ala Ala Lys
      85              90              95
Arg Ala Asp Thr Pro Val Lys Asn Asp Ala Lys Gln
      100              105

```

```

<210> 875
<211> 355
<212> DNA
<213> Homo sapiens

```

```

<400> 875
acgcgtgaag gggaccctaa ctcgtctggg ctgtaggatg cgggcgaggc ttccacaaac
60
tcactgtctg ggggagaaga aaagcagaaa acaactcgaa tcgctaccat tcaggacgaa
120
cccgccaagc accagctcaa gcgcaggtcc ccgggaaaaa gcgcgggctt ctctctccca
180
gcgctcagaa tccctgagcc ggaggccccc cgggattcag accgccagat ccccagggag
240
tgacaaatcg ccgcagaaac ttgggggaca actcggccct ggcaccgcgc ggcttccagg
300
cgcgggcagg cgcgcgccaa ctttccccgc gtgccacccc gcggctcccc cggn
355

```

```

<210> 876
<211> 106
<212> PRT
<213> Homo sapiens

```

```

<400> 876
Met Arg Ala Arg Leu Pro Gln Thr His Cys Leu Gly Glu Lys Lys Ser
 1              5              10              15
Arg Lys Gln Leu Glu Ser Leu Pro Phe Arg Thr Asn Pro Pro Ser Thr
      20              25              30
Ser Ser Ser Ala Gly Pro Arg Glu Lys Ala Arg Ala Ser Leu Ser Gln
      35              40              45
Arg Ser Glu Ser Leu Ser Arg Arg Pro Arg Gly Ile Gln Thr Ala Arg
      50              55              60
Ser Pro Gly Ser Asp Lys Ser Pro Gln Lys Leu Gly Gly Gln Leu Gly
65              70              75              80
Pro Gly Thr Ala Arg Leu Pro Gly Ala Gly Arg Arg Ala Pro Thr Phe
      85              90              95
Pro Ala Cys His Pro Ala Ala Pro Pro Ala
      100              105

```

```

<210> 877
<211> 487
<212> DNA
<213> Homo sapiens

```

```

<400> 877
acgcgtactt tgggtaatga actgacgacc gctgagatcg actgccttta tctgtgttac
60

```

caatccacct atgctaaacg tggtcagcaa gggtatctca cacgagaatt ctttggtttg  
 120  
 ttggccaata ccatgggaga tcaaatcctt ttagtacagg cgtacagaga aggcgaagcg  
 180  
 atcgccgcgt cgtggtgttt ctttgatgat cattcactat atgggcgtta ttggggctgt  
 240  
 atggaagaag tggattgcct gcattttgaa gcttggtatt accaaggaat cgagttttgt  
 300  
 ctcgaaaaag gggtacagca ttctgatccg ggtacacaag gggaacacaa gattgcgcgc  
 360  
 ggctttgaac ctgttttttag ccacagcgtg cattacattg ctcatcaagg ttttcgtgaa  
 420  
 gcgattggga atttctgtga ggaagaagcg caagctgtgc gcgagtatca tcaagatacc  
 480  
 cacgcgt  
 487

<210> 878  
 <211> 162  
 <212> PRT  
 <213> Homo sapiens

<400> 878  
 Thr Arg Thr Leu Gly Asn Glu Leu Thr Thr Ala Glu Ile Asp Cys Leu  
 1 5 10 15  
 Tyr Leu Cys Tyr Gln Ser Thr Tyr Ala Lys Arg Gly Gln Gln Gly Tyr  
 20 25 30  
 Leu Thr Arg Glu Phe Phe Gly Leu Leu Ala Asn Thr Met Gly Asp Gln  
 35 40 45  
 Ile Leu Leu Val Gln Ala Tyr Arg Glu Gly Glu Ala Ile Ala Ala Ser  
 50 55 60  
 Trp Cys Phe Phe Asp Asp His Ser Leu Tyr Gly Arg Tyr Trp Gly Cys  
 65 70 75 80  
 Met Glu Glu Val Asp Cys Leu His Phe Glu Ala Cys Tyr Tyr Gln Gly  
 85 90 95  
 Ile Glu Phe Cys Leu Glu Lys Gly Leu Gln His Phe Asp Pro Gly Thr  
 100 105 110  
 Gln Gly Glu His Lys Ile Ala Arg Gly Phe Glu Pro Val Phe Ser His  
 115 120 125  
 Ser Val His Tyr Ile Ala His Gln Gly Phe Arg Glu Ala Ile Gly Asn  
 130 135 140  
 Phe Cys Glu Glu Glu Ala Gln Ala Val Arg Glu Tyr His Gln Asp Thr  
 145 150 155 160  
 His Ala

<210> 879  
 <211> 993  
 <212> DNA  
 <213> Homo sapiens

<400> 879  
 nncttagcat ttaagccaac gaggcagcta atgtcctctg aacagcaaag gaaattcagc  
 60

agccagtcca gtagggctct gacccctcct tcctacagta ctgctaaaaa ttcattggga  
 120  
 tcaagatcca gtgaatcctt tgggaagtac acatcgccag taatgagtga gcatggggac  
 180  
 gagcacaggc agctcctctc tcacccaatg caaggccctg gactccgtgc agctacctca  
 240  
 tccaaccact ctgtggacga gcaactgaag aatactgaca cgcacctcat cgacctggta  
 300  
 accaatgaga ttatcaccca aggacctcca gtggactgga atgacattgc tggctctcgac  
 360  
 ctgggtgaagg ctgtcattaa agaggaggtt ttatggccag tgttgaggtc agacgcgttc  
 420  
 agtggactga cggccttacc tcggagcatc cttttatttg gacctcgggg gacaggcaaa  
 480  
 acattatttg gcagatgcat cgctagtcat ctggggggcca catttttcaa aattgccggt  
 540  
 tctggactag tcgccaaagg gttaggagaa gcagagaaaa ttatccatgc ctcttttctt  
 600  
 gtggccagggt gtcgccagcc ctcggtgatt tttgttagtg acattgacat gcttctctcc  
 660  
 tctcaagtga atgaggaaca tagtccagtc agtcggatga gaaccgaatt tctgatgcaa  
 720  
 ctggacactg tactaacttc ggctgaggac caaatcgtag taatttgtgc caccagtaaa  
 780  
 ccagaagaaa tagatgaatc ctttcggagg tacttcatga aacgactttt aatcccactt  
 840  
 cctgacagca cagcgaggca ccagataata gtacaactgc tctcacagca caattactgt  
 900  
 ctcaatgaca aggagtttgc actgctcgtc cagcgcacag aaggcttttc tggactagat  
 960  
 gtggctcatt tgtgtcagga agcagtgggtg ggc  
 993

&lt;210&gt; 880

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 880

Xaa	Leu	Ala	Phe	Lys	Pro	Thr	Arg	Gln	Leu	Met	Ser	Ser	Glu	Gln	Gln
1				5					10					15	
Arg	Lys	Phe	Ser	Ser	Gln	Ser	Ser	Arg	Ala	Leu	Thr	Pro	Pro	Ser	Tyr
			20					25				30			
Ser	Thr	Ala	Lys	Asn	Ser	Leu	Gly	Ser	Arg	Ser	Ser	Glu	Ser	Phe	Gly
		35				40					45				
Lys	Tyr	Thr	Ser	Pro	Val	Met	Ser	Glu	His	Gly	Asp	Glu	His	Arg	Gln
	50					55				60					
Leu	Leu	Ser	His	Pro	Met	Gln	Gly	Pro	Gly	Leu	Arg	Ala	Ala	Thr	Ser
65				70				75						80	
Ser	Asn	His	Ser	Val	Asp	Glu	Gln	Leu	Lys	Asn	Thr	Asp	Thr	His	Leu
			85					90						95	
Ile	Asp	Leu	Val	Thr	Asn	Glu	Ile	Ile	Thr	Gln	Gly	Pro	Pro	Val	Asp
		100					105					110			
Trp	Asn	Asp	Ile	Ala	Gly	Leu	Asp	Leu	Val	Lys	Ala	Val	Ile	Lys	Glu

115	120	125
Glu Val Leu Trp Pro Val Leu Arg Ser Asp Ala Phe Ser Gly Leu Thr		
130	135	140
Ala Leu Pro Arg Ser Ile Leu Leu Phe Gly Pro Arg Gly Thr Gly Lys		
145	150	155
Thr Leu Leu Gly Arg Cys Ile Ala Ser Gln Leu Gly Ala Thr Phe Phe		
165	170	175
Lys Ile Ala Gly Ser Gly Leu Val Ala Lys Gly Leu Gly Glu Ala Glu		
180	185	190
Lys Ile Ile His Ala Ser Phe Leu Val Ala Arg Cys Arg Gln Pro Ser		
195	200	205
Val Ile Phe Val Ser Asp Ile Asp Met Leu Leu Ser Ser Gln Val Asn		
210	215	220
Glu Glu His Ser Pro Val Ser Arg Met Arg Thr Glu Phe Leu Met Gln		
225	230	235
Leu Asp Thr Val Leu Thr Ser Ala Glu Asp Gln Ile Val Val Ile Cys		
245	250	255
Ala Thr Ser Lys Pro Glu Glu Ile Asp Glu Ser Leu Arg Arg Tyr Phe		
260	265	270
Met Lys Arg Leu Leu Ile Pro Leu Pro Asp Ser Thr Ala Arg His Gln		
275	280	285
Ile Ile Val Gln Leu Leu Ser Gln His Asn Tyr Cys Leu Asn Asp Lys		
290	295	300
Glu Phe Ala Leu Leu Val Gln Arg Thr Glu Gly Phe Ser Gly Leu Asp		
305	310	315
Val Ala His Leu Cys Gln Glu Ala Val Val Gly		
325	330	

<210> 881  
 <211> 313  
 <212> DNA  
 <213> Homo sapiens

<400> 881  
 cgcgtgagcg tcgacaatgc tccaggaacc ggtgtgtatg aggccgggga ttctaccggt  
 60  
 cgtgggtttgc agggcatgcg tgagcgcgcc cgtatccatg gcggcaccgc gcgctggggc  
 120  
 gactcgcagt attatgaagg cggtttcaac gtcacgggtg agattccaac atgagcggcc  
 180  
 aaaggatgaa catggacacg acgcgccccca atcacggtcg gggcttgccg acgatcagcc  
 240  
 ggctgggtgc gcaccggttt tgccatggtg ctggattcgc aggacgacat cacggtggcc  
 300  
 tggcaagccg acn  
 313

<210> 882  
 <211> 57  
 <212> PRT  
 <213> Homo sapiens

<400> 882  
 Arg Val Ser Val Asp Asn Ala Pro Gly Thr Gly Val Tyr Glu Ala Gly

```

      1           5           10           15
Asp Ser Thr Gly Arg Gly Leu Gln Gly Met Arg Glu Arg Ala Arg Ile
      20           25           30
His Gly Gly Thr Ala Arg Trp Gly Asp Ser Gln Tyr Tyr Glu Gly Gly
      35           40           45
Phe Asn Val Thr Val Glu Ile Pro Thr
      50           55

```

<210> 883  
 <211> 576  
 <212> DNA  
 <213> Homo sapiens

```

<400> 883
naattaagat ctggggtccc agtgtcattg gtgaaggcct tgggattcga ggcagctgag
60
tcctcactga ccaaggcaag ccatgcttct gagtgcctga ggccaccgaa atgaacaaat
120
ggaaaacact cccatctttt tcaagcctac cttttagcag aagaggcaga tacacaagcc
180
ctaaagatgt aacatcaggc tgagtggagg aaggctgaga agaaaaataa agcagggtca
240
ggaggagaga gtgatgtcag gatgcccttg tgcttactcc agcctccttg tgaaaacca
300
gctctcctgt ctccagtgga agacttgatg ggcagccatc aggggaaggct ggggtcccagc
360
tgaggagtatg ggtgtgagct ctatagacca tccctctctg caatcaataa acacttgctt
420
gtgaaagagg cccaagccac catccgcatg gacaccagtg caagtggccc caccgcctg
480
gtcctcagtg actgtgccac cagccatggg agcctgcgca tccaactgct gcataagctc
540
tccttcctgg tgaacgcctt agctaagcag gtcattg
576

```

<210> 884  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

```

<400> 884
Met Pro Leu Cys Leu Leu Gln Pro Pro Cys Glu Asn Pro Ala Leu Leu
      1           5           10           15
Ser Pro Ser Glu Asp Leu Asp Gly Ser His Gln Gly Arg Leu Gly Pro
      20           25           30
Ser Trp Glu Tyr Gly Cys Glu Leu Tyr Arg Pro Ser Leu Ser Ala Ile
      35           40           45
Asn Lys His Leu Pro Val Lys Glu Ala Gln Ala Thr Ile Arg Met Asp
      50           55           60
Thr Ser Ala Ser Gly Pro Thr Arg Leu Val Leu Ser Asp Cys Ala Thr
      65           70           75           80
Ser His Gly Ser Leu Arg Ile Gln Leu Leu His Lys Leu Ser Phe Leu
      85           90           95
Val Asn Ala Leu Ala Lys Gln Val Met

```

100

105

<210> 885  
 <211> 370  
 <212> DNA  
 <213> Homo sapiens

<400> 885  
 actagtggcg ccctcatccg ggccgctgtc ccgctctcgg agtcggctgc gttggagtcc  
 60  
 ggtgaggcga tgctgacgaa cgacacaccg gtgacttggg atggcgggaa agtacggggc  
 120  
 aggcggtgt cgccctcgg tgcatcgag ttgtcgtcga ccccggtccg ccagatccg  
 180  
 gtacgggctc gccacgtggc gctggaagca gtgaggtctg ggggacttga cgtacgagc  
 240  
 ctgacgaaga acggtgaatc tttgcgacgc cgtcttgccc tggcccatcg ggtgtttggt  
 300  
 gatccctggc ccgatgtcag cgatgaggct ctgctagcct gcgccgagga gtggcttgac  
 360  
 ctcgacgcgt  
 370

<210> 886  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 886  
 Thr Ser Gly Ala Leu Ile Arg Ala Ala Val Pro Leu Ser Glu Ser Ala  
 1 5 10 15  
 Ala Leu Glu Ser Gly Glu Ala Met Leu Thr Asn Asp Thr Pro Val Thr  
 20 25 30  
 Trp Asp Gly Gly Lys Val Arg Gly Arg Arg Val Ser Arg Leu Gly Ala  
 35 40 45  
 Ile Glu Leu Ser Ser Thr Pro Val Arg Pro Asp Pro Val Arg Ala Arg  
 50 55 60  
 His Val Ala Leu Glu Ala Val Arg Ser Gly Gly Leu Asp Val Ala Ser  
 65 70 75 80  
 Leu Thr Lys Asn Gly Glu Ser Leu Arg Arg Arg Leu Ala Leu Ala His  
 85 90 95  
 Arg Val Phe Gly Asp Pro Trp Pro Asp Val Ser Asp Glu Ala Leu Leu  
 100 105 110  
 Ala Cys Ala Glu Glu Trp Leu Asp Leu Asp Ala  
 115 120

<210> 887  
 <211> 447  
 <212> DNA  
 <213> Homo sapiens

<400> 887  
 cagggcggtg cgctcggtcg cgtgctgccg atggtcatgc tcggaggcctt aaccgccatc  
 60



attatctccg gctgcctgaa ccagcttggt aaacgctatc cgcattctgac cggcgaaggc  
 120  
 caactgatgc caaacctgac taatgctgat accacggctt cccaaccggc gttctccggt  
 180  
 aaagcggacg tgaccaccat tgcctccggc gcgttgctgg ccgtgctgct ttacatgggtg  
 240  
 ggtagggttg ttcacaagtt gattggcctg cctgctccgg ttggcatggt gtttgtggcg  
 300  
 gtgctgggtca aactgtgcaa cggcgcttct ccccgctgac tcgaaggctc gcagggtggtt  
 360  
 tacaattctt tccagacctc cgtcacctat ccgattctgt tcgccgttgg cgtggcgatt  
 420  
 acgccgtggc aggaactggt caacgcg  
 447

<210> 888  
 <211> 149  
 <212> PRT  
 <213> Homo sapiens

<400> 888  
 Gln Gly Val Ala Leu Gly Arg Val Leu Pro Met Val Met Leu Gly Gly  
 1 5 10 15  
 Leu Thr Ala Ile Ile Ser Gly Cys Leu Asn Gln Leu Gly Lys Arg  
 20 25 30  
 Tyr Pro His Leu Thr Gly Glu Gly Gln Leu Met Pro Asn Arg Ala Asn  
 35 40 45  
 Ala Asp Thr Thr Ala Ser Gln Pro Ala Phe Ser Gly Lys Ala Asp Val  
 50 55 60  
 Thr Thr Ile Ala Ser Gly Ala Leu Leu Ala Val Leu Leu Tyr Met Val  
 65 70 75 80  
 Gly Arg Leu Val His Lys Leu Ile Gly Leu Pro Ala Pro Val Gly Met  
 85 90 95  
 Leu Phe Val Ala Val Leu Val Lys Leu Cys Asn Gly Ala Ser Pro Arg  
 100 105 110  
 Leu Leu Glu Gly Ser Gln Val Val Tyr Lys Phe Phe Gln Thr Ser Val  
 115 120 125  
 Thr Tyr Pro Ile Leu Phe Ala Val Gly Val Ala Ile Thr Pro Trp Gln  
 130 135 140  
 Glu Leu Val Asn Ala  
 145

<210> 889  
 <211> 450  
 <212> DNA  
 <213> Homo sapiens

<400> 889  
 ggtaccaccc cacacctgac aagagggtggc cagggaggaa gggagggttc ttacctcccc  
 60  
 atctcccctc agtaaaattc aggatgccca gtgaagtttg aatgtcagat aaacaatttg  
 120  
 ttagtataag gatgtaccta gcattgaaat gatgccttgt aatttactaa atctgcaact  
 180

atgcagcctt atttcatggc gggcagtggc ggtgatccca ggtttcaggg gcggggaagg  
 240  
 gtgctgggga gatcctgagg tcaggaaccc gtacacctct gcttctgccc tctcttccct  
 300  
 gtgccggcca caaggcaatg actcctgtgt gggcgcagag gcagaaatgg gtctggaagg  
 360  
 ggattcccag tgtctggcaa gttctggtta attctgcatt ggaggttctc tctgtagtaa  
 420  
 ggggagttgg cctggccgcc cttcacgcgt  
 450

<210> 890  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 890  
 Met Met Pro Cys Asn Leu Leu Asn Leu Gln Leu Cys Ser Leu Ile Ser  
 1 5 10 15  
 Trp Arg Ala Val Ala Val Ile Pro Gly Phe Arg Gly Gly Glu Gly Cys  
 20 25 30  
 Trp Gly Asp Pro Glu Val Arg Asn Pro Tyr Thr Ser Ala Ser Ala Leu  
 35 40 45  
 Ser Ser Leu Cys Arg Pro Gln Gly Asn Asp Ser Cys Val Gly Ala Glu  
 50 55 60  
 Ala Glu Met Gly Leu Glu Gly Asp Ser Gln Cys Leu Ala Ser Ser Gly  
 65 70 75 80  
 Lys Phe Cys Ile Gly Gly Ser Leu Cys Ser Lys Gly Ser Trp Pro Gly  
 85 90 95  
 Arg Pro Ser Arg  
 100

<210> 891  
 <211> 318  
 <212> DNA  
 <213> Homo sapiens

<400> 891  
 nncaccgtcc ccgtactgga tccgcgcgag gatttcgccg actgcatgca cattgacgta  
 60  
 ctggatccct tccacactga caacaccagt gagcacagt acctggccac agatggccag  
 120  
 actaacggcc cggctgatag cgggactggc acccactctg agcagggaaa ctccgacata  
 180  
 tctagccccg tcagctctag tgacgtgct aacaccaccg acagcactgc tggcaatacc  
 240  
 ggtgaaggta ctgccgcgaa tatgcctggt gacatggctc attcttcgac ggctaccac  
 300  
 ccctatgcaa gcaccggt  
 318

<210> 892  
 <211> 106  
 <212> PRT

<213> Homo sapiens

<400> 892

```

Xaa Thr Val Pro Val Leu Asp Pro Arg Glu Asp Phe Ala Asp Cys Met
 1           5           10           15
His Ile Asp Val Leu Asp Pro Phe His Thr Asp Asn Thr Ser Glu His
      20           25           30
Ser Asp Leu Ala Thr Asp Gly Gln Thr Asn Gly Pro Ala Asp Ser Gly
      35           40           45
Thr Gly Thr His Ser Glu Gln Gly Asn Ser Asp Ile Ser Ser Pro Val
      50           55           60
Ser Ser Ser Asp Ala Ala Asn Thr Thr Asp Ser Thr Ala Gly Asn Thr
      65           70           75           80
Gly Glu Gly Thr Ala Ala Asn Met Pro Gly Asp Met Ala His Ser Ser
      85           90           95
Thr Ala Thr His Pro Tyr Ala Ser Thr Gly
      100           105

```

<210> 893

<211> 510

<212> DNA

<213> Homo sapiens

<400> 893

```

nnggatccta tccctgaatc taagggtggg gacacatgtg tttgggatag caaggtagag
60
aagtcacaga aaaagcctgt ggaaaacagg atgaaggagg acaaaagcag catcagggaa
120
gcaatcagca aagccaagag tacagcaaata ataaagacag aacaggaagg tgaggcatct
180
gagaagagct tgcattctgag cccacagcat atcacacacc agactatgcc tataggacag
240
agaggcagtg agcaaggcaa acgtgtggag aacattaatg gaacctccta ccctagtcta
300
cagcagaaaa ccaatgctgt taagaaatta cataaatgtg atgaatgtgg gaaatccttc
360
aaatataatt cccgccttgt tcaacataaa attatgcaca ctggggaaaa gcgctatgaa
420
tgtgatgact gtggaggggac tttccggagc agctcgagcc ttcgggtcca caaacggatc
480
cacactgggt acggagagaa gacaacgcgt
510

```

<210> 894

<211> 170

<212> PRT

<213> Homo sapiens

<400> 894

```

Xaa Asp Pro Ile Pro Glu Ser Lys Val Gly Asp Thr Cys Val Trp Asp
 1           5           10           15
Ser Lys Val Glu Lys Ser Gln Lys Lys Pro Val Glu Asn Arg Met Lys
      20           25           30
Glu Asp Lys Ser Ser Ile Arg Glu Ala Ile Ser Lys Ala Lys Ser Thr

```

		35					40					45				
Ala	Asn	Ile	Lys	Thr	Glu	Gln	Glu	Gly	Glu	Ala	Ser	Glu	Lys	Ser	Leu	
	50					55					60					
His	Leu	Ser	Pro	Gln	His	Ile	Thr	His	Gln	Thr	Met	Pro	Ile	Gly	Gln	
65					70					75					80	
Arg	Gly	Ser	Glu	Gln	Gly	Lys	Arg	Val	Glu	Asn	Ile	Asn	Gly	Thr	Ser	
				85					90					95		
Tyr	Pro	Ser	Leu	Gln	Gln	Lys	Thr	Asn	Ala	Val	Lys	Lys	Leu	His	Lys	
			100					105					110			
Cys	Asp	Glu	Cys	Gly	Lys	Ser	Phe	Lys	Tyr	Asn	Ser	Arg	Leu	Val	Gln	
	115						120					125				
His	Lys	Ile	Met	His	Thr	Gly	Glu	Lys	Arg	Tyr	Glu	Cys	Asp	Asp	Cys	
	130					135					140					
Gly	Gly	Thr	Phe	Arg	Ser	Ser	Ser	Ser	Leu	Arg	Val	His	Lys	Arg	Ile	
145					150					155					160	
His	Thr	Gly	Tyr	Gly	Glu	Lys	Thr	Thr	Arg							
				165					170							

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<210> 895
<211> 1119
<212> DNA
<213> Homo sapiens
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<400> 895
cggccgcaga attgggtcgg gcatttccag atgttcccgt ggttgattcg tccggcaatc
60
acgttcggga gagggtcgat tcaactcccc gattaatcgt tgccacccca agggccgaac
120
ccgcaccgga atcggggcttt tcctgggggt gccttcctaa atgcggtgtc ctccctgtcg
180
aggcctggcc tggcggcggt ggagcagacc gtcgatcggg ggatggcaat cctggccttg
240
gtccgatcag tgcgggatgg gggccgggca gttatcgteg ggccttcgga ggacgccgcc
300
ttgcaggcca tggttcgaaa tgatccagtc ggggtggcga cacgtgaact cgccgatcgt
360
cgggaggcac atttcccgcc cgcggtgccg tgcggaattg tcgacggtga cccgaaagcg
420
gtggctacag cggcacagcg actacgcgag tggttcgga ccgaccttga gatgcttggc
480
ccagctccac aaccacgccg tgccagcgaa tcggaacggg atcgaattat cgtgctcct
540
cgtagcacga tgcctctcgc cgagctttcc cagggctcat ttcggctacg ttccaaacac
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<212> PRT

<213> Homo sapiens

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Thr	Ile	Ala	Asn	Cys	Lys	Arg	Leu	His	Thr	Leu	Val	Ala	His	Ser	Asn
		100					105						110		
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Thr	Val	Ala	Asn	Val	Gly
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Lys	Val	Asn	Gly	Val	Thr
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Leu	Tyr	Pro	Trp	Ile	Leu
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Thr	Ile	Gln	Asp	Glu	Leu
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His	Leu	Ser	Tyr	Thr	Glu
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Pro	Leu	Ala	Ala	Ala	Lys
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Cys	Gln	Asp	Ser	Val	Gly
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			450		455
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Pro	Ser	Ser	Ser	Ser	Gly
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Thr	Ser	Glu	Val	Ser	Ser
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Asn	Ala	Gly	Gly	Leu	Asp
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Cys	Ser	Leu	His	Pro	Thr
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Asp	Asp	Asp	Gln	Pro	Val
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<212> DNA
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Ile Arg Leu Pro Ser Val Ser Val Val Ser Ser Asp Gly His Leu Trp
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Ser Phe Gln Arg Leu Met His Trp Val Thr Arg His Cys Lys Arg Pro
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Gln Ile Ala Gln His His Leu Thr Phe Thr Pro His His Ile Asn Ile
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 gggctctgcg acaggctggc tggacatggc gtgacctcaa cgggtggttcc caacatcggt  
 180  
 gacgtcgagc tgtttgaccg tcttgatcga cgacatgagg ggacgatcgt cgtcagcgtc  
 240

gccaccctca acccgggaaa gggcatgatt gagttagctc aggctgttga gcgtcttccc  
 300  
 gaggttcagt tgagaatcat cggagatgga ccgcagcggc accaactgga ggccattgcc  
 360  
 gctgataatc cacgcgt  
 377

<210> 906  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 906  
 Xaa Pro Glu Pro Val Val Trp Thr Glu His Asp Ser His Leu Ala His  
 1 5 10 15  
 Pro Asp Gln Arg Leu Asn Glu Asp Ile Ile Ile Ala Gly Asp Arg Ala  
 20 25 30  
 Asp Ala Val Ile Ser Val Ser Gln Gly Leu Cys Asp Arg Leu Ala Gly  
 35 40 45  
 His Gly Val Thr Ser Thr Val Val Pro Asn Ile Val Asp Val Glu Leu  
 50 55 60  
 Phe Asp Arg Pro Asp Arg Arg His Glu Gly Thr Ile Val Val Ser Val  
 65 70 75 80  
 Ala Thr Leu Asn Pro Gly Lys Gly Met Ile Glu Leu Ala Gln Ala Val  
 85 90 95  
 Glu Arg Leu Pro Glu Val Gln Leu Arg Ile Ile Gly Asp Gly Pro Gln  
 100 105 110  
 Arg His Gln Leu Glu Ala Ile Ala Ala Asp Asn Pro Arg  
 115 120 125

<210> 907  
 <211> 332  
 <212> DNA  
 <213> Homo sapiens

<400> 907  
 acgcgtagga tgatgaagtc cgctcactgga tcgttcttgg gtggcaaccg ggaagtcggt  
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 gaccagttct tcaacggcga gggtcaactg aaccttgtgc cgcagggtac attcgccgag  
 120  
 cgcattcgtg ccggcgctgc tggattgca gcattcttca cgcctactgg ctatggtaca  
 180  
 gccgtgcaga agggtagct tgttcttaag tatgaaaaga aggacggtaa ggctgtgcc  
 240  
 gtcatgacgt ccaagccgcg tgaagtgcgc tcgtttgacg gccgtgacta tataatagaa  
 300  
 gaggttatta aggatgaata ggatatggtg aa  
 332

<210> 908  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 908

```

Thr Arg Arg Met Met Lys Ser Val Thr Gly Ser Phe Leu Gly Gly Asn
 1           5           10           15
Arg Glu Val Gly Asp Gln Phe Phe Asn Gly Glu Val Gln Leu Asn Leu
 20           25           30
Val Pro Gln Gly Thr Phe Ala Glu Arg Ile Arg Ala Gly Ala Ala Gly
 35           40           45
Ile Ala Ala Phe Phe Thr Pro Thr Gly Tyr Gly Thr Ala Val Gln Lys
 50           55           60
Gly Glu Leu Val Leu Lys Tyr Glu Lys Lys Asp Gly Lys Ala Val Pro
65           70           75           80
Val Met Thr Ser Lys Pro Arg Glu Val Arg Ser Phe Asp Gly Arg Asp
 85           90           95
Tyr Ile Ile Glu Glu Val Ile Lys Asp Glu
100           105

```

&lt;210&gt; 909

&lt;211&gt; 318

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 909

```

acgcgtcggg catggcagct gtacagatct atcgcgtcag cagggcctac gcacacatga
60
tgccgcaggg gcaccgacgc tgctgccatc aaaagagccg cctcgcgccc gcagcgcctc
120
ccagggacgg cgactcacgt ggctcgacac gcgcgcgcga gtcgcgtggg tgtgtcacgc
180
cccttttttt cccaccccaa caccgaaccg gcgggcatg gctgaggatt cgaccccat
240
tcgctccggc ttgcgcatgc tcaagcgctc ctggagctcg aatgagaatg taccgccgcc
300
acaaagctcg ccgccggc
318

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&lt;210&gt; 910

&lt;211&gt; 102

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 910

```

Met Ala Ala Val Gln Ile Tyr Arg Val Ser Arg Ala Tyr Ala His Met
 1           5           10           15
Met Pro Gln Gly His Arg Arg Cys Arg His Gln Lys Ser Arg Leu Ala
 20           25           30
Pro Ala Ala Pro Pro Arg Asp Gly Asp Ser Arg Gly Ser Thr Arg Ala
 35           40           45
Arg Glu Ser Arg Gly Cys Val Thr Pro Leu Phe Phe Pro Pro Gln His
 50           55           60
Arg Thr Gly Gly Pro Trp Leu Arg Ile Arg Thr Pro Phe Ala Pro Ala
65           70           75           80
Cys Ala Cys Ser Ser Ala Pro Gly Ala Arg Met Arg Met Tyr Arg Arg
 85           90           95
His Lys Ala Arg Arg Arg

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100

<210> 911  
 <211> 506  
 <212> DNA  
 <213> Homo sapiens

<400> 911  
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 caaccttatg aggctggcct tgggggaacc ctgttttagg gatgagctga acttaccggg  
 120  
 aggctgcatg cgaggttggt gtgaaatgca tatctggctt tgtagctggt cggtcacct  
 180  
 ctgggggttg cacaggggcg ggggttctgc catggctaga atgcgctaag gggtggaac  
 240  
 gaagcctgct gggcccgga accacagagc agcctggcct ttgaaggaga ccctgtggca  
 300  
 cccctgccc accccaagt ccagccattt cacttcctg gagatggtgc aaagcaagaa  
 360  
 aaaaaaaaa atccagtgtt ctgaggtcag cctccacca gccaggattc atcgtctgat  
 420  
 ctgtttgggg agagagcatg gagtgggtga gatgggttg gcccagtggt tttctgatta  
 480  
 actcgcagtt cacctgaaac attttg  
 506

<210> 912  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

<400> 912  
 Met Phe Gln Val Asn Cys Glu Leu Ile Arg Lys His Trp Gly Pro Thr  
 1 5 10 15  
 His Leu His His Ser Met Leu Ser Pro Gln Thr Asp Gln Thr Met Asn  
 20 25 30  
 Pro Gly Trp Trp Lys Ala Asp Leu Arg Thr Leu Asp Phe Phe Phe  
 35 40 45  
 Leu Ala Leu His His Leu Gln Gly Ser Glu Met Ala Gly Leu Gly Gly  
 50 55 60  
 Gly Gln Gly Val Pro Gln Gly Leu Leu Gln Arg Pro Gly Cys Ser Val  
 65 70 75 80  
 Val Pro Gly Pro Ser Arg Leu Arg Phe His Pro Leu Ala His Ser Ser  
 85 90 95  
 His Gly Arg Thr Pro Ala Pro Val Pro Thr Pro Glu Val Ser Arg Pro  
 100 105 110  
 Ala Thr Lys Pro Asp Met His Phe Thr Pro Thr Ser His Ala Ala Ser  
 115 120 125  
 Arg

<210> 913  
 <211> 339



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 913

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 60  
 tttttcgttc gcgagaacgg taaaaccctc gcaacctcga tgttcacggt ttgtgtcgcc  
 120  
 ctggggcgcca cggacctgct ttctgccttc gactcgattc cggcgctccta tggtttcacc  
 180  
 aacgaggggt accttatcct taccgctaac gtctttgctc tcatgggctt gcgtcagttg  
 240  
 tatttcctta ttggaagcct gttggaacgt ctggtgtact tgctgctggg actgggtcgtg  
 300  
 attttgggct ttatcgccct caagctcatt ggccacgcg  
 339

&lt;210&gt; 914

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 914

Arg	Phe	Met	Ala	Trp	Phe	Arg	Arg	Thr	Val	Pro	Ala	Thr	Gly	Asp	Tyr
1				5					10					15	
Arg	Gly	Thr	Lys	Phe	Phe	Val	Arg	Glu	Asn	Gly	Lys	Thr	Leu	Ala	Thr
			20					25					30		
Ser	Met	Phe	Met	Val	Cys	Val	Ala	Leu	Gly	Ala	Thr	Asp	Leu	Leu	Phe
		35				40					45				
Ala	Leu	Asp	Ser	Ile	Pro	Ala	Ser	Tyr	Gly	Phe	Thr	Asn	Glu	Gly	Tyr
	50					55				60					
Leu	Ile	Leu	Thr	Ala	Asn	Val	Phe	Ala	Leu	Met	Gly	Leu	Arg	Gln	Leu
65				70				75					80		
Tyr	Phe	Leu	Ile	Gly	Ser	Leu	Leu	Glu	Arg	Leu	Val	Tyr	Leu	Ser	Leu
			85					90					95		
Gly	Leu	Val	Val	Ile	Leu	Gly	Phe	Ile	Ala	Leu	Lys	Leu	Ile	Gly	His
		100					105						110		

Ala

&lt;210&gt; 915

&lt;211&gt; 663

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 915

nnggtacctg tcaatcagta tgtaaaccctc actttatgtc gtgggttatcc acttctctgat  
 60  
 gacagtgaag atcctgttgt ggacattggt gctgctaccc ctgtcatcaa tggacagtca  
 120  
 ttaaccaagg gagagacttg catgaatcct caggatttta agccaggagc aatgggtctg  
 180  
 gaggagaatg gaaaatcggg acacactttg actgggtgatg gtctcaatgg accatcagat  
 240

gcaagtgagc agagagtatc catggcatcg tcaggcagct cccagcctga actagtgact  
 300  
 atccctttga ttaagggccc taaaggggtt gggtttgcaa ttgctgacag ccctactgga  
 360  
 cagaaggtga aaatgatact ggatagtcag tgggtgtcaag gccttcagaa aggagatata  
 420  
 attaaggaaa tataccatca aaatgtgcag aatttaacac atctccaagt ggtagaggtg  
 480  
 ctaaagcagt ttccagtagg tgctgatgta ccattgctta tcttaagagg aggtccccct  
 540  
 tcaccaacca aaagtgccaa aatgaaaaca gataaaaagg aaaatgcagg aagtttggag  
 600  
 gccataaatg agcctattcc tcagcctatg ccttttccac cgagcattat caggtcagga  
 660  
 tcc  
 663

<210> 916

<211> 221

<212> PRT

<213> Homo sapiens

<400> 916

Xaa	Val	Pro	Val	Asn	Gln	Tyr	Val	Asn	Leu	Thr	Leu	Cys	Arg	Gly	Tyr
1				5				10						15	
Pro	Leu	Pro	Asp	Asp	Ser	Glu	Asp	Pro	Val	Val	Asp	Ile	Val	Ala	Ala
		20					25						30		
Thr	Pro	Val	Ile	Asn	Gly	Gln	Ser	Leu	Thr	Lys	Gly	Glu	Thr	Cys	Met
		35					40					45			
Asn	Pro	Gln	Asp	Phe	Lys	Pro	Gly	Ala	Met	Val	Leu	Glu	Gln	Asn	Gly
	50					55				60					
Lys	Ser	Gly	His	Thr	Leu	Thr	Gly	Asp	Gly	Leu	Asn	Gly	Pro	Ser	Asp
65				70					75					80	
Ala	Ser	Glu	Gln	Arg	Val	Ser	Met	Ala	Ser	Ser	Gly	Ser	Ser	Gln	Pro
			85					90						95	
Glu	Leu	Val	Thr	Ile	Pro	Leu	Ile	Lys	Gly	Pro	Lys	Gly	Phe	Gly	Phe
		100					105						110		
Ala	Ile	Ala	Asp	Ser	Pro	Thr	Gly	Gln	Lys	Val	Lys	Met	Ile	Leu	Asp
		115					120					125			
Ser	Gln	Trp	Cys	Gln	Gly	Leu	Gln	Lys	Gly	Asp	Ile	Ile	Lys	Glu	Ile
	130					135				140					
Tyr	His	Gln	Asn	Val	Gln	Asn	Leu	Thr	His	Leu	Gln	Val	Val	Glu	Val
145				150					155					160	
Leu	Lys	Gln	Phe	Pro	Val	Gly	Ala	Asp	Val	Pro	Leu	Leu	Ile	Leu	Arg
			165					170					175		
Gly	Gly	Pro	Pro	Ser	Pro	Thr	Lys	Ser	Ala	Lys	Met	Lys	Thr	Asp	Lys
		180					185					190			
Lys	Glu	Asn	Ala	Gly	Ser	Leu	Glu	Ala	Ile	Asn	Glu	Pro	Ile	Pro	Gln
	195					200						205			
Pro	Met	Pro	Phe	Pro	Pro	Ser	Ile	Ile	Arg	Ser	Gly	Ser			
	210					215					220				

<210> 917

<211> 615

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 917

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 ttcaaacatg accccacgtc ggccaacctc ctgcagctgg tgcgctcgtc cggagacatc  
 120  
 caggagggcg acctggtgga ggtggtgctg tcggcctcgg ccaccttcga ggacttccag  
 180  
 atccgccccg acgccctcac ggtgcactcc tatcggggcg ctgccttctg tgatcactgc  
 240  
 ggggagatgc tcttcggcct agtgcgccag ggccctcaagt gcgatggctg cgggctgaac  
 300  
 taccacaagc gctgtgcctt cagcatcccc aacaactgta gtggggcccg caaacggcgc  
 360  
 ctgtcatcca cgtctctggc cagtggccac tcggtgcgcc tcggcacctc cgagtcacctg  
 420  
 ccctgcacgg ctgaagagga gccgtagcac caccgaactc ctgcctcgcc gtccccgtea  
 480  
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 540  
 ctgctctcca aggtcaaggt gccgcacacc ttctcatcc acagctatac acggcccacc  
 600  
 gtttgccagg cttgc  
 615

&lt;210&gt; 918

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 918

Ile Val Asp Gln Lys Phe Pro Glu Cys Gly Phe Tyr Gly Leu Tyr Asp  
 1 5 10 15  
 Lys Ile Leu Leu Phe Lys His Asp Pro Thr Ser Ala Asn Leu Leu Gln  
 20 25 30  
 Leu Val Arg Ser Ser Gly Asp Ile Gln Glu Gly Asp Leu Val Glu Val  
 35 40 45  
 Val Leu Ser Ala Ser Ala Thr Phe Glu Asp Phe Gln Ile Arg Pro His  
 50 55 60  
 Ala Leu Thr Val His Ser Tyr Arg Ala Pro Ala Phe Cys Asp His Cys  
 65 70 75 80  
 Gly Glu Met Leu Phe Gly Leu Val Arg Gln Gly Leu Lys Cys Asp Gly  
 85 90 95  
 Cys Gly Leu Asn Tyr His Lys Arg Cys Ala Phe Ser Ile Pro Asn Asn  
 100 105 110  
 Cys Ser Gly Ala Arg Lys Arg Arg Leu Ser Ser Thr Ser Leu Ala Ser  
 115 120 125  
 Gly His Ser Val Arg Leu Gly Thr Ser Glu Ser Leu Pro Cys Thr Ala  
 130 135 140  
 Glu Glu Glu Pro  
 145

<210> 919  
 <211> 294  
 <212> DNA  
 <213> Homo sapiens

<400> 919  
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 60  
 acaaatgcga tcctgctcga tagcgagcgg ggtgagtacc tcgccaagat gggcccgcg  
 120  
 gaagaagact tcatttcgaa cgcgacccat cgtggcgatc acctgaccgc acagcgcgcc  
 180  
 accttcgcca acccgacctt gctcaacgag atggccgtag tcgatggtga agtgaagaaa  
 240  
 ggctcgcttg cccgcgtgga accggaaggc catgtgatgc gcatgtggga agcc  
 294

<210> 920  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 920  
 Thr Gly Met Arg Pro Leu Ala Val Leu Gly Asp Asn Ile Thr Thr Asp  
 1 5 10 15  
 His Leu Ser Pro Thr Asn Ala Ile Leu Leu Asp Ser Ala Ala Gly Glu  
 20 25 30  
 Tyr Leu Ala Lys Met Gly Pro Pro Glu Glu Asp Phe Ile Ser Asn Ala  
 35 40 45  
 Thr His Arg Gly Asp His Leu Thr Ala Gln Arg Ala Thr Phe Ala Asn  
 50 55 60  
 Pro Thr Leu Leu Asn Glu Met Ala Val Val Asp Gly Glu Val Lys Lys  
 65 70 75 80  
 Gly Ser Leu Ala Arg Val Glu Pro Glu Gly His Val Met Arg Met Trp  
 85 90 95  
 Glu Ala

<210> 921  
 <211> 378  
 <212> DNA  
 <213> Homo sapiens

<400> 921  
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 60  
 aaccaggacg tgctgttggt catcgacaac atcttccggc tctcccaggc tggttctgag  
 120  
 gtttcaaccc tgctaggtcg tatgccctcg gcggtgggct accagcccaa cttggccgac  
 180  
 gagatgggccc aattgcagga gcgaatcacc tcgaccctg gtcactccat cacctcgatg  
 240  
 caggccgtct acgtccccgc tgacgattac accgaccggg ctccggcgac gaccttcgcc  
 300

cacctggatg ccaccacgga gctttctcgt gagattgcct ctggtggcct gtaccgggcc  
 360  
 gtggatccgc tggcgctcg  
 378

<210> 922  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<400> 922  
 Thr Arg Leu Arg Ile Ala Leu Thr Gly Leu Thr Met Ala Glu Tyr Phe  
 1 5 10 15  
 Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn Ile Phe  
 20 25 30  
 Arg Phe Ser Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly Arg Met  
 35 40 45  
 Pro Ser Ala Val Gly Tyr Gln Pro Asn Leu Ala Asp Glu Met Gly Gln  
 50 55 60  
 Leu Gln Glu Arg Ile Thr Ser Thr Arg Gly His Ser Ile Thr Ser Met  
 65 70 75 80  
 Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala  
 85 90 95  
 Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu Leu Ser Arg Glu Ile  
 100 105 110  
 Ala Ser Arg Gly Leu Tyr Pro Ala Val Asp Pro Leu Ala Ser  
 115 120 125

<210> 923  
 <211> 571  
 <212> DNA  
 <213> Homo sapiens

<400> 923  
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 ctggacaccg cgctggagca cgtgcgcgga gaaatccgca ttaccctgga gcatgcacgc  
 120  
 caacgcaaga atgtcgaaga agaagacatc ttcgccgccc accttgcgct attggaagac  
 180  
 cccacgctgc tggacgccgc cactggtgcc atcgaacacg gcagcgccgc caccacgcc  
 240  
 tggcgcgatg caatccaggc gcaatgcgcc gtgttgctgg ccctgggcaa accgctgttt  
 300  
 gccgagcgcg ccaacgacct gcgcgatctg caacagcgag tactgcgtgc gctgttggg  
 360  
 gaagcctggc acttcgaatt gccggccggg ccgattttca ggnnggcat taacttacc  
 420  
 cttccgcct tgttgcaact gagtgcctaa aacgccgtgg gtatttgcac ggccgaaggc  
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 540  
 ctgggcgcgc aagtgtctga cgtgcccac g  
 571

<210> 924  
 <211> 190  
 <212> PRT  
 <213> Homo sapiens

<400> 924  
 Thr Gly Ile Glu Leu Pro Gln Asp Thr Gly Lys His Val Ala Asp Glu  
 1 5 10 15  
 Gln Leu Gln Arg Leu Asp Thr Ala Leu Glu His Val Arg Gly Glu Ile  
 20 25 30  
 Arg Ile Thr Leu Glu His Ala Arg Gln Arg Lys Asn Val Glu Glu Glu  
 35 40 45  
 Asp Ile Phe Ala Ala His Leu Ala Leu Leu Glu Asp Pro Thr Leu Leu  
 50 55 60  
 Asp Ala Ala Thr Gly Ala Ile Glu His Gly Ser Ala Ala Thr His Ala  
 65 70 75 80  
 Trp Arg Asp Ala Ile Gln Ala Gln Cys Ala Val Leu Leu Ala Leu Gly  
 85 90 95  
 Lys Pro Leu Phe Ala Glu Arg Ala Asn Asp Leu Arg Asp Leu Gln Gln  
 100 105 110  
 Arg Val Leu Arg Ala Leu Leu Gly Glu Ala Trp His Phe Glu Leu Pro  
 115 120 125  
 Ala Gly Pro Ile Phe Arg Xaa Ala Ile Asn Leu Pro Pro Ser Ala Leu  
 130 135 140  
 Leu Gln Leu Ser Ala Gln Asn Ala Val Gly Ile Cys Met Ala Glu Gly  
 145 150 155 160  
 Gly Ala Thr Ser His Val Ala Ile Leu Ala Arg Gly Lys Gly Leu Pro  
 165 170 175  
 Cys Val Val Ala Leu Gly Ala Glu Val Leu Asp Val Pro Gln  
 180 185 190

<210> 925  
 <211> 620  
 <212> DNA  
 <213> Homo sapiens

<400> 925  
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 120  
 gtggtgtgta tgcattggtg gtgcacgtgt gcactgtgtg tgtgtgtatg catgtgtgtg  
 180  
 cacgtgtgcc tgtgtgtatg catggtaatg tgcgtgtgca ctgtgtggtg tgtatgcatg  
 240  
 tgtgtgcacg tgtgcactgt gtatgcatag tgtgtgcacg tgtgcactgt gtgtggatgc  
 300  
 atggtaatgt gcacgtgtgc actgtgtgtg gtgtgtatga tgggtgtgtgc acgtgtgcac  
 360  
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 420  
 tgtgtgcatg tatgcatggt gtgtgcatac gtgtgcagca gcacctggtc ccatctccag  
 480

tgcccagcag catcacacgc actttggtgc ttataaatg catggtcagt gaggtgcca  
 540  
 gcaccaagct gtccctttac cataaacacct ggaatagtca cctgtgataa gctatcacat  
 600  
 aggaaacatt tttaaaattt  
 620

<210> 926  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

<400> 926  
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys  
 1 5 10 15  
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met  
 20 25 30  
 Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val Cys  
 35 40 45  
 Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Val Cys Leu  
 50 55 60  
 Cys Val Cys Met Val Met Cys Val Cys Thr Val Trp Cys Val Cys Met  
 65 70 75 80  
 Cys Val His Val Cys Thr Val Tyr Ala  
 85

<210> 927  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 927  
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 aagaggcatt tggggctctg ttcagatcat tccaacagca aaccgggcat ggagacccca  
 120  
 tctcaggtct gtgcttctct gggggccacc cagccatcct gccaccagc tcagaggcag  
 180  
 ggacaaaagc ctcccaagag gcagcaggca gcaagggtca gccagcgag tggggacagg  
 240  
 caggtacaac ctggaaaccc caaaggaccc cagatggcaa tgtgacacgg cccatccacc  
 300  
 aagcacctgt aatgccggct tcccacagag gcgagccaga tcctggcact attctttaag  
 360

<210> 928  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 928  
 Met Glu Leu Leu Glu Ile Val Arg His Asp Gln Arg Glu Glu Ala Phe  
 1 5 10 15  
 Gly Val Leu Phe Arg Ser Phe Gln Gln Gln Thr Gly His Gly Asp Pro

[illegible]



caagatttcc tgaacaactt cacgctcctg gagatctgca acctcacgcc tgatacactc  
 1140  
 tctggggact acaagagcta ctggcacacc accttctacg agggcagctg gcgcagaggc  
 1200  
 agctccgcag ggggctgcag gaaccacctt ggcacgttct ggaccaacct ccagtttaag  
 1260  
 atctctcttc ctgaggggga tgaccagag gatgacgcag agggcaatgt tgtggtctgc  
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 1380  
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 cacagcgagt catgggaatt ggatgaagtc aactatgctg agcaactcca agaggaaaag  
 1680  
 gtctctgagg atgacatgga ccaggacttc ctacatttgt ttaagatagt ggcaggagag  
 1740  
 ggcaaggaga taggggtgta tgagctccag aggctgctca acaggatggc catcaaattc  
 1800  
 aaaagcttca agaccaaggg ctttggcctg gatgcttgcc gctgcatgat caacctcatg  
 1860  
 gataaagatg gctctggcaa gctggggctt ctagagttca agatcctgtg gaaaaaactc  
 1920  
 aagaaatgga tggacatctt cagagagtgt gaccaggacc attcaggcac cttgaactcc  
 1980  
 tatgagatgc gcctggttat tgagaaagca ggcacaaagc tgaacaacaa ggtaatgcag  
 2040  
 gtcctgggtg ccaggatgac agatgatggc ctgatcatag actttgacag cttcatcagc  
 2100  
 tgtttcctga ggctaaagac catgttcaca ttctttctaa ccatggacct caagaatact  
 2160  
 ggccatattt gcttgagcct ggaacagtgg ctgcagatga ccatgtgggg atagaggcgc  
 2220  
 tgtaggagcc tggatcatct taccagcagc agcagcagcg aggttctagc ccaggagggg  
 2280  
 ggggtgcttc ttgtagccct cagctctcca gtctctgctg atgaaatggg atccagggtg  
 2340

<210> 930

<211> 702

<212> PRT

<213> Homo sapiens

<400> 930

Met	Val	Ala	His	Ile	Asn	Asn	Ser	Arg	Leu	Lys	Ala	Lys	Gly	Val	Gly
1				5					10				15		
Gln	His	Asp	Asn	Ala	Gln	Asn	Phe	Gly	Asn	Gln	Ser	Phe	Glu	Glu	Leu
			20					25					30		
Arg	Ala	Ala	Cys	Leu	Arg	Lys	Gly	Glu	Leu	Phe	Glu	Asp	Pro	Leu	Phe

35	40	45
Pro Ala Glu Pro Ser Ser Leu Gly Phe Lys Asp Leu Gly Pro Asn Ser		
50	55	60
Lys Asn Val Gln Asn Ile Ser Trp Gln Arg Pro Lys Asp Ile Ile Asn		
65	70	75
Asn Pro Leu Phe Ile Met Asp Gly Ile Ser Pro Thr Asp Ile Cys Gln		
85	90	95
Gly Ile Leu Gly Asp Cys Trp Leu Leu Ala Ala Ile Gly Ser Leu Thr		
100	105	110
Thr Cys Pro Lys Leu Leu Tyr Arg Val Val Pro Arg Gly Gln Ser Phe		
115	120	125
Lys Lys Asn Tyr Ala Gly Ile Phe His Phe Gln Ile Trp Gln Phe Gly		
130	135	140
Gln Trp Val Asn Val Val Val Asp Asp Arg Leu Pro Thr Lys Asn Asp		
145	150	155
Lys Leu Val Phe Val His Ser Thr Glu Arg Ser Glu Phe Trp Ser Ala		
165	170	175
Leu Leu Glu Lys Ala Tyr Ala Lys Leu Ser Gly Ser Tyr Glu Ala Leu		
180	185	190
Ser Gly Gly Ser Thr Met Glu Gly Leu Glu Asp Phe Thr Gly Gly Val		
195	200	205
Ala Gln Ser Phe Gln Leu Gln Arg Pro Pro Gln Asn Leu Leu Arg Leu		
210	215	220
Leu Arg Lys Ala Val Glu Arg Ser Ser Leu Met Gly Cys Ser Ile Glu		
225	230	235
Val Thr Ser Asp Ser Glu Leu Glu Ser Met Thr Asp Lys Met Leu Val		
245	250	255
Arg Gly His Ala Tyr Ser Val Thr Gly Leu Gln Asp Val His Tyr Arg		
260	265	270
Gly Lys Met Glu Thr Leu Ile Arg Val Arg Asn Pro Trp Gly Arg Ile		
275	280	285
Glu Trp Asn Gly Ala Trp Ser Asp Ser Ala Arg Glu Trp Glu Glu Val		
290	295	300
Ala Ser Asp Ile Gln Met Gln Leu Leu His Lys Thr Glu Asp Gly Glu		
305	310	315
Phe Trp Met Ser Tyr Gln Asp Phe Leu Asn Asn Phe Thr Leu Leu Glu		
325	330	335
Ile Cys Asn Leu Thr Pro Asp Thr Leu Ser Gly Asp Tyr Lys Ser Tyr		
340	345	350
Trp His Thr Thr Phe Tyr Glu Gly Ser Trp Arg Arg Gly Ser Ser Ala		
355	360	365
Gly Gly Cys Arg Asn His Pro Gly Thr Phe Trp Thr Asn Pro Gln Phe		
370	375	380
Lys Ile Ser Leu Pro Glu Gly Asp Asp Pro Glu Asp Asp Ala Glu Gly		
385	390	395
Asn Val Val Val Cys Thr Cys Leu Val Ala Leu Met Gln Lys Asn Trp		
405	410	415
Arg His Ala Arg Gln Gln Gly Ala Gln Leu Gln Thr Ile Gly Phe Val		
420	425	430
Leu Tyr Ala Val Pro Lys Glu Phe Gln Asn Ile Gln Asp Val His Leu		
435	440	445
Lys Lys Glu Phe Phe Thr Lys Tyr Gln Asp His Gly Phe Ser Glu Ile		
450	455	460
Phe Thr Asn Ser Arg Glu Val Ser Ser Gln Leu Arg Leu Pro Pro Gly		

```

465          470          475          480
Glu Tyr Ile Ile Ile Pro Ser Thr Phe Glu Pro His Arg Asp Ala Asp
          485          490          495
Phe Leu Leu Arg Val Phe Thr Glu Lys His Ser Glu Ser Trp Glu Leu
          500          505          510
Asp Glu Val Asn Tyr Ala Glu Gln Leu Gln Glu Glu Lys Val Ser Glu
          515          520          525
Asp Asp Met Asp Gln Asp Phe Leu His Leu Phe Lys Ile Val Ala Gly
          530          535          540
Glu Gly Lys Glu Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu Asn Arg
545          550          555          560
Met Ala Ile Lys Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly Leu Asp
          565          570          575
Ala Cys Arg Cys Met Ile Asn Leu Met Asp Lys Asp Gly Ser Gly Lys
          580          585          590
Leu Gly Leu Leu Glu Phe Lys Ile Leu Trp Lys Lys Leu Lys Lys Trp
          595          600          605
Met Asp Ile Phe Arg Glu Cys Asp Gln Asp His Ser Gly Thr Leu Asn
          610          615          620
Ser Tyr Glu Met Arg Leu Val Ile Glu Lys Ala Gly Ile Lys Leu Asn
625          630          635          640
Asn Lys Val Met Gln Val Leu Val Ala Arg Tyr Ala Asp Asp Gly Leu
          645          650          655
Ile Ile Asp Phe Asp Ser Phe Ile Ser Cys Phe Leu Arg Leu Lys Thr
          660          665          670
Met Phe Thr Phe Phe Leu Thr Met Asp Pro Lys Asn Thr Gly His Ile
          675          680          685
Cys Leu Ser Leu Glu Gln Trp Leu Gln Met Thr Met Trp Gly
          690          695          700

```

<210> 931  
 <211> 297  
 <212> DNA  
 <213> Homo sapiens

```

<400> 931
tcgcgaaggg agcctgacat gggccagaaa atcaatcccc atggtttccg tctcgggtg
60
acgaccgatc acaagaccgg ctggtacgcc gagaagcagt acgccgagct cgtgggtgag
120
gatgtcaaga tccgagagtg gctccacaag aatctggagc gcgccgtctt ttcgtccatc
180
gagatcgagc gtcgctccga gcgcgtgacc attttccttt acgccgctcg cccgggcatc
240
gttatcgggc gcaatggccg ggaggccgag cgcgtgcgtn ntgagctcga aaagctt
297

```

<210> 932  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

```

<400> 932
Met Gly Gln Lys Ile Asn Pro His Gly Phe Arg Leu Gly Val Thr Thr

```

```

      1           5           10           15
Asp His Lys Thr Arg Trp Tyr Ala Glu Lys Gln Tyr Ala Glu Leu Val
      20           25           30
Gly Glu Asp Val Lys Ile Arg Glu Trp Leu His Lys Asn Leu Glu Arg
      35           40           45
Ala Gly Leu Ser Ser Ile Glu Ile Glu Arg Arg Ser Glu Arg Val Thr
      50           55           60
Ile Phe Leu Tyr Ala Ala Arg Pro Gly Ile Val Ile Gly Arg Asn Gly
      65           70           75           80
Arg Glu Ala Glu Arg Val Arg Xaa Glu Leu Glu Lys Leu
      85           90

```

&lt;210&gt; 933

&lt;211&gt; 305

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 933

```

nnacgcgtcg ccaagctgtt gatggccgaa tacaaggggc tcaacgtcat cgtcaaaacc
60
tccgccgatac cggcaagcca agccaatgcc gtgcaggatc tggcgggggc aggcacgcac
120
gcgctggcca tcctgccgac cgacccggat cagctggttt cggcgatcca gcaggtcaag
180
gacgacggca agttcgtggc gctggtcgac cgtgcgcctt ccgtcaacga caacacgac
240
cgcgatctct acgtggccgg caacaacccg gcgctcggcg aagtggcggg caaattcatg
300
ggcga
305

```

&lt;210&gt; 934

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 934

```

Xaa Arg Val Ala Lys Leu Leu Met Ala Glu Tyr Lys Gly Leu Asn Val
1           5           10           15
Ile Val Lys Thr Ser Ala Asp Pro Ala Ser Gln Ala Asn Ala Val Gln
      20           25           30
Asp Leu Ala Gly Ala Gly Ile Asp Ala Leu Ala Ile Leu Pro Thr Asp
      35           40           45
Pro Asp Gln Leu Val Ser Ala Ile Gln Gln Val Lys Asp Asp Gly Lys
      50           55           60
Phe Val Ala Leu Val Asp Arg Ala Pro Ser Val Asn Asp Asn Thr Ile
      65           70           75           80
Arg Asp Leu Tyr Val Ala Gly Asn Asn Pro Ala Leu Gly Glu Val Ala
      85           90           95
Gly Lys Phe Met Gly
100

```

&lt;210&gt; 935

&lt;211&gt; 333

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 935

acgcgtgaag ggctgatgag tgctatgaaa aagccagggg cccgaggaca ctgggggtgga  
 60  
 caggctcccc tggggaagtc ctcttagaac tgagggatca acactggagg agactgcaag  
 120  
 gggtagcgga taaatgttcc tggatgaagga aacagcaggg gcaaaggccc tgcagcagaa  
 180  
 aggagcgagg cccttttgagg taacagaaag accatggtga caggagctca gaaagaccac  
 240  
 tgggtgttaag actataagcc agtggaggcc agattgggga atgggatggg aggggtgctt  
 300  
 gaagaccatg gtgaggtctt ctgggtcttt act  
 333

&lt;210&gt; 936

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 936

Met	Val	Phe	Lys	His	Pro	Ser	His	Pro	Ile	Pro	Gln	Ser	Gly	Leu	His
1				5					10					15	
Trp	Leu	Ile	Val	Leu	Thr	Pro	Val	Val	Phe	Leu	Ser	Ser	Cys	His	His
			20					25					30		
Gly	Leu	Ser	Val	Thr	Pro	Lys	Gly	Leu	Ala	Pro	Phe	Cys	Cys	Arg	Ala
			35				40					45			
Phe	Ala	Pro	Ala	Val	Ser	Phe	Thr	Arg	Asn	Ile	Tyr	Pro	Val	Pro	Leu
	50					55				60					
Ala	Val	Ser	Ser	Ser	Val	Asp	Pro	Ser	Val	Leu	Arg	Gly	Leu	Pro	Gln
65					70					75				80	
Gly	Ser	Leu	Ser	Thr	Pro	Val	Ser	Ser	Gly	Pro	Trp	Leu	Phe	His	Ser
				85					90					95	
Thr	His	Gln	Pro	Phe	Thr	Arg									
				100											

&lt;210&gt; 937

&lt;211&gt; 464

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 937

nnnttatctg cggagggggg ggccaccctg cccacactca tgctgcaggc ctccaccgac  
 60  
 ccggcgggacg acgagctcaa ggatctgttg acggccgacc tcatggacca gcacaacctc  
 120  
 gaccgtgccc tggcaggggt gcgtgccagt cacgtcatcg acgaagctcg cgccgagggtg  
 180  
 cagcggcggtg ccgatctcgc ccgtggccat ctgcgccatc tccccgagg cgatgcccggt  
 240  
 acggcggttg agaccctgtg cgacgaggtg ggttcccggg cggcctgaac cccgaccctg  
 300

ccagnctgcg tcccatctcc tggccgggac cgctccagcg tctgctctct gacagctcat  
 360  
 cgttcttccg acaccaagga gtttctcgtg gcccgctcgc tcgatctcat cggcattggg  
 420  
 cccggcaacc cggactggat caccctggct gccgtcaagg ccan  
 464

<210> 938  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 938  
 Xaa Leu Ser Ala Glu Gly Val Ala Thr Leu Pro Thr Leu Met Leu Gln  
 1 5 10 15  
 Ala Ser Thr Asp Pro Ala Asp Asp Glu Leu Lys Asp Leu Leu Thr Ala  
 20 25 30  
 Asp Leu Met Asp Gln His Asn Leu Asp Arg Ala Leu Ala Gly Leu Arg  
 35 40 45  
 Ala Ser His Val Ile Asp Glu Ala Arg Ala Glu Val Gln Arg Arg Ala  
 50 55 60  
 Asp Leu Ala Arg Gly His Leu Ala Ile Leu Pro Ala Gly Asp Ala Arg  
 65 70 75 80  
 Thr Ala Leu Glu Thr Leu Cys Asp Glu Val Gly Ser Arg Ala Ala  
 85 90 95

<210> 939  
 <211> 385  
 <212> DNA  
 <213> Homo sapiens

<400> 939  
 ntgactatcc tcgaccccca tggtcaggag acgactccag gaagtgtcat cgaagggtt  
 60  
 ggactgctgc cggctcgagg ggaacttcgcc gccacgaaga cccttgccct gtcgcacggg  
 120  
 acatggcggg ggatcgagg tggcggctat gaaatccatc acgggcgtct gtcgttcgct  
 180  
 gaggacgctg aagccttctt cgacggcgta cacgtcggtc cggtatgggg gacgatgtgg  
 240  
 cacggggcat tcgagcacga cgaattccgt cgcacgtggc tggctgacgc ggcccgtcac  
 300  
 gctggatcat cctggcgctc gcactccgac gagctgggtt atcaggctcg acgcgaggcg  
 360  
 atgatcgaaa ccctcgccga cgcgt  
 385

<210> 940  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 940  
 Xaa Thr Ile Leu Asp Pro Asp Gly Gln Glu Thr Thr Pro Gly Ser Val

```

      1             5             10             15
Ile Glu Gly Leu Gly Leu Leu Pro Val Glu Val Asp Phe Ala Ala Thr
      20             25             30
Lys Thr Leu Ala Leu Ser His Gly Thr Trp Arg Gly Ile Glu Val Gly
      35             40             45
Gly Tyr Glu Ile His His Gly Arg Leu Ser Phe Ala Glu Asp Ala Glu
      50             55             60
Ala Phe Leu Asp Gly Val His Val Gly Pro Val Trp Gly Thr Met Trp
65             70             75             80
His Gly Ala Phe Glu His Asp Glu Phe Arg Arg Thr Trp Leu Ala Asp
      85             90             95
Ala Ala Arg His Ala Gly Ser Ser Trp Arg Pro His Ser Asp Glu Leu
      100            105            110
Gly Tyr Gln Ala Arg Arg Glu Ala Met Ile Glu Thr Leu Ala Asp Ala
      115            120            125

```

<210> 941  
 <211> 348  
 <212> DNA  
 <213> Homo sapiens

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<400> 941
atcttctggt cgccggtgat cacgctggtg accatcggcc tgctgtttgc cggcaacttc
60
gaagccatgc aaaccatggt cgtgctggcc gggtgcctt tctcggtggt gctgattttc
120
ttcatgttcg gtttgacaaa ggcatgctgc caggacgtgg ccatggagca ggagcaggca
180
caattggctg aacgtggtcg ccgtgggttc agcagcgccc tgaccgcgct ggacctgcaa
240
ccgagccagg gcaccgtgca acgctttatg gacaaacatg tgacgccggc gttggaacaa
300
gcggcgactg cgttgctgta tcaagggtg gaagtgcaga ccctgctt
348

```

<210> 942  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

```

<400> 942
Ile Phe Trp Ser Ala Val Ile Thr Leu Val Thr Ile Gly Leu Leu Phe
      1             5             10             15
Ala Gly Asn Phe Glu Ala Met Gln Thr Met Val Val Leu Ala Gly Leu
      20             25             30
Pro Phe Ser Val Val Leu Ile Phe Met Phe Gly Leu His Lys Ala
      35             40             45
Met Arg Gln Asp Val Ala Met Glu Gln Glu Gln Ala Gln Leu Ala Glu
      50             55             60
Arg Gly Arg Arg Gly Phe Ser Glu Arg Leu Thr Ala Leu Asp Leu Gln
65             70             75             80
Pro Ser Gln Gly Thr Val Gln Arg Phe Met Asp Lys His Val Thr Pro
      85             90             95
Ala Leu Glu Gln Ala Ala Thr Ala Leu Arg Asp Gln Gly Leu Glu Val

```

100 105 110  
 Gln Thr Leu Leu  
 115  
 <210> 943  
 <211> 439  
 <212> DNA  
 <213> Homo sapiens  
 <400> 943  
 ccatggcagg agcagagcag atagagcagg acctcgtctc cttctctttg cattttgtgc  
 60  
 ctctctaat gcacccctggg ctcttgctaa ccctgtggga aacaccgtct cttctctcct  
 120  
 ttgccctctt ctgtgatcac atcctcactt ctgagcctat ctgcccaccc agtcaatccc  
 180  
 ccttggttct gggatgctat ttccctggcc gcctccctct aggagtgttt agaaccctca  
 240  
 ctgtgggcag aaggaggga agatggctga ggtacctgga aagggacgtg tggatccccg  
 300  
 ggcattggaag gaaggaggca ggagagctag aaaaagggat gagatctaata gttccctaag  
 360  
 gaacctggct tagtgctggc ctttcacata ctgagacatg gaatccctac tactgttctc  
 420  
 tgaggaaaga ggctgttcc  
 439  
 <210> 944  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens  
 <400> 944  
 Met Ala Gly Ala Glu Gln Ile Glu Gln Asp Leu Val Ser Phe Ser Leu  
 1 5 10 15  
 His Phe Val Pro Pro Leu Met His Pro Gly Leu Leu Leu Thr Leu Trp  
 20 25 30  
 Glu Thr Pro Ser Leu Leu Ser Phe Ala Leu Phe Cys Asp His Ile Leu  
 35 40 45  
 Thr Ser Glu Pro Ile Cys Pro Ser Ser Gln Ser Pro Leu Val Leu Gly  
 50 55 60  
 Cys Tyr Phe Pro Gly Arg Leu Pro Leu Gly Val Phe Arg Thr Leu Thr  
 65 70 75 80  
 Val Gly Arg Arg Glu Gly Arg Trp Leu Arg Tyr Leu Glu Arg Asp Val  
 85 90 95  
 Trp Ile Pro Gly His Gly Arg Lys Glu Ala Gly Glu Leu Glu Lys Gly  
 100 105 110  
 Met Arg Ser Asn Val Pro  
 115  
 <210> 945  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens



&lt;400&gt; 945

ngaattcgtg aagcggtcca ttttttttc cttttaataa tttcaattgc actttatgtc  
 60  
 gagatgggtga tatatatata tactcacaca catatatatg tgtgtgtgtg tatatatgta  
 120  
 tatatatata gcgtgtacaa caaaacatgc actgtttact cagcaccctg tgtttgtctc  
 180  
 agcaatagct tttctaaaga actgctacta tttgaaatgg agggggaggg gggctctgga  
 240  
 cagagtattg tgcaagtga aagtctctgg atggggctat gtatatacta ccagccaatt  
 300  
 tgggtgcaaa ttggatttga aggcctgcct ctgtccacn  
 339

&lt;210&gt; 946

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 946

Xaa	Ile	Arg	Glu	Ala	Phe	His	Ile	Phe	Phe	Leu	Leu	Ile	Ile	Ser	Ile
1				5					10					15	
Ala	Leu	Tyr	Val	Glu	Met	Val	Ile	Tyr	Ile	Tyr	Thr	His	Thr	His	Ile
		20						25					30		
Tyr	Val	Cys	Val	Cys	Ile	Tyr	Val	Tyr	Ile	Tyr	Ser	Val	Tyr	Asn	Lys
		35					40					45			
Thr	Cys	Thr	Val	Tyr	Ser	Ala	Pro	Arg	Val	Cys	Leu	Ser	Asn	Ser	Phe
	50					55				60					
Ser	Lys	Glu	Leu	Leu	Leu	Phe	Glu	Met	Glu	Gly	Glu	Gly	Gly	Pro	Gly
65					70					75				80	
Gln	Ser	Ile	Val	Gln	Val	Glu	Ser	Leu	Trp	Met	Gly	Leu	Cys	Ile	Ser
			85						90				95		
Tyr	Gln	Pro	Ile	Trp	Val	Gln	Ile	Gly	Phe	Glu	Gly	Leu	Pro	Leu	Ser
			100					105					110		

Thr

&lt;210&gt; 947

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 947

tctagatctg ttctcagga agctgagatg gagatgagtg ggcagcaggt ttatggagtg  
 60  
 ctctgtggcat cacacctgtg cacgggggtg ggggaaggagt ggacaggagt ggacaagtca  
 120  
 agtagtgctg ccggctcaag cgatgcctca gcctttctgc tgtgtgcaaa gctttgcaga  
 180  
 ggagatgatg cttcaaagt gtccctgttg gggatgagca gccaggcctt tatacactgg  
 240  
 gacagtcagt catggatacg tggatactct ggaaccctc atccctggag gtctgagccc  
 300

ctggatacca tgcccttctt aggctggagt tgctgccctt gtccatttac cataaaaatt  
 360  
 ggacaagaga ataccaggac acacctgagt ttctcatcgt atgctaaacc tgttcttcca  
 420  
 cgtacatccc caatgtgtac agccctactt tttctgtctg atcaagttca attacttctg  
 480  
 ctaagatggg gactattctt gcctgctggg ccttgatgc aaggacccca atgttcaggc  
 540  
 agcctttggg gccttctagc atacgaatca gagcattatc tttagggtg gaataagctg  
 600  
 ccccaaaacc tgttgaagcc agccaggcac tgtgtccct tcacgcgt  
 648

<210> 948  
 <211> 154  
 <212> PRT  
 <213> Homo sapiens

<400> 948  
 Met Glu Met Ser Gly Gln Gln Val Tyr Gly Val Leu Val Ala Ser His  
 1 5 10 15  
 Leu Cys Thr Gly Val Gly Lys Glu Trp Thr Gly Val Asp Lys Ser Ser  
 20 25 30  
 Ser Ala Ala Gly Ser Ser Asp Ala Ser Ala Phe Leu Leu Cys Ala Lys  
 35 40 45  
 Leu Cys Arg Gly Asp Asp Ala Ser Lys Leu Ser Leu Leu Gly Met Ser  
 50 55 60  
 Ser Gln Ala Phe Ile His Trp Asp Ser Gln Ser Trp Ile Arg Gly Tyr  
 65 70 75 80  
 Ser Gly Asn Pro His Pro Trp Arg Ser Glu Pro Leu Asp Thr Met Pro  
 85 90 95  
 Phe Leu Gly Trp Ser Cys Cys Pro Cys Pro Phe Thr Ile Lys Ile Gly  
 100 105 110  
 Gln Glu Asn Thr Arg Thr His Leu Ser Phe Ser Ser Tyr Ala Lys Pro  
 115 120 125  
 Val Leu Pro Arg Thr Ser Pro Met Cys Thr Ala Leu Leu Phe Ser Ala  
 130 135 140  
 Asp Gln Val Gln Leu Leu Leu Arg Trp  
 145 150

<210> 949  
 <211> 661  
 <212> DNA  
 <213> Homo sapiens

<400> 949  
 acgcgtactg gttggctcat tcaactgaaa tatgatgaca tttaaaggaa atgcaagaat  
 60  
 aagtaatgtg gaattttatc acagtgggtca agaaggcttc agggatagca cagatccaag  
 120  
 atatgctgta acgtttctta acctaggaca gattcaagaa catggctcat cttatatctg  
 180  
 aggcgtgtgt tttcaccatg gcttctctcc agcaattggg gtatttggga cagatggatt  
 240

ggacatagat gacaacatca ttcactttac agtgggggaa ggcataagaa tatgggggaa  
 300  
 tgccaaccga gtccgagga atttgattgc actttcggtt tggccaggaa cctatcagaa  
 360  
 cagaaaagat ttaagttcaa ctctctggca tgcagcaatt gagataaata gagggaccaa  
 420  
 tacagtttta cagaataatg tagtggctgg atttgggaaga gcaggatacc gcattgatgg  
 480  
 tgaaccttgc ccaggccagt ttaatcctgt ggaaaagtgg tttgacaatg aagcccatgg  
 540  
 aggtttatat gggatctata tgaaccaaga tggccttcct ggatgttctc ttatacaagg  
 600  
 atttaccatt tggacatgct gggattatgg aatttatttt cagaccacag agagtgtgca  
 660  
 c  
 661

<210> 950

<211> 210

<212> PRT

<213> Homo sapiens

<400> 950

Met	Met	Thr	Phe	Lys	Gly	Asn	Ala	Arg	Ile	Ser	Asn	Val	Glu	Phe	Tyr
1				5					10					15	
His	Ser	Gly	Gln	Glu	Gly	Phe	Arg	Asp	Ser	Thr	Asp	Pro	Arg	Tyr	Ala
			20					25					30		
Val	Thr	Phe	Leu	Asn	Leu	Gly	Gln	Ile	Gln	Glu	His	Gly	Ser	Ser	Tyr
		35				40						45			
Ile	Arg	Gly	Cys	Ala	Phe	His	His	Gly	Phe	Ser	Pro	Ala	Ile	Gly	Val
		50				55					60				
Phe	Gly	Thr	Asp	Gly	Leu	Asp	Ile	Asp	Asp	Asn	Ile	Ile	His	Phe	Thr
65					70					75				80	
Val	Gly	Glu	Gly	Ile	Arg	Ile	Trp	Gly	Asn	Ala	Asn	Arg	Val	Arg	Gly
				85					90					95	
Asn	Leu	Ile	Ala	Leu	Ser	Val	Trp	Pro	Gly	Thr	Tyr	Gln	Asn	Arg	Lys
			100					105					110		
Asp	Leu	Ser	Ser	Thr	Leu	Trp	His	Ala	Ala	Ile	Glu	Ile	Asn	Arg	Gly
		115					120					125			
Thr	Asn	Thr	Val	Leu	Gln	Asn	Asn	Val	Val	Ala	Gly	Phe	Gly	Arg	Ala
		130				135					140				
Gly	Tyr	Arg	Ile	Asp	Gly	Glu	Pro	Cys	Pro	Gly	Gln	Phe	Asn	Pro	Val
145					150					155				160	
Glu	Lys	Trp	Phe	Asp	Asn	Glu	Ala	His	Gly	Gly	Leu	Tyr	Gly	Ile	Tyr
				165					170					175	
Met	Asn	Gln	Asp	Gly	Leu	Pro	Gly	Cys	Ser	Leu	Ile	Gln	Gly	Phe	Thr
			180					185					190		
Ile	Trp	Thr	Cys	Trp	Asp	Tyr	Gly	Ile	Tyr	Phe	Gln	Thr	Thr	Glu	Ser
		195					200					205			
Val	His														
															210

<210> 951

<211> 2615

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 951

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60  
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120  
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180  
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240  
tcggtgttgg cggggccggg ctacacgacg ttggctggcc tggatctcag ccacaacctg  
300  
ctcaccagca tctcaccac tgccttctcc cgccttcgct acctggagtc gcttgacctc  
360  
agccacaatg gcctgacagc cctgccagcc gagagcttca ccagctcacc cctgagcgac  
420  
gtgaacctta gccacaacca gctccgggag gtctcagtgt ctgccttcac gacgcacagt  
480  
cagggccggg cactacacgt ggacctctcc cacaacctct caccgcctcg tgccccaccc  
540  
cacgagggcc ggcctgcctg cgcaccacat tcagagcctg aacctggcct ggaaccggct  
600  
ccatgccgtg cccaacctcg agacttgccc ctgcgctacc tgagcctgga tgggaaccct  
660  
ctagctgtca ttggtccggg tgccttcgcg gggctgggag gccttacaca cctgtctctg  
720  
gccagcctgc agaggtctcc tgagctggcg cccagtggct tccgtgagct accgggcctg  
780  
caggtcctgg acctgtcggg caacccaag cttaactggg caggagctga ggtgttttca  
840  
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900  
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960  
cggcgcttgg tgcgggaggg cacctacccc cggaggcctg gctccagccc caaggtggcc  
1020  
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1080  
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1140  
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1320  
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1380  
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1440  
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 1680  
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 1740  
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 1800  
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 1860  
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 1920  
 gggcacattg gttccagcct agccagtttc tcacctggg ttgggggtccc ccagcatcca  
 1980  
 gactggaaac ctacccattt tccctgagc atcctctaga tgctgccccca aggagttgct  
 2040  
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 2100  
 tggccctgag cagcagagcc cttcttacct tcccaggaat gccgtgaaag gagacaaggt  
 2160  
 ctgcccagcc catgtctatg ctctaccccc agggtagcat ctacgcttcc gaacctggg  
 2220  
 ctgtttcctt agtcttcatt ttataaaagt tgttgccctt ttaacggagt gtcactttca  
 2280  
 accggcctcc cctaccctg ctggccgggg atggagacat gtcatttgta aaagcagaaa  
 2340  
 aagggtgcat ttgttcacat ttgtaatat gtctgggcc tgtgttgggg tgttggggga  
 2400  
 agctgggcat cagtggccac atgggcatca ggggctggcc ccacagagac cccacagggc  
 2460  
 agtgagctct gtcttcccc accctgctag cccatcatct atctaaccgg tccttgattt  
 2520  
 aataaacact ataaaatgaa gactaaggaa acagcccagg gttcggaagc tgagatgcta  
 2580  
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 2615

&lt;210&gt; 952

&lt;211&gt; 357

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 952

Xaa	Pro	Ala	Pro	Thr	Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Ala	Val	
1				5				10					15		
Ser	Gly	Ala	Gln	Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu
			20				25						30		
Val	Glu	Thr	Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp
		35				40						45			
Cys	Ser	Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp
	50					55					60				
Thr	Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu

```

65          70          75          80
Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu
          85          90          95
Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser Arg Leu
          100          105          110
Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu Thr Ala Leu
          115          120          125
Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp Val Asn Leu Ser
          130          135          140
His Asn Gln Leu Arg Glu Val Ser Val Ser Ala Phe Thr Thr His Ser
          145          150          155          160
Gln Gly Arg Ala Leu His Val Asp Leu Ser His Asn Leu Ser Pro Pro
          165          170          175
Arg Ala Pro Pro His Glu Gly Arg Pro Ala Cys Ala His His Ser Glu
          180          185          190
Pro Glu Pro Gly Leu Glu Pro Ala Pro Cys Arg Ala Gln Pro Arg Asp
          195          200          205
Leu Pro Leu Arg Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Val Ile
          210          215          220
Gly Pro Gly Ala Phe Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu
          225          230          235          240
Ala Ser Leu Gln Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu
          245          250          255
Leu Pro Gly Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn
          260          265          270
Trp Ala Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu
          275          280          285
Asp Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
          290          295          300
His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg Cys
          305          310          315          320
Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly Ser Ser
          325          330          335
Pro Lys Val Ala Leu His Cys Val Asp Thr Arg Glu Ser Ala Ala Arg
          340          345          350
Gly Pro Thr Ile Leu
          355

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<210> 953  
 <211> 347  
 <212> DNA  
 <213> Homo sapiens

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<400> 953
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60
accacacttt ccccatccct tgatccatca ttgggcgttg aggttttccc atgtcttgac
120
tgttgtacct ggcggctctg cggagtaacc gctgcggaca cacagtagga cgggaggagg
180
aagccattgc gtttcacct ttcattgccc ttcctttccc cttccaagt agctctttga
240
ggtagtcat ggagggcagt gtccctctgc atcctgtctg gggttgtcaa atatggccaa
300

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gtgggctcca tcggggcagc ggggtggggtg ggggggtgtct gtcagag  
347

<210> 954  
<211> 103  
<212> PRT  
<213> Homo sapiens

<400> 954  
Met Glu Pro Thr Trp Pro Tyr Leu Thr Thr Pro Asp Arg Met Gln Arg  
1 5 10 15  
Asp Thr Ala Leu His Asp Ser Pro Gln Arg Ala His Leu Glu Gly Glu  
20 25 30  
Arg Lys Gly His Glu Arg Val Lys Arg Asn Gly Phe Ser Leu Pro Ser  
35 40 45  
Tyr Cys Val Ser Ala Ala Val Thr Pro Gln Ser Arg Gln Val Gln Gln  
50 55 60  
Ser Arg His Gly Lys Thr Ser Thr Pro Asn Asp Gly Ser Arg Asp Gly  
65 70 75 80  
Glu Ser Val Val His Thr Leu Arg Gly Asp Pro Arg Glu Thr Gly Leu  
85 90 95  
Arg Thr Gly Met Ala Ser Arg  
100

<210> 955  
<211> 634  
<212> DNA  
<213> Homo sapiens

<400> 955  
acgcgtgaag ggctctgcag gtgagcggt ctgcaggtga aggggtctgc aggtgagcgg  
60  
ctctgcaggt gaatggttct gcaggtgaag ggctctgcag gtgaacgggt ctgcaggtga  
120  
agggctctgc aggtgaacgg ttctgcaggt gagcggtct ctgcaggtgagc ggctctgcat  
180  
gtgagtgacct ctgtgactgg ctgcgaagca gcatttgtgc acacttgact ggccacaaca  
240  
gaatgttctt ctctgttgc agcactgagg aggaagctcc tgcctaagcg accacagcca  
300  
ggcaccgct ccatggagac attgctctct ccagactcca ttcagactca ggaaacctga  
360  
gctcctggaa tgcaggtga ggcagctccc acacaaaagc tatctactct ggcagttatc  
420  
agaggcctcc gttgcacaaa tcacacacct actgtgcctg acgtggctgg gcctccagca  
480  
ggaccgctc ctgagaacac acgggtgcta gtccaagttc acagcacggc tcaagtcact  
540  
cccacaaacc tctctatata aacacacaaa gctctgggag gctaccctgc atccaagagt  
600  
caccatctca cacctggaac aagggttacg gccg  
634

<210> 956

<211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 956  
 Met Glu Ser Gly Glu Ser Asn Val Ser Met Glu Arg Val Pro Gly Cys  
 1 5 10 15  
 Gly Arg Leu Gly Arg Ser Phe Leu Leu Ser Ala Asp Asn Arg Glu Glu  
 20 25 30  
 His Ser Val Val Ala Ser Gln Val Cys Thr Asn Ala Ala Cys Glu Pro  
 35 40 45  
 Val Thr Glu Ala Leu Thr Cys Arg Ala Ala His Leu Gln Ser Arg Ser  
 50 55 60  
 Pro Ala Glu Pro Phe Thr Cys Arg Ala Leu His Leu Gln Asn Arg Ser  
 65 70 75 80  
 Pro Ala Glu Pro Phe Thr Cys Arg Thr Ile His Leu Gln Ser Arg Ser  
 85 90 95  
 Pro Ala Glu Pro Phe Thr Cys Arg Ala Ala His Leu Gln Ser Pro Ser  
 100 105 110  
 Arg

<210> 957  
 <211> 823  
 <212> DNA  
 <213> Homo sapiens

<400> 957  
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 gcgctccaag cttcaggagg cccagggaga gcacgtcctg ccggccaccc agcacagcgt  
 120  
 gtacctcctg gccaccacgc actgcgcagc cgtgggtgtcc agcctcctgg gcagcccctt  
 180  
 gcccttggaac aggtaccacg ctccagactcc aggccttaggg gtccctctgg aatgatgctc  
 240  
 cccctggaat gatgtcccc gagccctcca cccggctctg caccctgact ttctgcatga  
 300  
 gttcccatgg ctgtaggcca cgtgggacag aaagtgcacat ggagccaggc cccagtctct  
 360  
 caggtaacca cggggacctc tctctccag gcgttttggg atcctcactg gctccgggtg  
 420  
 gccctgcaca gcaccccccac agggaagctg ctgtttctgc ctctctctaa ggtcccaaaa  
 480  
 ctgcctgggt gctctgttgg cccaggtc cagcacacac tggaggctgc ccctcaccct  
 540  
 gtgtcttgggt tccggtact ccaagccttg tctctgcag ggcatccact gctgcctgtg  
 600  
 agcagacccc tgggaactgc ctgatctgag cccctcagg agcccaagga caacctgtc  
 660  
 tgtaccatac atcactatgt ctcccaagc tcacacctcc cagctcccag caaagggcag  
 720  
 ggcggtgcta ccacccacca gccactggg gtcccccttc ctgcccagg cctccggagc  
 780



atgggtctgc tggcccttcc tttctttgcc tcttagtctg gaa  
823

<210> 958

<211> 105

<212> PRT

<213> Homo sapiens

<400> 958

Met	Ala	Val	Gly	His	Val	Gly	Gln	Lys	Val	Thr	Trp	Ser	Gln	Ala	Pro
1				5					10					15	
Val	Ser	Gln	Val	Pro	Thr	Gly	Thr	Ser	Pro	Leu	Gln	Ala	Phe	Trp	Asp
		20						25					30		
Pro	His	Trp	Leu	Arg	Trp	Ala	Leu	His	Ser	Thr	Pro	Thr	Gly	Lys	Leu
		35					40					45			
Leu	Phe	Leu	Pro	Ser	Ser	Lys	Val	Pro	Lys	Leu	Pro	Gly	Cys	Ser	Val
	50					55					60				
Gly	Pro	Arg	Leu	Gln	His	Thr	Leu	Glu	Ala	Ala	Pro	His	Pro	Val	Ser
65					70				75					80	
Trp	Phe	Arg	Leu	Leu	Gln	Ala	Leu	Ser	Ser	Ala	Gly	His	Pro	Leu	Leu
			85					90						95	
Pro	Val	Ser	Arg	Pro	Leu	Gly	Thr	Ala							
			100				105								

<210> 959

<211> 586

<212> DNA

<213> Homo sapiens

<400> 959

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acagtggtag gcctgatcac cgacaacgat gaggcagcct atagggagga ggtagagagc  
120  
ctggcagtg ggtgccagga taacaacctc tccctcaacg tgatcaagac cacgaagatg  
180  
atcgtggact acaggaaaag gagggtcgag cagcggccca ttctcattga tggggctgta  
240  
tgggagccag ttgagagcct caagtccctt ggtgtccaca tcaccatcga actatcatgg  
300  
tccaaacaca ccaagacagt agtgaagagg gtgcgacaat gcctattcca cctcggtaga  
360  
caaaaaagat ttggaatgga tcctcagacc ctcaaaaagt ttgacatcta caccatcgag  
420  
agcatcatga ctggttgcac caccgcctgg tatggcaact gctcggcctc cgaccgcaag  
480  
gcactacaga gggtagtgcg tacggcccag tacatcactg gggctaagct tcctgccatc  
540  
caggacctct ataccaggcg gtgtcagcgg aagaccctga caattg  
586

<210> 960

<211> 195

<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 960

Xaa His Asp Cys Met Ala Lys His Asp Ser Asn Thr Ile Ile Lys Phe  
 1 5 10 15  
 Ala Asp Asp Thr Thr Val Val Gly Leu Ile Thr Asp Asn Asp Glu Ala  
 20 25 30  
 Ala Tyr Arg Glu Glu Val Arg Asp Leu Ala Val Trp Cys Gln Asp Asn  
 35 40 45  
 Asn Leu Ser Leu Asn Val Ile Lys Thr Thr Lys Met Ile Val Asp Tyr  
 50 55 60  
 Arg Lys Arg Arg Val Glu His Ala Pro Ile Leu Ile Asp Gly Ala Val  
 65 70 75 80  
 Trp Glu Pro Val Glu Ser Phe Lys Phe Leu Gly Val His Ile Thr Ile  
 85 90 95  
 Glu Leu Ser Trp Ser Lys His Thr Lys Thr Val Val Lys Arg Val Arg  
 100 105 110  
 Gln Cys Leu Phe His Leu Gly Arg Gln Lys Arg Phe Gly Met Asp Pro  
 115 120 125  
 Gln Thr Leu Lys Lys Phe Asp Ile Tyr Thr Ile Glu Ser Ile Met Thr  
 130 135 140  
 Gly Cys Ile Thr Ala Trp Tyr Gly Asn Cys Ser Ala Ser Asp Arg Lys  
 145 150 155 160  
 Ala Leu Gln Arg Val Val Arg Thr Ala Gln Tyr Ile Thr Gly Ala Lys  
 165 170 175  
 Leu Pro Ala Ile Gln Asp Leu Tyr Thr Arg Arg Cys Gln Arg Lys Thr  
 180 185 190  
 Leu Thr Ile  
 195

&lt;210&gt; 961

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 961

acgcgttggtc gtctctccgt agaccattca gtttggaaca acttccactg gagtctgtgc  
 60  
 atgactggat ggtctctttg acagccctgt caaggaatac caacagaata ttgattctcc  
 120  
 taaactgtat agtaacctgc taaccagtcg gaaagagcta ccaccaatg gagatactaa  
 180  
 atccatggta atggaccatc gagggcaacc tccagagttg gctgctcttc ccactcctga  
 240  
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 360  
 tcattcccca ataagtcatg ggcataatcc cagtgccatt gttcttccaa atgctaccca  
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 tgactacaac acgtctttct caaactccaa tgctcacaaa gctgaaaaga agcttcaaaa  
 480  
 cattgatcac cccttcacgc gt  
 502

<210> 962  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 962  
 Met Val Met Asp His Arg Gly Gln Pro Pro Glu Leu Ala Ala Leu Pro  
 1 5 10 15  
 Thr Pro Glu Ser Thr Pro Val Leu His Gln Lys Thr Leu Gln Ala Met  
 20 25 30  
 Lys Ser His Ser Glu Lys Ala His Gly His Gly Ala Ser Arg Lys Glu  
 35 40 45  
 Thr Pro Gln Phe Phe Pro Ser Ser Pro Pro Pro His Ser Pro Ile Ser  
 50 55 60  
 His Gly His Ile Pro Ser Ala Ile Val Leu Pro Asn Ala Thr His Asp  
 65 70 75 80  
 Tyr Asn Thr Ser Phe Ser Asn Ser Asn Ala His Lys Ala Glu Lys Lys  
 85 90 95  
 Leu Gln Asn Ile Asp His Pro Phe Thr Arg  
 100 105

<210> 963  
 <211> 1298  
 <212> DNA  
 <213> Homo sapiens

<400> 963  
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 gcgctctaga ggagatgaat tatggatccg ccctcccga atcctggctc ggccctcccc  
 120  
 acgccacca gggccagtcg ggtctgctca cagcccgagg aggccgctg tccagccgag  
 180  
 ggcaagagac agagcaggtc cctgtgtatc caagtcctg agcccgtag accggcccca  
 240  
 ggccctgtag agagccagca gccaccatgg cgaaggagga agatgaggag aagaaagcca  
 300  
 agaaagggaa gaaggggaag aaggcaccgg acccgagaga gcccaaacgg agcctgaagg  
 360  
 ggacgtcgcg ggtgttcagc ggcttcgcg accgaacacc caagatctac aagaagggcc  
 420  
 agttccgcag cgcctcggcc ttcttctggg gcctccacac cgccccccac aagaccaagc  
 480  
 gcacgaggaa ggcccgacc gtgctcgggt acacgtcaga gcttatgacg cacatgcgca  
 540  
 tgggcaagaa gaagcgggag atgaaggga agaagccgtc cttcatggtg atccgcttcc  
 600  
 caggccgccc tggctacggc cgcttcggc cgcgcgccc gtcactcagc aaagcgtcca  
 660  
 cggccatcaa ctggctcaca aaaaagttcc tcctcaagaa ggccgaggag tcgggcagcg  
 720  
 aacagggcac agtggacgcc tggctgcagc gctcgagctc ccgcatgggc tcccgcaaac  
 780

tcccccttccc gtcgggtgcc gagatcctgc ggccctggggg ccggctccgg aggttcccc  
 840  
 gcagccgcag catctacgcg tcaggcgagc ccctgggctt cctgcccttc gaggacgagg  
 900  
 cccattcca tcaactcgggc tcccgcaagt cgctgtacgg gcttgagggc ttccaggacc  
 960  
 tgggcgagta ttatgactat caccgcgacg gcgacgacta ctacgaccgg cagtcaactcc  
 1020  
 accgctacga ggagcaggaa ccctacctgg cgggcctcgg ccctacagc ccggcctggc  
 1080  
 caccctacgg cgaccactac tacgggtacc cgcccaggga tccctacgac tactaccacc  
 1140  
 ccgactatta cgggtggcccc gttgatccgg ggtacaccta cggctacggc tacgacgatt  
 1200  
 acgaaccccc atatgcgcc ccgtcggggg actcgtctcc ttacagctac cagcatgggt  
 1260  
 acgagggcga ggcgaccct tatggctact acctggat  
 1298

<210> 964

<211> 235

<212> PRT

<213> Homo sapiens

<400> 964

Ser	Ala	Ser	Gln	Ala	Ala	Val	Ala	Thr	Ala	Ala	Cys	Gly	Arg	Ala	Pro
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Gly	His	Ser	Ala	Lys	Arg	Pro	Arg	Pro	Ser	Thr	Gly	Ser	Gln	Lys	Ser
			20					25					30		
Ser	Ser	Ser	Arg	Arg	Pro	Arg	Ser	Arg	Ala	Ala	Asn	Arg	Pro	Gln	Trp
		35					40				45				
Thr	Pro	Gly	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Trp	Ala	Pro	Ala	Asn	Ser
	50					55					60				
Pro	Ser	Arg	Arg	Val	Pro	Arg	Ser	Cys	Gly	Leu	Gly	Ala	Gly	Ser	Gly
65				70					75					80	
Gly	Ser	Pro	Ala	Ala	Ala	Ala	Ser	Thr	Arg	Gln	Ala	Ser	Pro	Trp	Ala
			85					90					95		
Ser	Cys	Pro	Ser	Arg	Thr	Arg	Pro	His	Ser	Ile	Thr	Arg	Ala	Pro	Ala
		100					105					110			
Ser	Arg	Cys	Thr	Gly	Leu	Arg	Ala	Ser	Arg	Thr	Trp	Ala	Ser	Ile	Met
		115					120					125			
Thr	Ile	Thr	Ala	Thr	Ala	Thr	Thr	Thr	Thr	Thr	Gly	Ser	His	Ser	Thr
	130					135					140				
Ala	Thr	Arg	Ser	Arg	Asn	Pro	Thr	Trp	Arg	Ala	Ser	Ala	Pro	Thr	Ala
145					150					155				160	
Arg	Pro	Gly	His	Pro	Thr	Ala	Thr	Thr	Thr	Thr	Gly	Thr	Arg	Pro	Arg
			165					170					175		
Ile	Pro	Thr	Thr	Thr	Thr	Thr	Pro	Thr	Ile	Thr	Val	Ala	Pro	Leu	Ile
		180					185					190			
Arg	Gly	Thr	Pro	Thr	Ala	Thr	Ala	Thr	Thr	Ile	Thr	Asn	Pro	His	Met
		195				200					205				
Arg	Pro	Arg	Arg	Gly	Thr	Arg	Leu	Leu	Thr	Ala	Thr	Thr	Met	Gly	Thr
	210					215					220				
Arg	Ala	Arg	Arg	Thr	Leu	Met	Ala	Thr	Thr	Trp					

225

230

235

<210> 965  
 <211> 336  
 <212> DNA  
 <213> Homo sapiens

<400> 965  
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 cgggtcagcg atgccgaaaa ggctgaaatc ctcggccgcg ccgatgtgta tgcgcccc  
 120  
 aataccggcg gtgagagctt tggcattgtc ttggtggaag ccatggcggc aggcgcagcc  
 180  
 gttgttgctt cagacttga ggcttccgc gcagtgtgca acgccgattc cgatgatgtt  
 240  
 gccggcgcgc tatatcgcaa tgaggatagt aatgacctg ctcgtgtact caacgaggtg  
 300  
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 336

<210> 966  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

<400> 966  
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 Asp Phe Val Gly Arg Val Ser Asp Ala Glu Lys Ala Glu Ile Leu Gly  
 20 25 30  
 Arg Ala Asp Val Tyr Val Ala Pro Asn Thr Gly Gly Glu Ser Phe Gly  
 35 40 45  
 Ile Val Leu Val Glu Ala Met Ala Ala Gly Ala Val Val Ala Ser  
 50 55 60  
 Asp Leu Glu Ala Phe Arg Ala Val Cys Asn Ala Asp Ser Asp Asp Val  
 65 70 75 80  
 Ala Gly Ala Leu Tyr Arg Asn Glu Asp Ser Asn Asp Leu Ala Arg Val  
 85 90 95  
 Leu Asn Glu Val Leu Glu Asp Pro Glu Tyr Arg Ala Arg Leu Val His  
 100 105 110

<210> 967  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<400> 967  
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 ggcgccgagg cgctgggctc aagctccgct tcggcaccgg tcggcactga ggaatctccg  
 120  
 tcggcctccg cttcgccgc agcctgggct gcgccagact ctgcccggagg caccttctcc  
 180

cggggttcgcc agccaaatgg cgttgcaggc tccagcatcc agtccggtgc ctccggcacc  
 240  
 cccgcactgc gcagagaggc cgccagaaac gatggcaccg gcggcgcggg aggtgataca  
 300  
 ggcgcttcgg ccggagcgct cacggactcc ggcactacag gtgcagcttg cgcttcctgc  
 360  
 ggccggagcaa cagggtcact tcgaggcggg gat  
 393

<210> 968  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 968  
 Pro Ala Arg Ser Asp Thr Glu Leu Val Val Ser Thr Asp Ser Gly Ala  
 1 5 10 15  
 Glu Ala Ser Gly Ser Ser Ser Ala Ser Ala Pro Val Gly Thr Glu Glu  
 20 25 30  
 Ser Pro Ser Ala Ser Ala Ser Ala Ala Trp Ala Ala Pro Asp Ser  
 35 40 45  
 Ala Gly Gly Thr Phe Ser Arg Val Arg Gln Pro Asn Gly Val Ala Gly  
 50 55 60  
 Ser Ser Ile Gln Ser Gly Ala Phe Gly Thr Pro Ala Leu Arg Arg Glu  
 65 70 75 80  
 Ala Ala Arg Asn Asp Gly Thr Gly Gly Ala Gly Gly Asp Thr Gly Ala  
 85 90 95  
 Ser Ala Gly Ala Leu Thr Asp Ser Gly Thr Thr Gly Ala Ala Cys Ala  
 100 105 110  
 Ser Cys Gly Gly Ala Thr Gly Ser Leu Arg Gly Gly Asp  
 115 120 125

<210> 969  
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 <212> DNA  
 <213> Homo sapiens

<400> 969  
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 120  
 atgaattttc gagtaaaactt acatagaatg cctatgagac acaggaagaa ggcagcagac  
 180  
 aagaatctta ccctgccgtc tttagtatgt gaagtactgg acctgatggg agagtttatt  
 240  
 gtaacacaca tgatgaagga gtttcctatg gatctctata tacgctgcat ccaggtagta  
 300  
 cacaaactgc tctgctacca gaagaagtgt cgggtacgcc tgcattacac ctggcgaggag  
 360  
 ctctgggtcag ccttgataaa tttgctgaag ttccttatgt caaatgagac tgtacttttg  
 420  
 gccaaacaca acatttttac attagccctt atgattgtga acctatttaa tatgtttatc  
 480

acatatggcg acacatttct gccaaccccc agcagctatg atgaacttta ctatgagatt  
 540  
 atccgcatgc accagagctt tgacaacctc tactccatgg tcttgaggct ttctaccaat  
 600  
 gcaggccagt ggaaggaagc agctagcaag gtgacccatg cattgggttaa tatcagagcc  
 660  
 atcatcaacc actttaaccc caaaattgag tcctacgctg ctgtgaatca catatcccaa  
 720  
 ctgtcagagg agcaggtgct ggaggtggtg agagccaact atgacacgct cacgctgaag  
 780  
 ctgcaggatg gcctggacca gtatgagcgc tactcagagc agcacaagga agctgccttc  
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 880

<210> 970

<211> 263

<212> PRT

<213> Homo sapiens

<400> 970

Met	Thr	Met	His	Phe	Cys	Met	Met	Ile	Asn	Met	Asn	Phe	Arg	Val	Asn
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Leu	His	Arg	Met	Pro	Met	Arg	His	Arg	Lys	Lys	Ala	Ala	Asp	Lys	Asn
			20					25					30		
Leu	Thr	Leu	Pro	Ser	Leu	Val	Cys	Glu	Val	Leu	Asp	Leu	Met	Val	Glu
			35				40					45			
Phe	Ile	Val	Thr	His	Met	Met	Lys	Glu	Phe	Pro	Met	Asp	Leu	Tyr	Ile
	50					55					60				
Arg	Cys	Ile	Gln	Val	Val	His	Lys	Leu	Leu	Cys	Tyr	Gln	Lys	Lys	Cys
65					70					75				80	
Arg	Val	Arg	Leu	His	Tyr	Thr	Trp	Arg	Glu	Leu	Trp	Ser	Ala	Leu	Ile
			85						90				95		
Asn	Leu	Leu	Lys	Phe	Leu	Met	Ser	Asn	Glu	Thr	Val	Leu	Leu	Ala	Lys
			100					105					110		
His	Asn	Ile	Phe	Thr	Leu	Ala	Leu	Met	Ile	Val	Asn	Leu	Phe	Asn	Met
	115						120					125			
Phe	Ile	Thr	Tyr	Gly	Asp	Thr	Phe	Leu	Pro	Thr	Pro	Ser	Ser	Tyr	Asp
	130					135					140				
Glu	Leu	Tyr	Tyr	Glu	Ile	Ile	Arg	Met	His	Gln	Ser	Phe	Asp	Asn	Leu
145					150					155				160	
Tyr	Ser	Met	Val	Leu	Arg	Leu	Ser	Thr	Asn	Ala	Gly	Gln	Trp	Lys	Glu
			165						170					175	
Ala	Ala	Ser	Lys	Val	Thr	His	Ala	Leu	Val	Asn	Ile	Arg	Ala	Ile	Ile
			180					185					190		
Asn	His	Phe	Asn	Pro	Lys	Ile	Glu	Ser	Tyr	Ala	Ala	Val	Asn	His	Ile
	195					200						205			
Ser	Gln	Leu	Ser	Glu	Glu	Gln	Val	Leu	Glu	Val	Val	Arg	Ala	Asn	Tyr
	210					215					220				
Asp	Thr	Leu	Thr	Leu	Lys	Leu	Gln	Asp	Gly	Leu	Asp	Gln	Tyr	Glu	Arg
225					230					235				240	
Tyr	Ser	Glu	Gln	His	Lys	Glu	Ala	Ala	Phe	Phe	Lys	Glu	Leu	Val	Arg
			245					250					255		
Ser	Ile	Ser	Thr	Asn	Val	Arg									

260

<210> 971  
 <211> 337  
 <212> DNA  
 <213> Homo sapiens

<400> 971  
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 120  
 aatcccaacc ccaaatacct ggttgtaac ggagacgaat ccgaacccgg cacgtgcaag  
 180  
 gacatgccgc tcattatggc aagcccgac acgcttgctg aaggtgctct tatctccgc  
 240  
 tacgctttcg gatccgagca ggctttcatc tacctccgtg gagaagttgt tcaggtagcc  
 300  
 cggcgccttg aagaaaaaaa aaaaatgcga nnnnnnn  
 337

<210> 972  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

<400> 972  
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 Asp Ser Gly Leu Arg Gly Arg Gly Gly Ala Gly Phe Pro Thr Gly Val  
 20 25 30  
 Lys Trp Ser Phe Val Pro Gln Asn Asn Pro Asn Pro Lys Tyr Leu Val  
 35 40 45  
 Val Asn Gly Asp Glu Ser Glu Pro Gly Thr Cys Lys Asp Met Pro Leu  
 50 55 60  
 Ile Met Ala Ser Pro His Thr Leu Val Glu Gly Ala Leu Ile Ser Arg  
 65 70 75 80  
 Tyr Ala Phe Gly Ser Glu Gln Ala Phe Ile Tyr Leu Arg Gly Glu Val  
 85 90 95  
 Val Gln Val Ala Arg Arg Leu Glu Glu Lys Lys Lys Met Arg Xaa Xaa  
 100 105 110

<210> 973  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 973  
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 120  
 ccgggacctt ctgtataggc atcacttagg aaccagtcag accatcagat tctcaggacc  
 180



cactggatca actgagtcag gaactcaggg ttttcaacac atcctccggg gggattccag  
 240  
 tggctgtgta actttgagga ccactggcaa agtggctctg gggtcagaga tccgagttca  
 300  
 tattctgggt ctgcctctga ctgactgcaa cgggtgggcaa gtcacttgcc gtgcccagcc  
 360

<210> 974

<211> 91

<212> PRT

<213> Homo sapiens

<400> 974

Met	Ala	Trp	Ser	Cys	Cys	Met	Val	Leu	Ser	Gly	Val	Arg	Asp	Leu	Leu
1				5					10				15		
Tyr	Arg	His	His	Leu	Gly	Thr	Ser	Gln	Thr	Ile	Arg	Phe	Ser	Gly	Pro
			20					25				30			
Thr	Gly	Ser	Thr	Glu	Ser	Gly	Thr	Gln	Gly	Phe	Gln	His	Ile	Leu	Arg
		35				40				45					
Gly	Asp	Ser	Ser	Gly	Cys	Val	Thr	Leu	Arg	Thr	Thr	Gly	Lys	Val	Ala
	50					55				60					
Leu	Gly	Ser	Glu	Ile	Arg	Val	His	Ile	Leu	Gly	Leu	Pro	Leu	Thr	Asp
65					70				75					80	
Cys	Asn	Gly	Gly	Gln	Val	Thr	Cys	Arg	Ala	Gln					
				85					90						

<210> 975

<211> 2604

<212> DNA

<213> Homo sapiens

<400> 975

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 120  
 ccttgataa gtggtttctg attttgagag gacagcagag ggctgtatca cacaagacat  
 180  
 ttggcattag cctggaagag gtcctggtga acgagtttac ccgccgcaag catcttgaac  
 240  
 tgaccagcca cgatgcaggt tgaagaagcc accggtcagg ctgcgggccg tcgtcgggga  
 300  
 aacgtggtgc gaaggggtgt tggccgcac cggcgctttt tcagtcgcag gcggaatgag  
 360  
 cccaccttgc cccgggagtt cactcgccgt gggcgctcag gtgcagtgtc tgtggatagt  
 420  
 ctggctgagc tggaagacgg agccctgctg ctgcagaccc tgcagctttc aaaaatttcc  
 480  
 tttccaattg gccaacgact tctgggatcc aaaaggaaga tgagtctcaa tccgattgag  
 540  
 aaacaaatcc cccaggttgt tgaggcttgc tgccaattca ttgaaaaaca tggcttaagc  
 600  
 gcagtgggga tttttaccct tgaatactcc gtgcagcgag tgcgtcagct ccgtgaagaa  
 660

tttgcataag gtctggatgt agtgctggat gacaatcaga atgtgcatga tgtggctgca  
720  
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aaaatcactg agaactgcga ggactcaatt ggcattgatg gacagttggt cccaggcaac  
960  
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1020  
tttggcaaga gagagtccag gaaaacaaag ctggggattg atcactatgt tgcttctgtc  
1080  
aatgtggtcc gtgccatgat tgataactgg gatgtcctct tccaggtgcc tccccatatt  
1140  
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1200  
cgcaggaact tgagggaagat ccagagtga cgcataaaga tggaagagga tgcactactt  
1260  
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1320  
tctgatgaag gttcctctga ggagccagct gtgccttccg gcactgcccg tccccatgac  
1380  
gatgaggaag gagcgggtaa ccctcccatt ccggagcaag accgcccatt gctccgtgtg  
1440  
ccccgggaga aggaggccaa aactggcgtc agctacttct ttccttagat gtttttcctt  
1500  
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1560  
taaggagaga gttgaaggta aagatctgaa ggtaagaagg agttccacct gatgctcggg  
1620  
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1680  
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1740  
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ccccaaatgg gattgcatga tttccctgac tttctaccc tcctccagag agctcagttg  
1920  
gaaaggccct caagaggcat gctagaacgt taggtcagcc tactgacagc tgacaaacaa  
1980  
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2040  
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2100  
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2160  
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2220  
acaattggtg tttacacct cttgtcagca aaacagctag ttaggtaagg acatatagtt  
2280

ccaagtaggt aaagtcactt gattacaaat gttcttaact atcgtctctg taattccttt  
 2340  
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 2460  
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 2580  
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 2604

<210> 976

<211> 411

<212> PRT

<213> Homo sapiens

<400> 976

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			20				25					30		Arg
Arg	Arg	Asn	Glu	Pro	Thr	Leu	Pro	Arg	Glu	Phe	Thr	Arg	Arg	Gly
		35				40					45			Arg
Arg	Gly	Ala	Val	Ser	Val	Asp	Ser	Leu	Ala	Glu	Leu	Glu	Asp	Gly
	50					55				60				Ala
Leu	Leu	Leu	Gln	Thr	Leu	Gln	Leu	Ser	Lys	Ile	Ser	Phe	Pro	Ile
65					70				75				80	Gly
Gln	Arg	Leu	Leu	Gly	Ser	Lys	Arg	Lys	Met	Ser	Leu	Asn	Pro	Ile
			85					90				95		Ala
Lys	Gln	Ile	Pro	Gln	Val	Val	Glu	Ala	Cys	Cys	Gln	Phe	Ile	Glu
			100					105				110		Lys
His	Gly	Leu	Ser	Ala	Val	Gly	Ile	Phe	Thr	Leu	Glu	Tyr	Ser	Val
	115					120				125				Gln
Arg	Val	Arg	Gln	Leu	Arg	Glu	Phe	Asp	Gln	Gly	Leu	Asp	Val	Val
	130				135				140					
Leu	Asp	Asp	Asn	Gln	Asn	Val	His	Asp	Val	Ala	Ala	Leu	Leu	Lys
145					150				155				160	Glu
Phe	Phe	Arg	Asp	Met	Lys	Asp	Ser	Leu	Leu	Pro	Asp	Asp	Leu	Tyr
			165					170				175		Met
Ser	Phe	Leu	Leu	Thr	Ala	Thr	Leu	Lys	Pro	Gln	Asp	Gln	Leu	Ser
			180				185					190		Ala
Leu	Gln	Leu	Leu	Val	Tyr	Leu	Thr	Pro	Pro	Cys	His	Ser	Asp	Thr
	195					200					205			Leu
Glu	Arg	Leu	Leu	Lys	Ala	Leu	His	Lys	Ile	Thr	Glu	Asn	Cys	Glu
	210					215					220			Asp
Ser	Ile	Gly	Ile	Asp	Gly	Gln	Leu	Val	Pro	Gly	Asn	Arg	Met	Thr
225					230				235				240	Ser
Thr	Asn	Leu	Ala	Leu	Val	Phe	Gly	Ser	Ala	Leu	Leu	Lys	Lys	Gly
			245					250					255	Lys
Phe	Gly	Lys	Arg	Glu	Ser	Arg	Lys	Thr	Lys	Leu	Gly	Ile	Asp	His
			260				265					270		Tyr
Val	Ala	Ser	Val	Asn	Val	Val	Arg	Ala	Met	Ile	Asp	Asn	Trp	Asp
														Val

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      275              280              285
Leu Phe Gln Val Pro Pro His Ile Gln Arg Gln Val Ala Lys Arg Val
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Trp Lys Ser Ser Pro Glu Ala Leu Asp Phe Ile Arg Arg Arg Asn Leu
305              310              315              320
Arg Lys Ile Gln Ser Ala Arg Ile Lys Met Glu Glu Asp Ala Leu Leu
      325              330              335
Ser Asp Pro Val Glu Thr Ser Ala Glu Ala Arg Ala Ala Val Leu Ala
      340              345              350
Gln Ser Lys Pro Ser Asp Glu Gly Ser Ser Glu Glu Pro Ala Val Pro
      355              360              365
Ser Gly Thr Ala Arg Ser His Asp Asp Glu Glu Gly Ala Gly Asn Pro
      370              375              380
Pro Ile Pro Glu Gln Asp Arg Pro Leu Leu Arg Val Pro Arg Glu Lys
385              390              395              400
Glu Ala Lys Thr Gly Val Ser Tyr Phe Phe Pro
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<210> 977  
 <211> 378  
 <212> DNA  
 <213> Homo sapiens

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<400> 977
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gagggcaacc ttaactatgg aggagtttgc ctggcgtcgg acgcccagtt cagtgaacttc
180
ctgggaagca tggggccggc acagtttgtg ggccgccaga ccctggccac cacacccatg
240
ggggatgtgg agatcggtct gcaggagcgg aacggtcagt tggaggtgga cattatccag
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gctcggggac tgacagccaa gccaggctcc aagacactgc cagcggccta catcaaggcc
360
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378

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<210> 978  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

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<400> 978
Arg Val Lys Gly Ala Ile Gln Arg Ser Thr Glu Thr Gly Leu Ala Val
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Glu Met Pro Ser Arg Thr Leu Arg Gln Ala Ser His Glu Ser Ile Glu
      20              25              30
Asp Ser Met Asn Ser Tyr Gly Ser Glu Gly Asn Leu Asn Tyr Gly Gly
      35              40              45
Val Cys Leu Ala Ser Asp Ala Gln Phe Ser Asp Phe Leu Gly Ser Met
      50              55              60
Gly Pro Ala Gln Phe Val Gly Arg Gln Thr Leu Ala Thr Thr Pro Met

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65		70		75		80									
Gly	Asp	Val	Glu	Ile	Gly	Leu	Gln	Glu	Arg	Asn	Gly	Gln	Leu	Glu	Val
				85					90					95	
Asp	Ile	Ile	Gln	Ala	Arg	Gly	Leu	Thr	Ala	Lys	Pro	Gly	Ser	Lys	Thr
			100					105					110		
Leu	Pro	Ala	Ala	Tyr	Ile	Lys	Ala	Tyr	Leu	Leu	Glu	Met	Ala		
		115					120					125			

&lt;210&gt; 979

&lt;211&gt; 3500

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 979

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nntttttttt ttccagggga aaatgcttta ttgagtaaag tatccgagga agtgatgcag
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ggcaggtaaa cagctggtgc tcagcagcga gaggacgcgt cactctgccg ttctgcaggg
120
tgacgccctc cccgtacctc gctgagagcc acctgcagac acagcaggcc acagcagaat
180
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540
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780
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&lt;211&gt; 73

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 980

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65					70										

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&lt;211&gt; 404

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 981

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 35 40 45  
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 Leu Phe Phe Ser Leu Pro Glu Thr Pro Phe Leu Leu Asn Asn Leu Met  
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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 987

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